

GenCore version 5.1.6
Copyright (C) 1993 - 2003 Computer Ltd.

ON protein - nucleic search, using frame_plus_p2n model
Run on: August 11, 2003, 08:36:05 : Search time 610.591 Seconds
756,292 Million cell updates/sec

Title: US-10-000-039a-3
Perfect score: 103
Sequence: 1 DEPTFEETVFNISPOSS 19
Scoring table: BLOSUM62
Gapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-O/cspn2_1/usfpo.spool/us10000039/runat_01082003.085419.27521/app_query.fasta_1.661
-DB-EST -QWTF-FASTP -SUPERF-EST -MINMATCH-0.1 -LOOPEXT-0
-MAXLEN-2000000000 -STRAP-SCORES-0 -STRAP-LOCAL-LOCAL-500
-OUTFN-PLC -NORH-ext -HEAPSLE-500 -MINLEN-0 -MAXLEN-2000000000
-USER-us10000039.qcgl_1.1.6633 -runat_01082003.085419.27521 -NCFU-6 -ICPU-3
-NO-MAP -LARGESQUERY -NEG-SCORES-0 -WAIT -DSPBLOC-100 -LONGLOC
-ICPU-3 -ICPU-3 -ICPU-3 -ICPU-3 -ICPU-3 -ICPU-3 -ICPU-3 -ICPU-3
-FGAPEXT-7 -FGAPOP-10 -YGAPEXT-0.5 -DELOP-6 -DELEXT-7 -FGAPOP-6

Database :

1: EST*

2: em.estbta.*

3: em.estbun.*

4: em.estbun.*

5: em.estbun.*

6: em.estbun.*

7: em.estbun.*

8: em.estbun.*

9: em.estbun.*

10: em.estbun.*

11: em.estbun.*

12: em.estbun.*

13: em.estbun.*

14: em.estbun.*

15: em.estbun.*

16: em.estbun.*

17: em.gss.hum.*

18: em.gss.hum.*

19: em.gss.hum.*

20: em.gss.vrt.*

21: em.gss.fun.*

22: em.gss.fun.*

23: em.gss.fun.*

24: em.gss.fun.*

25: em.gss.fun.*

26: em.gss.fun.*

27: em.gss.fun.*

28: em.gss.fun.*

29: gb.gss2.*

Pred: No. is the number of results predicted by chance to have a
score at least as high as the observed score, assuming flatness,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	103	100	0	AA34258	EST50139
2	103	100	0	34	AA34258
3	103	100	0	34	AA34258
4	103	100	0	34	AA34258
5	103	100	0	34	AA34258
6	103	100	0	34	AA34258
7	103	100	0	34	AA34258
8	103	100	0	34	AA34258
9	103	100	0	34	AA34258
10	103	100	0	34	AA34258
11	103	100	0	34	AA34258
12	103	100	0	34	AA34258
13	103	100	0	34	AA34258
14	103	100	0	34	AA34258
15	103	100	0	34	AA34258
16	103	100	0	34	AA34258
17	103	100	0	34	AA34258
18	103	100	0	34	AA34258
19	103	100	0	34	AA34258
20	103	100	0	34	AA34258
21	103	100	0	34	AA34258
22	103	100	0	34	AA34258
23	103	100	0	34	AA34258
24	103	100	0	34	AA34258
25	103	100	0	34	AA34258
26	103	100	0	34	AA34258
27	103	100	0	34	AA34258
28	103	100	0	34	AA34258
29	103	100	0	34	AA34258
30	103	100	0	34	AA34258
31	103	100	0	34	AA34258
32	103	100	0	34	AA34258
33	103	100	0	34	AA34258
34	103	100	0	34	AA34258
35	103	100	0	34	AA34258
36	103	100	0	34	AA34258
37	103	100	0	34	AA34258
38	103	100	0	34	AA34258
39	103	100	0	34	AA34258
40	103	100	0	34	AA34258
41	103	100	0	34	AA34258
42	103	100	0	34	AA34258
43	103	100	0	34	AA34258
44	103	100	0	34	AA34258
45	103	100	0	34	AA34258

ALIGNMENTS

RESULT 1
AA34258

LOCUS

DEFINITION

AA34258 Gall bladder 1 Homo sapiens cDNA 5' end similar to similar

AA34258 Cholinergic kinase, mRNA sequence.

AA34258.1 GI:1996494

VERSION

EST.

WORDS

ORGANISM

Homo sapiens (human)

Chloridia: Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Carnivora; Hominoidea; Homo.

REFERENCE

1 (bases 1 to 259)


```

/organism="Homo sapiens"
/mol_type="mRNA"
/mol_size="1504"
/sex="F"
/sisus="SISUS-18-204"
/issue_type="Ascites"
/cell_type="Embryoblast-like"
/lab="LabHost"
/lab_host="Top10p"
/clone_lib="SISUS"
/notes="Organ: Stomach; Vector: pCNS; Site_1: EcoRI;
Site_2: HindIII; Site_3: HindIII. The cDNA was prepared with
bacterial alkaline phosphatase (BAP) and ligated into the
intact mRNA was ligated with DNA-RNA linker including EcoR
priming with 5' RNA ligase and the first strand
cDNA synthesis. The second strand was synthesized by
priming with 5' RNA ligase. The cDNA vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
the cDNA vector with EcoRI. The cDNA vector was
competent cells E. coli Top10p by electroporation method.
The cDNA library was constructed by this method are
full-length enriched cDNA library."
BASE COUNT      125 a 140 c 120 g 145 t
ORIGIN

```

```

Alignment Scores:
  Presl. No.:      1.29e-05      Length:      530
  Score:          103.00      Matches:      19
  Identical:      100.00%      Conservative: 0
  Positives:      100.00%      Gaps:        0
  Query Match:    100.00%      Indels:       0
  DB:             12          Gaps:        0

US-10-000-039a-3 (1-19) x BW756001 (1-530)
OY      1 Asproctuphertrugluiprowalproanseriledyllysserproaspsr 19
DB      200 GRACCCGAGTTCACCGAGAGGCTGTCTCCCACTTCATGGCAATGTCCCTGCACGC 256

```

Search completed: August 11, 2003, 11:27:47
 Job time : 614.591 secs

[illegible]

Richards J.S., Fitzpatrick S.L., Clemens J.W., Morris J.K.,
Allison T., Sirols J.;
Ovarian cell differentiation: a cascade of multiple hormones,
Recent Prog. Horm. Res. 50:223-254(1995).
[4]
INDUCTION BY P53
[4]
MEDLINE-96218163; PUBMED-8647846;
Malvar A.C., Huang A.J., Phu P.T., Cha H.H., Firestone G.L.;
"p53 stimulates promoter activity of the sgf."
Serum/glucocorticoid-inducible cells and the threonine protein kinase gene
J. Biol. Chem. 271:12414-12422(1996).
[5]
PHOSPHORYLATION ON THR-256 BY PDKP1.
Park J., Leong M.L., Buse P., Malvar A.C., Firestone G.L.,
Hemmings B.A.;
Serum and glucocorticoid-inducible kinase (SGK) is a target of the p1
ENK1 J. 18:1024-1033(1999).
-1- FUNCTION: Protein kinase that plays an important role in
activating certain potassium, sodium, and chloride channels,
regulating their regulation of ion transport processes such as
cell survival, neuronal excitability and cellular stress response (By
similarity). May also play an important role in the development of
catalytic activity after birth in the postnatal brain.
-1- SUBCELLULAR LOCATION: Cytoplasmic and nuclear, upon
phosphorylation (By similarity).
-1- TISSUE SPECIFICITY: Expressed in most tissues with highest levels
in brain and testis.
-1- INDUCTION: By dexamethasone and serum. By tumor suppressor p53 in
mammary epithelial tumor cells. By FSH in granulosa cells. By
injury to the central nervous system.
-1- FUNCTION: Belongs to the AGC FAMILY OF PROTEIN KINASES.
This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation
the European Bioinformatics Institute. There are no restrictions on its
use. The entry is made available under the terms of the EMBL/EBI
modified and this statement is not removed. Usage by for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/commence/>
or send an email to license@isb-sib.ch).
EMBL: L01624; AAA42137.1; .
HSP: P00517; YDR.
Interpro: IPR000961; PKinase_C.
Protein family (PF000433): Serine/threonine protein kinase.
Pfam: PF000433; pkInase_C.1.
SMART: SM00133; S_TKc_kinase.1.
SMART: SM00220; S_TKc.1.
PROSITE: PS001207; S_TKc.1.
PROSITE: PS001207; PROTEIN_KINASE_ATP.1.
PROSITE: PS001207; PROTEIN_KINASE_S7.1.
PROSITE: PS001207; PROTEIN_KINASE_S7.1.
APOLLOSIS: Transferase: Serine/threonine-protein kinase: ATP-binding;
phosphorylation.
DOMAIN 98 354 PROTEIN KINASE.
BINDING 127 127 ATP (By similarity).
ACT_SITE 127 127 ATP (By similarity).
FT FT ACT_SITE 222 222 ATP (By similarity).
FT FT MOD_RES 256 256 PHOSPHORYLATION (By PDKP1).
FT SQ MOD_RES 430 430 489?M; 005845801166726D CRC64;
Query Match 97.1%; Score 2204.5; DB 1: Length 430;
Best Local Similarity 96.8%; Score No. 2.3e152;
Matches 417; Conservative 8; Mismatches 5; Indels 1; Gaps 1;

OY 1 MYTKEAKGTLTYSMHHGKVVALLAPMKHRRNGLNDIFQK TANNSSVWHPKPVSLIKI 60
DB 1 MYTKEAKGTLTYSMHHGKVVALLAPMKHRRNGLNDIFQK TANNSSVWHPKPVSLIKI 60
OY 61 SPOPELWNPANPPSPSPQINLSPNSHPKYSDFPKVLIGKSGSKVLAHAKAE 140
DB 61 SPOPELWNPANPPSPSPQINLSPNSHPKYSDFPKVLIGKSGSKVLAHAKAE 140
OY 121 EYVYAPVYLOKATLAKKEPEKINSKSVLWKKVHPFLVGLJESVOTAKIKLYVLYIN 180
DB 121 EYVYAPVYLOKATLAKKEPEKINSKSVLWKKVHPFLVGLJESVOTAKIKLYVLYIN 180
OY 121 ENFYAVKVLQKATLAKKEPEKINSKSVLWKKVHPFLVGLJESVOTAKIKLYVLYIN 240
DB 121 ENFYAVKVLQKATLAKKEPEKINSKSVLWKKVHPFLVGLJESVOTAKIKLYVLYIN 240
OY 181 GSELYEHLQRECELEPPRAEYAEIASALCYLINSVTVEDVFNHLLNSCHLVLD 240
DB 181 GSELYEHLQRECELEPPRAEYAEIASALCYLINSVTVEDVFNHLLNSCHLVLD 240
OY 181 GSELYEHLQRECELEPPRAEYAEIASALCYLINSVTVEDVFNHLLNSCHLVLD 240
DB 181 GSELYEHLQRECELEPPRAEYAEIASALCYLINSVTVEDVFNHLLNSCHLVLD 240
OY 241 FOLCKVGLSEVATSGVSTVATKAVKLVKPKVGLVGLVGLVGLVGLVGLVGLV 400
DB 241 FOLCKVGLSEVATSGVSTVATKAVKLVKPKVGLVGLVGLVGLVGLVGLVGLV 400
OY 241 FOLCKVGLSEVATSGVSTVATKAVKLVKPKVGLVGLVGLVGLVGLVGLVGLV 400
DB 241 FOLCKVGLSEVATSGVSTVATKAVKLVKPKVGLVGLVGLVGLVGLVGLVGLV 400
OY 301 WTAVNTDINLKPFOIKVPIINSAHHLIGLQKUPKPKLQKADPKIKSNVPTSLIN 600
DB 301 WTAVNTDINLKPFOIKVPIINSAHHLIGLQKUPKPKLQKADPKIKSNVPTSLIN 600
OY 361 DOLINKMTTPPNVNSVPELHFDVPTTEPPVNSIGKSPDSVLTASVKAANALIG 420
DB 361 DOLINKMTTPPNVNSVPELHFDVPTTEPPVNSIGKSPDSVLTASVKAANALIG 420
OY 360 DOLINKMTTPPNVNSVPELHFDVPTTEPPVNSIGKSPDSVLTASVKAANALIG 419
DB 360 DOLINKMTTPPNVNSVPELHFDVPTTEPPVNSIGKSPDSVLTASVKAANALIG 419
OY 421 FSTAPPTDPSFL 431
DB 421 FSTAPPTDPSFL 431
OY 420 FSTAPPTDPSFL 430
DB 420 FSTAPPTDPSFL 430
AC OPERED:
ID SGK3 MOUSE STANDARD: PRT: 496 AA.
DT 28-FEB-2003 (Rel. 41, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DE Serine/threonine-protein kinase Sak3 (KC 2.7.1.37)
DE (Serine/glucocorticoid regulated kinase 3) (serum/glucocorticoid
regulated kinase like) (Cytokine independent survival kinase).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]-txid10-10090,
RN [1]-txid10-10090,
RP SEQUENCE FROM N.A. (ISUPFORM 1), AND MUTAGENESIS OF LYS-191.
RX MEDLINE-20504817; PUBMED-11050496;
RX MEDLINE-22354683; PubMed-12468851;
RT "Identification of Cdk5 as a member of the SGK kinase family that
promotes IL-3-dependent survival."
RL Curr. Biol. 10:1233-1236(2000).
RN STRAIN=57BL/6J; TISSUE=ovary, Ovary, and Uterus;
RX MEDLINE-22354683; PubMed-12468851;
RX Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono B., Kondo S.,
Yagi K., Tomaru Y., M. Saito T., Shinkai H., Yamazaki T., Yoshida H.,
RA Baladrelli R., Hill D.P., Buit C., Rume D.A., Quackenbush J.,
RA Schriber L.M., Kanapin A., Matsuda H., Batelov S., Beisel K.W.,
RA Drake J.A., Bradt D., Brusci V., Chethio C., Corbani L.E., Cousins S.,
RA Gaasterland T., Gariboldi M., Gissi C., Goddard A., Gough J.,
RA Grimonard S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kdzierski R.N., Lyons P.A.,
RA Mott G.D., Nishikawa T., Nishikawa T., Nishikawa T., Nishikawa T.,
RA Nagashima T., Numaoka K., Okido T., Pavan W.J., Pearce G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,

[illegible][illegible]

[illegible]

CC	QY	28	MCORGLNDQFQK	-----TANNYSCKHPE-----	-----VQSLKLSQPEELMANHP	73
CC	DB	84	MYEPFPRFIFLQGLVYIFVETPRFENKATQVADGLNGDEETPFS	143	-----	-----
CC	QY	74	SPSPSS	-----QQINLQSPNHP-----	-----SDFEFKLVGSGKGVLLARHAEWF	123
CC	DB	144	QSPDSQAGDEMSVL	-----AKPIRYNKEPEFILLQKQITGVLLMEKATGRF	196	-----
CC	QY	124	YAVYVQKALKLKEEKHSINERNYKLVKHFVGLGAFSTAKYLPVLYDINGE	183	-----	-----
CC	DB	197	TAKLLEMYVAVDVAHTEITL	-----NVKYNRHFPLTALATSTFQTHNCLCYVMEANGE	255	-----
CC	QY	184	LFYHLOERCTEFLPARYATAENAGTCLHS	-----LVTVYDLKPNILDSGSHVLDG	242	-----
CC	DB	256	LFYHLSHREEDMARTQVETVNSDGLKRVYVMDVGLVMDVYKIDYFG	315	-----	-----
CC	QY	243	LCENIEHNHSTSTFGCPYLPVLPYKQYDQVDMCLGAVLYEMVGLPPYFSRNT	302	-----	-----
CC	DB	316	LOEGLQKQNTKQCPPELVNLEVDQNTQVDMGLGAVVTRKMGCLPFIIDH	375	-----	-----
CC	QY	303	AMHYNTLNFQLKPNITNSHRLKELGOKFTELK	-----GAKDQFNKSHVFEFLNWD	361	-----
CC	DB	376	KNFUELLHMEFPRFLOENSLKSLQGLQKQNGSDENKZLMQHFANLWQ	435	-----	-----
CC	QY	362	DLNKLKTFPFPNENLHRDDEFEPEVNSKGFQSVLYTAKVEAAEALFG	421	-----	-----
CC	DB	436	DYERKLSYFAPQVSTQZTFDDEFTQNTTFFPDQDQSHSCVVS	-----ERRPHFQF	493	-----
CC	QY	422	SYA	424	-----	-----
CC	DB	494	SYA	496	-----	-----
RESULT 14						
CC	ID	KRAC_MOUSE	STANDARD:	PRT:	480 AA.	
CC	DT	P31750; Q62774;				
CC	DT	01-JUL-1993 (Ref. 26, Created)				
CC	DT	01-JUL-1993 (Ref. 26, Created)				
CC	DT	28-FEB-2003 (Ref. 41, Last annotation update)				
CC	DE	RAC-alpha serine/threonine kinase (EC 2.7.1.1) (RAC-PK-alpha) (AKT1 kinase) (Protein kinase B) (PKB) (C-AKT) (Thymoma viral proto-oncogene) AKT OR BCR.				
CC	OS	Mus musculus (Mouse).				
CC	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E				

GenCode version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OH protein - protein search, using sw model

Run on: August 11, 2003, 08:05:45 ; Search time 57.3433 seconds
(without alignments)
722,816 Million cell updates/sec

Title: US-10-000-039a-2

Perfect score: 2270

Sequence: 1 MYKTEAKTLYTSKHKH.....KEARAEFLGHSYAPPTDSEFL 431

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 283308 seqs, 9616862 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

PR:76:*

1: PID1:*

2: PID2:*

3: PID3:*

4: PID4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2222	97.9	431	2 A48094	serum and glucocorticoid-regulated kinase - rat
2	1072	47.2	422	2 Z63334	hypothetical prote
3	905	39.9	462	2 Z12877	protein kinase (EC
4	905	39.9	454	1 JC4345	protein kinase (EC
5	890	39.2	611	1 A55889	protein kinase (EC
6	885	38.1	763	1 A40831	gas-akt polyprotein
7	863	38.0	480	1 JC2437	protein kinase (EC
8	860.5	37.9	479	2 A38578	protein kinase 2
9	859	37.8	481	1 A42888	protein kinase (EC
10	847	37.3	480	1 A42888	protein kinase (EC
11	838	36.9	481	1 JC2438	protein kinase (EC
12	822.5	36.3	280	2 Z37955	protein kinase (EC
13	816.5	36.1	677	2 Z37955	protein kinase YKR
14	805.5	35.7	546	1 T43223	protein kinase (EC
15	808	35.6	451	1 Z65677	p150 kinase (EC
16	803	35.4	525	1 S12906	probable ribosomal
17	797	35.1	541	1 T43222	protein kinase (EC
18	795	35.0	634	1 B32352	protein kinase C
19	792.5	34.9	616	1 A60729	protein kinase C
20	792.5	34.9	1016	1 A60729	protein kinase C
21	791	34.8	672	1 K1RUC4	protein kinase C
22	791	34.8	672	1 K1RUC4	protein kinase C
23	790	34.8	672	1 K1RUC4	protein kinase C
24	790	34.8	672	1 K1RUC4	protein kinase C

30 788.5 34.7 672 1 K1RUC4
31 780 34.4 547 2 Z62856
32 780 34.4 671 1 K1RUC1
33 779 34.3 707 1 A55350
34 779 34.3 707 1 A55350
35 776 34.2 671 1 K1RUC1
36 775.5 34.2 676 2 A7237
37 775.5 34.2 988 1 S13362
38 775.5 34.2 988 1 S13362
39 773.5 34.1 537 2 A45909
40 772 34.0 696 2 S55694
41 772 34.0 737 1 Z28942
42 768.5 33.9 736 1 K1RUC2
43 768.5 33.9 736 1 K1RUC2
44 767 33.8 528 1 T21523
45 766 33.7 682 1 K1RUC3

ALIGNMENTS

RESULT 1
A48094

serum and glucocorticoid-regulated kinase - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 1993-08-11 Sequence revision 18-Nov-1994 #test_change 19-Dec-1997

C:Accession: A48094

C:Author: M. K. Goya, L. G. Y. Miyai, A. C. Firestone, G. L.

C:Journal: Cell, Biol. 13, 2031-2040, 1993

A:Title: Characterization of a novel member of the serine/threonine protein kinase

A:Note: Sequence extracted from NCBI backbone (NCBI:127618, NCBI:127619)

A:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; Protein kinase hom

F:96-355/pdomain; protein kinase homology <kin>

F:104-112/Region: protein kinase ATP-binding motif

Query Match 97.94; Score 2222; Dm 2; Length 431;

Best Local Similarity 97.04; Prod. No. 2.1e-94;

Matches 8; Mismatches 5; Indels 0; Gaps 0;

QY 1 MYKTEAKTLYTSKHKHALLAKPKQRMGLADFTOKLANNACKUPKQVSLK 60

DB 1 MYKTEAKTLYTSKHKHALLAKPKQRMGLADFTOKLANNACKUPKQVSLK 60

QY 61 SGPQPEFLMANSPSPSPQOINGRSSHPNAPKDPHEFLKVGKSGVLAHRAE 120

DB 61 SGPQPEFLMANSPSPSPQOINGRSSHPNAPKDPHEFLKVGKSGVLAHRAE 120

QY 121 EYFAVYKVKVALLKKEKKEKSHSNVYKLVKQVLPUSQADKLYPVLDVN 180

DB 121 EYFAVYKVKVALLKKEKKEKSHSNVYKLVKQVLPUSQADKLYPVLDVN 180

QY 181 GGEFLTHQREKTEFPAARFYAASATAGTJHSLNIVTRGLKPNILDSQGHVLD 240

DB 181 GGEFLTHQREKTEFPAARFYAASATAGTJHSLNIVTRGLKPNILDSQGHVLD 240

QY 241 FGLCKENHNTSTFCGTPEFLAPRVAKQPTVYKNSGLAVLYKVLKLPFSPR 300

DB 241 FGLCKENHNTSTFCGTPEFLAPRVAKQPTVYKNSGLAVLYKVLKLPFSPR 300

QY 301 NYAEDTMLPLQPKPNTNGSAILHLEGLQKSTRELGAQDPMEIKSHVYFSLNW 360

DB 301 NYAEDTMLPLQPKPNTNGSAILHLEGLQKSTRELGAQDPMEIKSHVYFSLNW 360

QY 361 DDLINKKITPPFNVSQPELHDFRTEEPVPSQSGVSLVTSVAKAAAEFLG 420

DB 361 DDLINKKITPPFNVSQPELHDFRTEEPVPSQSGVSLVTSVAKAAAEFLG 420

QY 361 DDLINKKITPPFNVSQPELHDFRTEEPVPSQSGVSLVTSVAKAAAEFLG 420

DB 361 DDLINKKITPPFNVSQPELHDFRTEEPVPSQSGVSLVTSVAKAAAEFLG 420

A:Residues: 1-462 <P0U>
 A:Cross-references: EMBL:U117525; GI:Q655977; NID:q5912043; PIDN:CA855977.1
 B:Nakatani, K.; Thompson, D.A.; Bartel, A.; Sakano, H.; Liu, W.; Weigel, R.J.; Roth, R.
 J. Biol. Chem. 274, 21528-21532, 1999
 A:Title: Up-regulation of Akt3 in estrogen receptor-deficient breast cancers and androgen
 receptor-deficient prostate cancers
 A:Accession: U041459; PMID:10419436
 A:Comments: This protein is increased in estrogen receptor-negative breast cancers and
 androgen receptor-negative prostate cancers
 A:Gene: GDB:4973
 A:Genes: GDB:4973
 A:Cross-references: GDB:9554867
 A:Map position: 1944-1944
 A:Function:
 A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine
 phosphate
 C:Superfamily: protein kinase act; pleckstrin repeat homology; protein kinase homology
 C:Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein
 kinase
 F:4-105/Domain: pleckstrin repeat homology <PK>
 F:154-162/Region: protein kinase ATP-binding motif
 F:177/Active site: Lys status predicted
 F:177/Active site: Lys status predicted

Query Match
 Best Local Similarity 39.98; Score 905; DB 1; Length 462;
 Matches 185; Conservative 61; Mismatches 115; Indels 28; Gaps 7;

Qy 28 MKORGMGNDFQK-----TANNYSACKHP-----VOSLKTSQPEPELNANP 73
 Db 62 MKTERKPNFTLIRCLQWTVYIERFDVPEREENETALQADRLQREENHNP 121
 Qy 74 SPPTSPSQNLG-----PSSNHAK-----PSDFELKVIKGGSGFKVLARHAKREVAT 126
 Db 122 T-----SQDINGEEDNASTTHIRKKTNDFTVLLQALQDGTGKVLVREKASQNTAM 176
 Qy 127 KYLQKALKLKKKEKHIMERNVLLKYNKHPFLVGLHFSTQADKLVFLVDTNGEELFY 186
 Db 177 KLUKKEVLIADQVATLTESV-LAKTRHPFLSLKTSQPEPELNANP 235
 Qy 187 HQRECRLESPARFATASALGYLSLNTVRLKPNILDSGGHVLTLQGLNKE 246
 Db 236 HLSRNYSDFDRFYGATYLSALGYLSLNTVRLKPNILDSGGHVLTLQGLNKE 245
 Qy 247 NTEHNSTSTFGCTPTLAPVLRHQRDYDMKGLGAVLYGLPPTYSNTAKY 406
 Db 296 GTDQATKCTPTLAPVLRHQRDYDMKGLGAVLYGLPPTYSNTAKY 355
 Qy 307 DNLKLPQKPNLNTSNHLLQDQKTKEL-GANQDPMELKSHVFSLLNMDLNL 365
 Db 356 ELLIMDEKEPFLSSDAKSLGLLQDKNRKLGGDPDPKEIHHNSSFSGVNNQIWD 415
 Qy 366 KKTTPPMNWSGPNELRHDFEETPEV 394
 Db 416 KKLVPFPKPVSTETDTRTFDEETPAQTI 444

RESULT 6
 A:Residues: 1-611 <AND>
 A:Cross-references: GI:M83510
 A:Gene: FlyBase:RacP
 A:Cross-references: FlyBase:Fgn0013324
 A:Start codon: ACG
 A:Title: Developmental regulation of expression and activity of multiple forms of the
 protein kinase (EC 2.7.1.37) akt (similarity) - fruit fly (Drosophila melanogaster)
 C:Species: Drosophila melanogaster
 C:Dates: 10-Sep-1999 sequence revision 10-Sep-1999 text_change 20-Apr-2001
 C:Accession: A55888
 A:Title: Molecular cloning and characterization of a new member of the Rac protein kinase
 family
 A:Accession: J03435
 A:Residues: 1-454 <RNA>
 A:Experimental source: brain

C:Function:
 A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threo-
 phosphate
 C:Superfamily: protein kinase act; pleckstrin repeat homology; protein kinase homology
 C:Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein
 kinase
 F:4-105/Domain: pleckstrin repeat homology <PK>
 F:154-162/Region: protein kinase ATP-binding motif
 F:177/Active site: Lys status predicted

Query Match
 Best Local Similarity 39.98; Score 905; DB 1; Length 454;
 Matches 185; Conservative 61; Mismatches 115; Indels 28; Gaps 7;

Qy 28 MKORGMGNDFQK-----TANNYSACKHP-----VOSLKTSQPEPELNANP 73
 Db 62 MKTERKPNFTLIRCLQWTVYIERFDVPEREENETALQADRLQREENHNP 121
 Qy 74 SPPTSPSQNLG-----PSSNHAK-----PSDFELKVIKGGSGFKVLARHAKREVAT 126
 Db 122 T-----SQDINGEEDNASTTHIRKKTNDFTVLLQALQDGTGKVLVREKASQNTAM 176
 Qy 127 KYLQKALKLKKKEKHIMERNVLLKYNKHPFLVGLHFSTQADKLVFLVDTNGEELFY 186
 Db 177 KLUKKEVLIADQVATLTESV-LAKTRHPFLSLKTSQPEPELNANP 235
 Qy 187 HQRECRLESPARFATASALGYLSLNTVRLKPNILDSGGHVLTLQGLNKE 246
 Db 236 HLSRNYSDFDRFYGATYLSALGYLSLNTVRLKPNILDSGGHVLTLQGLNKE 245
 Qy 247 NTEHNSTSTFGCTPTLAPVLRHQRDYDMKGLGAVLYGLPPTYSNTAKY 406
 Db 296 GTDQATKCTPTLAPVLRHQRDYDMKGLGAVLYGLPPTYSNTAKY 355
 Qy 307 DNLKLPQKPNLNTSNHLLQDQKTKEL-GANQDPMELKSHVFSLLNMDLNL 365
 Db 356 ELLIMDEKEPFLSSDAKSLGLLQDKNRKLGGDPDPKEIHHNSSFSGVNNQIWD 415
 Qy 366 KKTTPPMNWSGPNELRHDFEETPEV 394
 Db 416 KKLVPFPKPVSTETDTRTFDEETPAQTI 444

RESULT 6
 A:Residues: 1-611 <AND>
 A:Cross-references: GI:M83510
 A:Gene: FlyBase:RacP
 A:Cross-references: FlyBase:Fgn0013324
 A:Start codon: ACG
 A:Title: Developmental regulation of expression and activity of multiple forms of the
 protein kinase (EC 2.7.1.37) akt (similarity) - fruit fly (Drosophila melanogaster)
 C:Species: Drosophila melanogaster
 C:Dates: 10-Sep-1999 sequence revision 10-Sep-1999 text_change 20-Apr-2001
 C:Accession: A55888
 A:Title: Molecular cloning and characterization of a new member of the Rac protein kinase
 family
 A:Accession: J03435
 A:Residues: 1-454 <RNA>
 A:Experimental source: brain

A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threo-
 phosphate
 C:Superfamily: protein kinase act; pleckstrin repeat homology; protein kinase homology
 C:Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein
 kinase
 F:4-105/Domain: pleckstrin repeat homology <PK>
 F:154-162/Region: protein kinase ATP-binding motif
 F:177/Active site: Lys status predicted


```

Oy 277 TVMCLGAVLYENLYGLPPFYSRNTAEWDNIINKEPLQKPNITNSARHLLGELQKOR 336
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Oy 330 AVNMCLGVVWYEMWCGRLPTVQDHRLFELLWGEIRPPETLOPBNASGLGDLQKOR 389
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Oy 337 TKRL-GAKDPFMEKSHVFESLNDMLINKITPPFPNPNVSGMELRHFPDFTPEVP 394
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Oy 390 KQLCGGSDAKENHREHFFLSINQDQVQKGLPFPFVTSYDITNFDDEFQSI 448
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 15
C:Species: Schizosaccharomyces pombe
C:Probable proliferation-associated serine/threonine protein kinase [imported] - fission y
C:Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 02-Sep-2000
C:Accession: U0418, D.: Wood, V.: Rajandream, M.A.: Barrell, B.G.
P:Submitted to the EMBL Data Library, February 2000
A:Reference number: Z25039
A:Accession: F50414
A:Database: GenBank
A:Molecule type: DNA
A:Residues: 1-569 <SEE>
A:Cross-references: EMBL:AL157991; PDB:1CM76216.1; GSPDB:GN00068; SPDB:SPCC24B10.07
A:Protein source: strain 972h(-); cosmid c24b10
C:Genetics:
A:Map position: 3
A:Gene: SPDB:SPCC24B10.07
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo

Query Match 36.3%; Score 824; DB 2: Length 569;
Best Local Similarity 31.1%; Pred. No. 7.5e-31;
Matches 169; Conservative 42; Mismatches 110; Indels 10; Gaps 5;

Oy 98 FHLKTVKGSGKGVLLARHKAEEYFVAVKVLQKAKILKKKEKHINSERWLLANKYHP 157
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Oy 230 FELLVWKGSGKGVWVQKQRTSYIAKTKKGVSRSEVQHTLAERKVLQ-VNRP 288
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Oy 158 FVLGLHFSQTAKLYLVLDYINGGELFVHLQRECFLEPRARYAAETASALGYLHSLN 217
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Oy 289 FVPLRFSPQSGKLLVLAVVNGGRLHILQREGCOTTRAKFYIAELLVALECLEHPN 348
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Oy 218 IYNDLKPENILLDSGGHVLDTGCLCKENIHNSSTFSGCTPEYLAPEVLHKKPPDPT 277
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Oy 349 IYNDLKPENILLDTGHTLACQGLCKLNAKQRTMFCQTPPEYLAPELLIGHGYTKV 408
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Oy 278 VQNMCLGAVLYEHLGLPFPFYSRNTAEWDNIINAKPLQKPNITNSARHLLGELQKOR 337
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Oy 408 VQNMGLVLYEHLGLPFPFYSRNTAEWDNIINAKPLQKPNITNSARHLLGELQKOR 337
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Oy 338 KRLGAKDPFMEKSHVFESLNDMLINKITPPFPNPNVSGMELRHFPDFTPEVPNS 397
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Oy 469 KRLGS-GGAGETKNHFFDDIKKLCCKAKIOPPFKFSVESADITSNPFQSEFTSE-IP-- 524
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Oy 398 ICKSPDSVPLVTSVKEAA-EARLGSFYAPPT 427
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Oy 525 ----MDSVVAUSHLSETVQOORFANWYSQRT 551
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

Search completed: August 11, 2003, 08:23:24
 Job time : 59.3433 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

ON protein - nucleic search, using frame_plus_p2n model

Run on: August 11, 2003, 08:36:34 ; Search time 18.1364 Seconds

462.401 Million cell updates/sec

Title: us-10-000-039a-3

Perfect score: 103

Sequence: 1 DPEETPEPVNSIGSPDS 19

Scoring table: BLOSUM62

Xgapop 10.0, Xgapext 0.5

Ygapop 10.0, Ygapext 0.5

Zgapop 6.0, Zgapext 7.0

Delop 6.0, Delext 7.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum match 0%

Listing first 45 summaries

Command line parameters:

-MODEP1-2/USPFO spoof1 -DEV-x10

-Q-cgpn2.1/USPFO spoof1 -DEV-x10

-DB-Issued Patents-NA -QWt-fastap -SUFFIX-rni -MINMATCH=0.1 -LOOPCL=0

-LOOPEXT=0 -UNITS=bits -STAR=1 -END=1 -MATRIX=blom62 -TRANS-human40.cdi

-MODE-LOCAL -OUTPRF-pco -NORM-ext -HEAPSIZE=500 -NINLEN=0 -MAXLEN=0

-USER=US1000039.rgn1.1.145.rnunt.01082003.085419.27535 -NCPU=6 -ICPU=3

-DO-WAY-LATOPRNT -NEE-SOURCES=0 -WAT -DSPBLOCK=100 -LONGLOG

-DO-WAY-LATOPRNT -NEE-SOURCES=0 -WAT -DSPBLOCK=100 -LONGLOG

-FGAPEXT-7 -YGAPOP=10 -YGAPEXT=0.5 -DELPH=6 -DELEXT=7

-FGAPEXT-7 -YGAPOP=10 -YGAPEXT=0.5 -DELPH=6 -DELEXT=7

Database :

Issued Patents-NA: 1 /lin/5A.COMB.seq*

2: /cgn2.6/pdata1/lin/5B.COMB.seq*

3: /cgn2.6/pdata1/lin/5A.COMB.seq*

4: /cgn2.6/pdata1/lin/5B.COMB.seq*

5: /cgn2.6/pdata1/lin/5A.COMB.seq*

6: /cgn2.6/pdata1/lin/5B.COMB.seq*

7: /cgn2.6/pdata1/lin/5A.COMB.seq*

8: /cgn2.6/pdata1/lin/5B.COMB.seq*

9: /cgn2.6/pdata1/lin/5A.COMB.seq*

10: /cgn2.6/pdata1/lin/5B.COMB.seq*

11: /cgn2.6/pdata1/lin/5A.COMB.seq*

12: /cgn2.6/pdata1/lin/5B.COMB.seq*

13: /cgn2.6/pdata1/lin/5A.COMB.seq*

14: /cgn2.6/pdata1/lin/5B.COMB.seq*

15: /cgn2.6/pdata1/lin/5A.COMB.seq*

16: /cgn2.6/pdata1/lin/5B.COMB.seq*

17: /cgn2.6/pdata1/lin/5A.COMB.seq*

18: /cgn2.6/pdata1/lin/5B.COMB.seq*

19: /cgn2.6/pdata1/lin/5A.COMB.seq*

20: /cgn2.6/pdata1/lin/5B.COMB.seq*

21: /cgn2.6/pdata1/lin/5A.COMB.seq*

22: /cgn2.6/pdata1/lin/5B.COMB.seq*

23: /cgn2.6/pdata1/lin/5A.COMB.seq*

24: /cgn2.6/pdata1/lin/5B.COMB.seq*

25: /cgn2.6/pdata1/lin/5A.COMB.seq*

26: /cgn2.6/pdata1/lin/5B.COMB.seq*

27: /cgn2.6/pdata1/lin/5A.COMB.seq*

28: /cgn2.6/pdata1/lin/5B.COMB.seq*

29: /cgn2.6/pdata1/lin/5A.COMB.seq*

30: /cgn2.6/pdata1/lin/5B.COMB.seq*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Qty	Match	Length	DB ID	Description
1	103	100.0	2311	2	US-08-712-709-6	Sequence 6, Appl
2	103	100.0	2311	3	US-09-11-724-6	Sequence 6, Appl
3	103	100.0	2311	3	US-09-11-724-6	Sequence 6, Appl
4	103	100.0	2311	4	US-09-016-434-772	Sequence 772, Appl
5	103	100.0	2310	4	US-09-031-295-1	Sequence 1, Appl
6	51	49.5	2286	4	US-09-073-009-9	Sequence 9, Appl
7	51	49.5	2286	4	US-09-073-009-9	Sequence 9, Appl
8	51	49.5	441529	3	US-09-103-8408-2	Sequence 2, Appl
9	50	48.5	910	4	US-09-103-8408-2	Sequence 88, Appl
10	50	48.5	55827	4	US-09-813-1334-3	Sequence 3, Appl
11	46	44.7	2533	3	US-09-262-773-209	Sequence 209, Appl
12	46	44.7	2531	3	US-09-262-773-210	Sequence 210, Appl

13	46	44.7	4403765	3	US-09-103-840A-2	Sequence 2, Appl
14	46	44.7	4411529	3	US-09-103-840A-1	Sequence 1, Appl
15	45	43.7	1116	3	US-09-104-308-2	Sequence 2, Appl
16	45	43.7	1116	3	US-09-104-308-2	Sequence 2, Appl
17	45	43.7	1116	4	US-09-729-881A-2	Sequence 2, Appl
18	45	43.7	1116	4	US-09-729-881A-2	Sequence 2, Appl
19	45	43.7	1158	4	US-09-729-881A-2	Sequence 246, App
20	45	43.7	1158	4	US-09-328-352-246	Sequence 2, Appl
21	45	43.7	1158	4	US-09-328-352-246	Sequence 2, Appl
22	45	43.7	1158	4	US-09-328-352-246	Sequence 4, Appl
23	45	43.7	1158	4	US-09-328-352-246	Sequence 4, Appl
24	45	43.7	1158	4	US-09-328-352-246	Sequence 4, Appl
25	45	43.7	1158	4	US-09-328-352-246	Sequence 4, Appl
26	45	43.7	1158	4	US-09-328-352-246	Sequence 4, Appl
27	44	42.7	257	4	US-09-193-881-2	Sequence 20, Appl
28	44	42.7	257	4	US-09-193-881-2	Sequence 20, Appl
29	44	42.7	257	4	US-09-193-881-2	Sequence 20, Appl
30	44	42.7	257	4	US-09-193-881-2	Sequence 20, Appl
31	44	42.7	257	4	US-09-193-881-2	Sequence 20, Appl
32	44	42.7	257	4	US-09-193-881-2	Sequence 20, Appl
33	44	42.7	257	4	US-09-193-881-2	Sequence 20, Appl
34	44	42.7	257	4	US-09-193-881-2	Sequence 20, Appl
35	44	42.7	257	4	US-09-193-881-2	Sequence 20, Appl
36	43	41.7	1725	4	US-09-134-001C-1868	Sequence 1868, Ap
37	43	41.7	1725	4	US-09-134-001C-1868	Sequence 1868, Ap
38	43	41.7	1725	4	US-09-134-001C-1868	Sequence 1868, Ap
39	43	41.7	1725	4	US-09-134-001C-1868	Sequence 1868, Ap
40	43	41.7	1725	4	US-09-134-001C-1868	Sequence 1868, Ap
41	43	41.7	1725	4	US-09-134-001C-1868	Sequence 1868, Ap
42	43	41.7	1725	4	US-09-134-001C-1868	Sequence 1868, Ap
43	43	41.7	1725	4	US-09-134-001C-1868	Sequence 1868, Ap
44	43	41.7	1725	4	US-09-134-001C-1868	Sequence 1868, Ap
45	43	41.7	1725	4	US-09-134-001C-1868	Sequence 1868, Ap

ALIGNMENTS

RESULT 1
US-09-103-840A-2
Sequence 6, Application US/08712709
Patent No. 4863780
GENERAL INFORMATION:
INVENTOR: Gung, Jancie
APPLICANT: Gung, Jancie
TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES
INVENTOR'S ADDRESS: 3174 Porter Drive
CORRESPONDENCE ADDRESS: 3174 Porter Drive
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
COMPUTER TYPE: Disquette
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA: /08/712,709
FILING DATE: Filled Hereafter
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REFERENCE/DOCKET NUMBER: 7,716
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-445-4166
INVOICE NUMBER: 7777777777
SEQUENCE CHARACTERISTICS: 6
LENGTH: 2311 base pairs
TYPE: nucleic acid

```

STRANDNESS: single
SEQUENCE: 4638-08
MOLECULE TYPE: cDNA
IMMEDIATE SOURCE:
LIBRARY: Consensus
US-08-712-709-6

```

```

Alignment Scores: 4,638-08 2311
Seq. No.: 19
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 0
Mismatches: 0
Indels: 0
Gaps: 0

```

US-10-000-039A-3 (1-19) x US-08-712-709-6 (1-2311)

```

QY 1 AspProGluPheHbduGluProValProAsnSerIleGlyLysSerProAspSer 19
|||||
DB 1165 GACCCCGAGTTTACCGAGAGCCTCTCCCACTTCATTCGACAGTCCCTGCACGC 1221

```

```

RESULT 2
US-09-111-444-6 Application US/09111444
Sequence 6, 4091777
GENERAL INFORMATION:
APPLICANT: Au-Young, Janice
APPLICANT: Guebler, Karl J.
APPLICANT: HAKLOS, PAUL J. R.
TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESS: Novartis Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
SOFTWARE: FASTSEQ Version 1.5
OPERATING SYSTEM: DOS
CURRENT APPLICATION DATA:
FILING DATE: 08/09/111.444
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/712.709
ATTORNEY AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
TELEPHONE: 415-855-0555
TELECOMMUNICATION INFORMATION:
TELEFAX: 415-855-0555
INVENTOR INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
TELEPHONE: 415-855-0555
SEQUENCE CHARACTERISTICS: 6:
LENGTH: 2311 base pairs
TYPE: nucleic acid
STRANDNESS: single
MOLECULE TYPE: cDNA
IMMEDIATE SOURCE:
LIBRARY: Consensus
US-09-111-444-6

```

```

Alignment Scores: 4,638-08 2311
Seq. No.: 19
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 0
Mismatches: 0
Indels: 0
Gaps: 0

```

```

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

```

US-10-000-039A-3 (1-19) x US-09-111-444-6 (1-2311)

```

QY 1 AspProGluPheHbduGluProValProAsnSerIleGlyLysSerProAspSer 19
|||||
DB 1165 GACCCCGAGTTTACCGAGAGCCTCTCCCACTTCATTCGACAGTCCCTGCACGC 1221

```

```

RESULT 3
US-09-541-228-6 Application US/0951228
Sequence 6, 4091777
GENERAL INFORMATION:
APPLICANT: Au-Young, Janice
APPLICANT: Guebler, Karl J.
APPLICANT: HAKLOS, PAUL J. R.
TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESS: Novartis Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
SOFTWARE: FASTSEQ Version 1.5
OPERATING SYSTEM: DOS
CURRENT APPLICATION DATA:
FILING DATE: 08/09/541.228
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/712.709
ATTORNEY AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
TELEPHONE: 415-855-0555
TELECOMMUNICATION INFORMATION:
TELEFAX: 415-855-0555
INVENTOR INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
TELEPHONE: 415-855-0555
SEQUENCE CHARACTERISTICS: 6:
LENGTH: 2311 base pairs
TYPE: nucleic acid
STRANDNESS: single
MOLECULE TYPE: cDNA
IMMEDIATE SOURCE:
LIBRARY: Consensus
US-09-541-228-6

```

```

Alignment Scores: 4,638-08 2311
Seq. No.: 19
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 0
Mismatches: 0
Indels: 0
Gaps: 0

```

US-10-000-039A-3 (1-19) x US-09-541-228-6 (1-2311)

```

QY 1 AspProGluPheHbduGluProValProAsnSerIleGlyLysSerProAspSer 19
|||||
DB 1165 GACCCCGAGTTTACCGAGAGCCTCTCCCACTTCATTCGACAGTCCCTGCACGC 1221

```

```

RESULT 4
US-09-016-434-772

```



```

Sequence 772, Application US/09016434
GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Sellhammer
TITLE OF INVENTION: METHOD FOR THE DETECTION OF SIGNALING
OPERATING SYSTEM: PC-DOS/MS-DOS
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
APPLICATION NUMBER: 1490
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Trezeller, Karen J
REFERENCE/DOCKET NUMBER: PA-0002 US
TELEPHONE: (650) 855-0555
FAX: (650) 855-0555
INFORMATION FOR SEQ ID NO: 772:
SEQUENCE CHARACTERISTICS:
LENGTH: 2311 base pairs
MOL. WEIGHT: 150000
STANDARDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: 477243
US-09-016-434-772
Alignment Scores:
Pred. No.: 4,63e-08 Length: 2311
Score: 103.00 Matches: 19
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 100.00%
DB: Gaps: 0

US-10-000-039A-3 (1-19) x US-09-016-434-772 (1-2311)
QY 1 AsprrGluPheThrGluGluProValProAsnSerIleGlySerProAspSer 19
DB 1165 GACCCCGATTACGAGAGGCTGTCCCACTCATGTGCAAGTCCCTCCGACG 1221

RESULT 5
US-09-031-295-1
Sequence 1, Application US/09031295
GENERAL INFORMATION:
APPLICANT: LANG, Florian
APPLICANT: WALDEGER, Tubingen
TITLE OF INVENTION: CELL VOLUME-REGULATED HUMAN KINASE H-56K
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
STREET: 3000 K Street, N.W.
CITY: Washington
US-09-031-295-1
Alignment Scores:
Pred. No.: 4,63e-08 Length: 2311
Score: 103.00 Matches: 19
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 100.00%
DB: Gaps: 0

US-10-000-039A-3 (1-19) x US-09-016-434-772 (1-2311)
QY 1 AsprrGluPheThrGluGluProValProAsnSerIleGlySerProAspSer 19
DB 1165 GACCCCGATTACGAGAGGCTGTCCCACTCATGTGCAAGTCCCTCCGACG 1221

Sequence 772, Application US/09016434
GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Sellhammer
TITLE OF INVENTION: METHOD FOR THE DETECTION OF SIGNALING
OPERATING SYSTEM: PC-DOS/MS-DOS
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
APPLICATION NUMBER: 1490
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Trezeller, Karen J
REFERENCE/DOCKET NUMBER: PA-0002 US
TELEPHONE: (650) 855-0555
FAX: (650) 855-0555
INFORMATION FOR SEQ ID NO: 772:
SEQUENCE CHARACTERISTICS:
LENGTH: 2311 base pairs
MOL. WEIGHT: 150000
STANDARDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: 477243
US-09-016-434-772
Alignment Scores:
Pred. No.: 4,63e-08 Length: 2311
Score: 103.00 Matches: 19
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 100.00%
DB: Gaps: 0

US-10-000-039A-3 (1-19) x US-09-031-295-1 (1-2370),
QY 1 AsprrGluPheThrGluGluProValProAsnSerIleGlySerProAspSer 19
DB 1198 GACCCCGATTACGAGAGGCTGTCCCACTCATGTGCAAGTCCCTCCGACG 1294

RESULT 6
US-09-073-009-9/c Application US/09073009
Sequence 9, Application US/09073009
GENERAL INFORMATION:
APPLICANT: Alderson, Mark
APPLICANT: Alderson, Kevin C. W.
APPLICANT: SWANSON, Kevin C. W.
APPLICANT: Campos-Melo, Antonio
TITLE OF INVENTION: COMPOUNDS AND DIAGNOSIS OF
NUMBER OF SEQUENCES: 144
CORRESPONDENCE ADDRESS:
STREET: 6300 Columbia Center, 701 Fifth Ave.
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
APPLICATION NUMBER: US/09/071,009

```

```

; FILING DATE: 05-MAY-1998
; CLONING POSITION INFORMATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: MAXI, DAVID J.
; REGISTRATION NUMBER: 31,992
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-522-4900
; TELEFAX: 206-682-6031
; MAILING ADDRESS: 120121.441C1
; INVENTOR INFORMATION: 9;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2286 base pairs
; TYPE: nucleic acid
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORGANISM SOURCE: Mycobacterium tuberculosis
US-09-073-009-9

```

```

Alignment Scores: 31.3 Length: 2286
Score: 51.00 Matches: 10
Percent Similarity: 70.59% Conservative: 2
Best Local Similarity: 49.51% Mismatches: 0
Query Match: 49.51% Indels: 0
DB: 0

```

US-10-000-039a-3 (1-19) x US-09-073-009-9 (1-2286)

```

QY 1 AspProGluPheThrGluIuproValProAsnSerIleGlyLysSerPro 17
DB 137 GACCCAGATTACGCGAGATCCGTCCTCCGTTCCGCGGTGGCAATCCG 87

```

```

RESULT 7
US-09-103-840A-2/c
; Sequence 2, Application US/09103840A
; CLONING POSITION INFORMATION:
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: VENTER, John C.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM TUBERCULOSIS
; CURRENT FILING DATE: 1998-06-24
; CURRENT APPLICATION NUMBER: US/09/103-840A
; EARLIER FILING DATE: 1998-06-24
; EARLIER APPLICATION NUMBER: 60/092,956
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 1: Patent In Ver. 2.1
; SEQ ID NO 2: Patent In Ver. 2.1
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: 16* bases at various positions throughout the sequence
US-09-103-840A-2

```

```

Alignment Scores: 3.69e+05 Length: 4403765
Score: 51.00 Matches: 10
Percent Similarity: 70.59% Conservative: 2
Best Local Similarity: 49.51% Mismatches: 5
Query Match: 49.51% Indels: 0
DB: 0

```

US-10-000-039a-3 (1-19) x US-09-103-840A-2 (1-4403765)

```

QY 1 AspProGluPheThrGluIuproValProAsnSerIleGlyLysSerPro 17
DB 1234985 GNCCAGCAATTACGCGAGATCCGTCCTCCGTTCCGCGGTGGCAATCCG 1234935

```

```

RESULT 8
US-09-103-840A-1/c
; Sequence 1, Application US/09103840A
; CLONING POSITION INFORMATION:
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: VENTER, John C.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: TUBERCULOSIS
; CURRENT FILING DATE: 1998-06-24
; CURRENT APPLICATION NUMBER: US/09/103-840A
; EARLIER FILING DATE: 1998-06-24
; EARLIER APPLICATION NUMBER: 60/092,956
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 1: Patent In Ver. 2.1
; SEQ ID NO 2: Patent In Ver. 2.1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: H37Nv
US-09-103-840A-1

```

```

Alignment Scores: 3.69e+05 Length: 4411529
Score: 51.00 Matches: 10
Percent Similarity: 70.59% Conservative: 2
Best Local Similarity: 49.51% Mismatches: 0
Query Match: 49.51% Indels: 0
DB: 0

```

US-10-000-039a-3 (1-19) x US-09-103-840A-1 (1-4411529)

```

QY 1 AspProGluPheThrGluIuproValProAsnSerIleGlyLysSerPro 17
DB 1235456 GACCCAGATTACGCGAGATCCGTCCTCCGTTCCGCGGTGGCAATCCG 1235406

```

```

RESULT 9
US-09-482-273-88/c
; Sequence 88, Application US/09482273
; CLONING POSITION INFORMATION:
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 771 Human Secreted Proteins
; CURRENT FILING DATE: 2000-01-13
; CURRENT APPLICATION NUMBER: US/09/482,273
; EARLIER FILING DATE: 2000-01-13
; EARLIER APPLICATION NUMBER: US/99/070899/15849
; EARLIER FILING DATE: 1999-07-07
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/092,922
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/092,956
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 1: Patent In Ver. 2.0
; SEQ ID NO 88
; LENGTH: 910
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-482-273-88

```

```

Alignment Scores: 14.5 Length: 910
Score: 50.00 Matches: 9
Percent Similarity: 64.71% Conservative: 2
Best Local Similarity: 52.94% Mismatches: 6
Query Match: 48.54% Indels: 0
DB: 0

```

US-10-000-039a-3 (1-19) x US-09-482-273-88 (1-910)

```

Oy 1 AsprogluPherthgluProvalProasnSerIleGlylysserPro 17
Db 123 GATCCACCCACACCCAGCCGCTGGCGAGCTCTGGGAAATCGCG 73
RESULT 10
US-09-813-133A-3/C
; Sequence 20, Application US/09813133A
; Patent No. 6455294
; ORGANISM: Human
; APPLICANT: GAN, Weiniu et al
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASES ENCODING HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CLO01173
; CURRENT APPLICATION NUMBER: US/09/813,133A
; CURRENT FILING DATE: 1999-03-04
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3: 5827
; LENGTH: 5827
; TYPE: DNA
; ORGANISM: Human
US-09-813-133A-3
Alignment Scores:
Pred. No.: 2,63e+03 Length: 55827
Score: 50.00 Matches: 10
Percent Similarity: 66.67% Conservative: 2
Best Local Similarity: 66.67% Mismatches: 0
Query Match: 44.66% Indels: 0
Gaps: 0
DB: 48071 CCTCCACACTCTCCCTCCCTGCTTATTCACAGTCGAGCCCAACGC 48018

US-10-000-039A-3 (1-19) x US-09-813-133A-3 (1-55827)
Oy 2 ProgluPherthgluProvalProasnSerIleGlylysserProaspSer 19
Db 48071 CCTCCACACTCTCCCTCCCTGCTTATTCACAGTCGAGCCCAACGC 48018
RESULT 11
US-09-262-773-209
; Sequence 209, Application US/09262773
; Patent No. 6252773
; ORGANISM: Human
; APPLICANT: Ballinger, Dennis G.
; APPLICANT: Ding, Wei
; APPLICANT: Wagner, Susanne
; APPLICANT: Fraser, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: CHROMOSOME 11-LINKED CORONARY HEART DISEASE
; TITLE OF INVENTION: SUSCEPTIBILITY GENE CHD1
; FILE REFERENCE: MY140
; CURRENT APPLICATION NUMBER: US/09/262,773
; CURRENT FILING DATE: 1999-03-04
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2: 2933
; LENGTH: 2933
; TYPE: DNA
; ORGANISM: Human
US-09-262-773-209
Alignment Scores:
Pred. No.: 304 Length: 2933
Score: 46.00 Matches: 8
Percent Similarity: 66.67% Conservative: 1
Best Local Similarity: 66.67% Mismatches: 0
Query Match: 44.66% Indels: 0
Gaps: 0
DB: 48071 CCTCCACACTCTCCCTCCCTGCTTATTCACAGTCGAGCCCAACGC 48018

US-10-000-039A-3 (1-19) x US-09-262-773-209 (1-2933)
Oy 6 GluGluproValProasnSerIleGlylysserPro 17
Db 123 GATCCACCCACACCCAGCCGCTGGCGAGCTCTGGGAAATCGCG 73
RESULT 12
US-09-262-773-210
; Sequence 210, Application US/09262773
; Patent No. 6252451
; ORGANISM: Human
; APPLICANT: Ballinger, Dennis G.
; APPLICANT: Ding, Wei
; APPLICANT: Wagner, Susanne
; APPLICANT: HESS, Mark A.
; TITLE OF INVENTION: CHROMOSOME 11-LINKED CORONARY HEART DISEASE
; TITLE OF INVENTION: SUSCEPTIBILITY GENE CHD1
; FILE REFERENCE: MY140
; CURRENT APPLICATION NUMBER: US/09/262,773
; CURRENT FILING DATE: 1999-03-04
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 210
; LENGTH: 23071
; TYPE: DNA
; ORGANISM: Human
US-09-262-773-210
Alignment Scores:
Pred. No.: 4,17e+03 Length: 23071
Score: 46.00 Matches: 1
Percent Similarity: 75.00% Conservative: 1
Best Local Similarity: 66.67% Mismatches: 3
Query Match: 44.66% Indels: 0
Gaps: 0
DB: 48071 CCTCCACACTCTCCCTCCCTGCTTATTCACAGTCGAGCCCAACGC 48018

US-10-000-039A-3 (1-19) x US-09-262-773-210 (1-23071)
Oy 6 GluGluproValProasnSerIleGlylysserPro 17
Db 2625 GAGACCCGCGCCCGCCGAGAGTCCTGGGAAATCGCG 2660
RESULT 13
US-09-103-840A-2
; Sequence 2, Application US/09103840A
; Patent No. 6284328
; ORGANISM: Human
; APPLICANT: TROTTMAN, Robert D.
; APPLICANT: WHITE, Owen Robert D.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: CHROMOSOMES FOR STAPH ANALYSIS IN MYCOMA-THERIUM
; TITLE OF INVENTION: SUSCEPTIBILITY GENE CHD1
; FILE REFERENCE: 24166-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2
Alignment Scores:
Pred. No.: 1,06e+06 Length: 4403765
Score: 46.00 Matches: 1
Percent Similarity: 82.50% Conservative: 1
Best Local Similarity: 56.25% Mismatches: 6
Query Match: 44.66% Indels: 0
Gaps: 3
DB: 48071 CCTCCACACTCTCCCTCCCTGCTTATTCACAGTCGAGCCCAACGC 48018

US-10-000-039A-3 (1-19) x US-09-103-840A-2 (1-4403765)

```

```

Oy      2 ProdiuphethgluiprovAlProAnSerIleGlyLysSerPro 17
DB 3136791 CGGGCAGCAGCGAGAGCTGACCCCTAGGAGCGCGTCCCAAAATGCC 3136838
RESULT 14
US-09-103-840A-1
1 TITLE OF INVENTION: Application US/09103840A
2 PATENT NO.: 6294328
3 GENERAL INFORMATION:
4 APPLICANT: FLEISCHMAN, Robert D.
5 APPLICANT: FRASER, Claire M.
6 APPLICANT: VENTER, John C.
7 APPLICANT: VAN DER KLEIJ, Wilhelmus A.H.
8 TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
9 TUBERCULOSIS
10 FILE REFERENCE: 24366-20007.00
11 CURRENT APPLICATION NUMBER: US/09/103,840A
12 CURRENT FILING DATE: 1998-06-24
13 INVENTOR: FRASER, Claire M.
14 SOFTWARE: PatentIn Ver. 2.1
15 SEQ ID NO 1
16 LENGTH: 441529
17 ORGANISM: Mycobacterium tuberculosis
18 OTHER INFORMATION: H37RV
US-09-103-840A-1
Alignment Scores:
Pred. No.: 1,06e+06 Length: 441529
Score: 46.00 Matches: 9
Percent Similarity: 52.50A Conservative: 1
Best Local Similarity: 52.50A Mismatches: 0
Query Match: 44.66A Indels: 0
DB: 3 Gaps: 0
US-10-000-039A-3 (1-19) x US-09-103-840A-1 (1-441529)
Oy      2 ProdiuphethgluiprovAlProAnSerIleGlyLysSerPro 17
DB 3142522 CGGGCAGCAGCGAGAGCTGACCCCTAGGAGCGCGTCCCAAAATGCC 3142669
RESULT 15
US-09-104-308-2/c
1 Sequence 2, Application US/09104308
2 TITLE OF INVENTION: Application US/09104308
3 GENERAL INFORMATION:
4 APPLICANT: Jones, Brian E.
5 APPLICANT: Van Der Kleij, Wilhelmus A.H.
6 APPLICANT: FRASER, Claire M.
7 APPLICANT: VENTER, John C.
8 APPLICANT: WEGYLER, Walter
9 TITLE OF INVENTION: No. 6187577e1 Cellulase Producing Actinomycetes,
10 TITLE OF INVENTION: Cellulase Produced Therefrom and Method of Producing Same
11 CORRESPONDENCE ADDRESS:
12 ADDRESSEE: Genencor International, Inc.
13 STREET: 925 Page Mill Road
14 CITY: Palo Alto
15 STATE: California
16 COUNTRY: USA
17 ZIP: 94304-1013
18 COMPUTER READABLE FORM:
19 SOURCE: FTS
20 OPERATING SYSTEM: IBM Compatible
21 SOFTWARE: FASTSEQ for Windows Version 2.0
22 CURRENT APPLICATION NUMBER: US/09/104,308
23 FILING DATE: 24-JUN-1998
24 PRIOR APPLICATION DATA:
25 APPLICATION NUMBER: 08/974,042
26 FILING DATE: 24-JUN-1997
27 ATTORNEY/AGENT INFORMATION:

```

```

1 NAME: Stone, Christopher L.
2 REGISTRATION NUMBER: 35,696
3 REFERENCE/DOCKET NUMBER: GC539
4 TELEPHONE: 650-846-7552
5 TELEFAX: 650-845-6504
6 INFORMATION FOR SEQ ID NO: 2:
7 SEQUENCE CHARACTERISTICS:
8 LENGTH: 1116 base pairs
9 TYPE: nucleic acid
10 STRANDEDNESS: single
11 TOPOLOGY: linear
12 US-09-104-308-2
Alignment Scores:
Pred. No.: 122 Length: 1116
Score: 60.00 Matches: 0
Percent Similarity: 60.00A Conservative: 0
Best Local Similarity: 60.00A Mismatches: 6
Query Match: 43.69A Indels: 0
DB: 3 Gaps: 0
US-10-000-039A-3 (1-19) x US-09-104-308-2 (1-1116)
Oy      3 GhuPhethgluiprovAlProAnSerIleGlyLysSerPro 17
DB 737 GAGTTCAGCGCCAGACCGCGTGGCCCTCCACAGCGCTGAGTCCC 693
Search completed, August 11, 2003, 12:07:09
Job time : 2223.14 secs

```

GenCode version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

ON protein - nucleic search, using frame_plus_p2n model

Run on: August 11, 2003, 08:23:34 ; Search time 70.8182 Seconds
724.239 Million cell updates/sec

Title: US-10-000-039a-3

Sequence: 1 DEETEPVNSIGKSPDS 19

Scoring table:
BLOSUM62 0, Gapcost 0.5
Xgapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
delop 6.0, delext 7.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Maximum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Command line parameters: gview3p
-O -C/92.7/USPFO.spool/US1000039/rnaal_Q1082003.085418.27503/seq_query.fasta.1.661
-Db-N Geneseq-19jun03 -OFMT-fastap -SUFFIX-rng -MINMATCH=0.1 -LOEPL=0
-LOOPEXT=0 -UNITS-bits -START=1 -END=1 -MATRIX-blosum62 -TRANS-human40.cdi
-LIST=45 -DOCAATCH=200 -THR_SCORE=PC -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-USER=US1000039 -GCN1.1.740 -rtnaol_Q1082003.085418.27503 -NCPU=6 -ICPU=3
-NO_MMAR -LARGEQUERY -NEG_SCORES=0 -NAT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -MARL_TIMEOUT=30 -THREADS=1 -XGAPOP=0.5 -XGAPEXT=0.5 -PGAPOP=6
-FONFMT=7 -FONOP=0.5 -FONPAP=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq-19jun03.*

1: /SIDSI/gcdgata/geneseq-emb1/NA1980.DAT.*
2: /SIDSI/gcdgata/geneseq-emb1/NA1981.DAT.*
3: /SIDSI/gcdgata/geneseq-emb1/NA1982.DAT.*
4: /SIDSI/gcdgata/geneseq-emb1/NA1983.DAT.*
5: /SIDSI/gcdgata/geneseq-emb1/NA1984.DAT.*
6: /SIDSI/gcdgata/geneseq-emb1/NA1985.DAT.*
7: /SIDSI/gcdgata/geneseq-emb1/NA1986.DAT.*
8: /SIDSI/gcdgata/geneseq-emb1/NA1987.DAT.*
9: /SIDSI/gcdgata/geneseq-emb1/NA1988.DAT.*
10: /SIDSI/gcdgata/geneseq-emb1/NA1989.DAT.*
11: /SIDSI/gcdgata/geneseq-emb1/NA1990.DAT.*
12: /SIDSI/gcdgata/geneseq-emb1/NA1991.DAT.*
13: /SIDSI/gcdgata/geneseq-emb1/NA1992.DAT.*
14: /SIDSI/gcdgata/geneseq-emb1/NA1993.DAT.*
15: /SIDSI/gcdgata/geneseq-emb1/NA1994.DAT.*
16: /SIDSI/gcdgata/geneseq-emb1/NA1995.DAT.*
17: /SIDSI/gcdgata/geneseq-emb1/NA1996.DAT.*
18: /SIDSI/gcdgata/geneseq-emb1/NA1997.DAT.*
19: /SIDSI/gcdgata/geneseq-emb1/NA1998.DAT.*
20: /SIDSI/gcdgata/geneseq-emb1/NA1999.DAT.*
21: /SIDSI/gcdgata/geneseq-emb1/NA2000.DAT.*
22: /SIDSI/gcdgata/geneseq-emb1/NA2001A.DAT.*
23: /SIDSI/gcdgata/geneseq-emb1/NA2001B.DAT.*
24: /SIDSI/gcdgata/geneseq-emb1/NA2001C.DAT.*
25: /SIDSI/gcdgata/geneseq-emb1/NA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed.

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB IU	Description
1	103	100.0	2281	20	Human breast tumor
2	103	100.0	2281	20	Human breast tumor
3	103	100.0	2311	19	Human protein kinase
4	103	100.0	2311	25	AAV52174
5	103	100.0	2348	25	AB741395
6	103	100.0	2348	25	AB741395
7	103	100.0	2370	19	AAV48311
8	103	100.0	2370	24	ABK84749
9	103	100.0	2370	24	ABK97360
10	103	100.0	2370	24	ABK97360
11	100	97.1	404	25	ABX42261
12	100	97.1	433	25	ABX438963
13	95	92.2	431	24	ABJ99409
14	95	92.2	431	24	ABJ99409
15	95	92.2	432	22	AAK46240
16	64	62.1	1333	22	AAI99535
17	64	62.1	1346	22	AAK44641
18	64	62.1	1365	22	AAK44987
19	64	62.1	1365	22	AAK44987
20	64	62.1	1812	24	ADP38341
21	64	62.1	1834	21	AAA27856
22	64	62.1	2146	21	AAA27857
23	64	62.1	2146	21	AAA27857
24	54	52.4	3953	25	ABX60036
25	51	49.5	2286	20	AAK01152
26	51	49.5	2286	20	AAK01156
27	51	49.5	2286	22	AAK12464
28	51	49.5	2286	22	AAK12464
29	51	49.5	2965	22	AAK48332
30	51	49.5	3872	24	ABK41310
31	51	49.5	11809	22	ABK21072
32	51	49.5	11809	22	ABK21072
33	51	49.5	440765	22	AAI99683
34	51	49.5	441529	22	AAI99682
35	50	48.5	583	24	ABO33516
36	50	48.5	583	24	ABO33516
37	50	48.5	910	20	AAK00677
38	50	48.5	910	21	AAK98094
39	50	48.5	910	22	AAJ01707
40	50	48.5	910	22	AAK09803
41	50	48.5	910	25	ABZ71201
42	50	48.5	910	25	ABZ71201
43	50	48.5	5915	24	ABK93210
44	50	48.5	5915	24	ABK93210
45	50	48.5	5915	24	ABK93210

ALIGNMENTS

RESULT 1

AAKF4639

ID AAF44639 standard; cDNA; 1236 BP.

XX

XX AAF44639;

XX

DT 27-MAR-2001 (first entry)

XX

XX Novel protein kinase cDNA, SEQ ID NO: 18.

XX

KM Human; mouse; protein kinase; antiarthritic; antisclerotic; osteopathic;

KM immunosuppressive; cardiac; renal; antiinflammatory; antistatic;

KM dermatological; anticatabolic; antifertility; gene therapy; vaccine;

KM immunological; antiinflammatory; antisclerotic; osteopathic;

KM cancer; autoimmune disorder; stroke; of the brain; of the

KM inflammatory pelvic disease; multiple sclerosis; psoriasis; ss.

XX

(INCY-) INCYTE PHARM INC.
 PA Au-Young J, Guegler KJ, Hawkins PR;
 PI WPI: 1998-207394/18.
 DR P-NSDB: A6A4205.
 CC
 PT New isolated human protein kinase(s) - used to develop products for
 PT diagnosis of a variety of diseases, including, but not limited to, cancers,
 PT asthma, multiple sclerosis or rheumatoid arthritis.
 CC
 PS Cista 25; Fig 3; 75pp: Human.
 CC This sequence encodes a human protein kinase (HPK) of the invention. The
 CC HPK protein can be used to develop products for studying signalling
 CC cascades in various cells and tissues, diagnosing disease and selecting
 CC inhibitors of drug-induced altered kinase expression is implicated. The
 CC products can be used to e.g. reverse memory loss such as due to
 CC Alzheimer's disease, for cancer treatment or to provide anti-inflammatory
 CC and immunosuppressive effects in the treatment of multiple
 CC lymphocytic leukemias or lymphomas.
 CC
 SQ Sequence 2311 BP: 604 A; 508 G; 506 G; 692 T; 1 other:
 Alignment Scores:
 Pred. No.: 9,676-07 Length: 2311
 Score: 103.00 Matches: 19
 Percent Similarity: 100.00% Mismatches: 0
 Best Local Similarity: 100.00% Indels: 0
 Query Match: 19 Gaps: 0
 DB: 19
 US-10-000-039A-3 (1-19) x ANV23833 (1-2311)
 QY 1 AsprGluPheThrGluCupProValProAnSerIleClySerProAspSer 19
 Db 1165 GACCCGAGGTTCACCGAAGACGTCTCCCAACACGTCATTCGACATGCTCCCTGACAGC 1221
 RESULT 4
 ID ACA56174 standard; cDNA; 2311 BP.
 AC ACA56174;
 AT
 CT 06-JUN-2003 (first entry)
 DT 06-JUN-2003 (first entry)
 DE Human signalling pathway polynucleotide probe SEQ ID NO 772.
 KW Human; probe; ss; array element; Parkinson's disease;
 KW immunopathology; AIDS; Asthma; neuropathy; Alzheimer's disease; microarray.
 XX
 OS Homo sapiens.
 PX US6500938-B1.
 PD 31-DEC-2002.
 PR 30-JAN-1998; 98US-0016434.
 PR 30-JAN-1998; 98US-0016434.
 XX (INCY-) INCYTE GENOMICS INC.
 XX Au-Young J, Seilhamer JJ;
 PI WPI: 2003-352189/33.
 DR
 PT Combination of polynucleotide probes, useful as array elements in a
 PT microarray for monitoring the expression of a number of target
 PT polynucleotides

Claim 1; SEQ ID NO 772; 65pp; English.
 The invention relates to a combination which, comprises a number of
 polynucleotide probes comprising a sequence selected from one of the 1490
 array element in the sequence of the invention. The combination is useful as an
 array element in the expression of the invention. The microarray is particularly useful in the
 diagnosis and treatment of cancer and immunopathology and neuropathology.
 The microarray is useful in diagnostics and treatment regimens, drug
 discovery and development, toxicology and carcinogenesis studies,
 monitoring progression of diseases and for developing sophisticated
 profiles for the effects of currently available therapeutic drugs. The
 combination is also useful for purifying a subpopulation of cells. The
 array can detect changes in expression in a large number of genes coding
 for different signaling pathway populations which can be used to diagnose
 various diseases including cancer e.g. adenocarcinoma and leukemia disease
 immunopathology's disease. The present sequence represents a polynucleotide
 probe of the invention.
 Note: The sequence data for this patent did not form part of the printed
 specification but was obtained from the sequence data directly from USPTO
 at sequen2.uspto.gov/sequence.html?DocID=06500938B1.
 SQ Sequence 2311 BP: 604 A; 508 G; 506 G; 692 T; 1 other:
 Alignment Scores:
 Pred. No.: 9,676-07 Length: 2311
 Score: 103.00 Matches: 19
 Percent Similarity: 100.00% Mismatches: 0
 Best Local Similarity: 100.00% Indels: 0
 Query Match: 19 Gaps: 0
 DB: 19
 US-10-000-039A-3 (1-19) x ACA56174 (1-2311)
 QY 1 AsprGluPheThrGluCupProValProAnSerIleClySerProAspSer 19
 Db 1165 GACCCGAGGTTCACCGAAGACGTCTCCCAACACGTCATTCGACATGCTCCCTGACAGC 1221
 RESULT 5
 ID ABX74395
 AC ABX74395
 AT
 CT 21-MAR-2003 (first entry)
 DT 21-MAR-2003 (first entry)
 DE Human cDNA sequence #6 up-regulated in non-aggressive CC-RCC.
 KW Human; microarray; solid surface; immobilised probe; CC-RCC;
 KW differential expression profile; aggressive CC-RCC tumour type;
 KW non-aggressive CC-RCC tumour type; renal cell carcinoma; carcinoma;
 KW gene expression profiling; tumour tissue; gene; ss.
 XX Homo sapiens.
 PX WO200279411-A2.
 PD 10-OCT-2002.
 PR 29-MAR-2002; 2002MO-US095576.
 PR 29-MAR-2001; 2001US-279411P.
 XX (VAND-) VAN ANDEL INST.
 XX Habb B, Rhodes D, Teh BT, Takashi M;
 PI WPI: 2003-040579/03.
 DR

FF New microarray, comprising a matrix of cDNA probe from a set of probes
 FF immobilised to a solid surface in predetermined order, useful in the
 FF prognosis of patients with clear cell renal carcinoma -
 PS Claim 1: Page 79-80; 17pp: English.

CC The present invention relates to a microarray comprising a matrix of
 CC cDNA probes immobilised on a solid surface in predetermined order,
 CC surface in a predetermined order, where a row of pixels corresponds
 CC to replicates of one distinct probe from the set. The probes are
 CC complementary to nucleic acid sequences that are expressed
 CC under high stringency conditions. The microarray is useful for the
 CC diagnosis of patients with clear cell renal carcinoma (CC-RC) and
 CC prognosis of patients with CC-RC, wherein aggressive and
 CC expression profiles of genes that hybridise with one or more probes
 CC are used to predict the clinical course and prognosis of the disease.
 CC The arrays are useful for gene
 CC expression profiling of tumour and normal tissues. The present
 CC invention represents a novel cDNA sequence up-regulated in
 CC non-aggressive CC-RC phenotypes.

XX Alignment Scores: 2343 BP; 612 A; 517 G; 703 T; 0 other;

Pred. No.: 9,83e-07 Length: 2343
 Score: 103.00 Matches: 19
 Percent Similarity: 100.00% Conservative: 0
 Query Match: 100.00% Mismatches: 0
 DB: 25 Indels: 0
 Gaps: 0

US-10-000-039a-3 (1-19) x AAU74395 (1-2343)

Oy 1 AspProGluPheThrGluUpProValProAsnSerIleGlyLysSerProAspSer 19
 Db 1191 GACCCGAGTTACCGAGAGCCCTCCCACTCCATTCGCAAGTCCCTGCACAGC 1247

RESULT 6

ID AAU74190 standard; DNA; 2346 BP.

AC AAU74190;

XX 15-MAY-1999 (first entry)

DT Homo sapiens.

XX Serum glucocorticoid regulated kinase; sgk; human; treatment; inhibitor;

XX serine/threonine protein kinase family; antagonist; diabetic nephropathy;
 XX chronic renal failure, inflammation, Alzheimer's disease, wound; 68.

XX Homo sapiens.

OS Key

XX Location/Qualifiers

FF CDS 45..1340

FF /tag= a

FF /product= "sgk"

FF /trans_except= (pos:1185..1187, aa:Asp)

FF EP887081-A2.

XX 30-DEC-1996.

XX 27-MAY-1998; 98EP-0304189.

XX 27-JUN-1997; 97US-0051124.

PA (SMK) X SMITHKLINE BEECHAM CORP.

XX Kumar JN;

XX HPI; 1999-047627/05.

XX

XX

XX

XX

DR P-PSDB; AAU70139.

XX Treating chronic renal failure, diabetic nephropathy and Alzheimer's
 XX administration of nucleic acids and antagonists which
 XX inhibit activation of the renin-angiotensin system
 XX regulated kinase (sgk), a serine/threonine protein kinase

XX Disclosure: Page 14-15; 17pp: English.

CC This sequence encodes a novel human serum glucocorticoid regulated kinase
 CC (sgk) protein which is a member of the serine/threonine protein kinase
 CC family. This protein is used for the treatment of a subject having need
 CC for a protein kinase inhibitor, e.g., for the treatment of chronic renal failure,
 CC e.g., for the treatment of chronic renal failure, diabetic nephropathy,
 CC inflammation, Alzheimer's disease and wounds.

XX Sequence 2346 BP; 608 A; 520 C; 518 G; 700 T; 0 other;

XX Alignment Scores:

Pred. No.: 9,85e-07 Length: 2346
 Score: 103.00 Matches: 19
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 20 Gaps: 0

US-10-000-039a-3 (1-19) x AAU74190 (1-2346)

Oy 1 AspProGluPheThrGluUpProValProAsnSerIleGlyLysSerProAsnSer 19
 Db 1200 GACCCGAGTTACCGAGAGCCCTCCCACTCCATTCGCAAGTCCCTGCACAGC 1256

RESULT 7

ID AAU74311 standard; CDNA; 2370 BP.

AC AAU74311;

XX 15-NOV-1998 (first entry)

DT Homo sapiens.

XX Human cell-volume regulating kinase h-sgk.

XX sgk; human; cell-volume; kinase; h-sgk; diabetes mellitus;

XX renal insufficiency; inflammation; Alzheimer's disease.

XX Homo sapiens.

OS Key

XX Location/Qualifiers

FF CDS 43..1338

FF /tag= a

FF /product= "Kinase h-sgk"

FF EP861896-A2.

XX 02-SEP-1998.

XX 27-JAN-1998; 98EP-0101338.

XX 28-FEB-1997; 97DE-1008173.

XX (DADB-) DADE BEHNING MAKING OHM.

XX Lang F, Waldegg S;

XX HPI; 1998-149109/39.

DR P-PSDB; AAU7219.

XX New nucleic acid encoding cell-volume regulating kinase h-sgk and
 XX related proteins used for diagnosis and treatment of diseases
 XX associated with chronic renal failure, e.g. renal insufficiency,
 XX inflammation, infections etc.

XX Disclosure: Fig 1; 15pp: German.

Alignment Scores:

```

Pred. No.: 9,96e-07 Length: 2370
Score: 103.00 Matches: 19
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Gaps: 0
Query Match: 24 DB: 0

US-10-000-039a-3 (1-19) x ABX170006 (1-2370)
Oy 1 AspProGluPheHrCluGluProValProHsnSerIleGlyLysSerProAspSer 19
Db 1198 GACCCCGGATTACCGAAGACCCCTCCCACTCTCTGGAGATGCCCTGACACG 1254
RESULT 11
ABX42261
ID ABX42261 standard; cDNA: 404 BP.
AC ABX42261;
XX
XX
XX 20-FEB-2003 (first entry)
DT 20-FEB-2003 (first entry)
DE Bovine EST associated with lactation/muscle/fat deposition #7426.
KM Bovine; ss: EST; expressed sequence tag; lactation; LMPD;
KM muscle deposition; fat deposition; genome mapping; gene identification;
XX gene analysis; cattle breeding.
OS Bos Taurus.
XX
XX US2002137139-A1.
XX
XX 26-SEP-2002.
XX
XX 24-SEP-2001; 2001US-0960352.
XX
XX 12-JAN-1999; 99US-115707P.
XX 11-JAN-2000; 2000US-0480902.
XX
XX (BVAT//) BYATT J C.
XX (MATH//) MATHIALAGAN N.
XX (TAON//) TAO N.
XX (WARR//) WARREN W C.
XX
XX Byatt JC, Mathialagan N, Tao N, Warren WC;
XX WPI; 2003-110599/10.
XX
XX New nucleic acid associated with lactation, and muscle and fat
XX deposition, useful for genome mapping, gene identification and
XX analysis, cattle breeding, or for genetically improving cattle
XX
XX Claim 2: SEQ ID NO 7426; 245pp: English.
XX
XX The invention relates to a purified nucleic acid molecule associated with
XX lactation or muscle and fat deposition (designated LMPD), derived to a
XX second nucleic acid molecule comprising any of 15112 nucleotide
XX sequences, appearing as ABX34836-ABX49947, or complements of them.
XX Also included are: (1) a transfected cell having a nucleic acid
XX comprising an insert nucleic acid linked to the cell to cause termination of
XX transcription and addition of polyadenylated ribonucleotides to a 3' end
XX of the mRNA molecule; and (2) determining a level or pattern of a
XX molecule in a bovine cell or tissue comprising: (a) incubating a marker
XX complement or fragment with a complementary nucleic acid molecule
XX obtained from the bovine cell or tissue, where hybridization between the
XX marker nucleic acid and the complementary nucleic acid permits the
XX detection of the molecule; and (b) detecting the level or pattern of the
XX nucleic acid is predictive of the level or pattern of the molecule.
XX The LMPD nucleic acid is used for determining a level or pattern
XX of a molecule in a bovine cell or tissue. It is useful for genome

```

```

CC mapping, gene identification and analysis, cattle breeding, preparation
CC of constructs for use in cattle gene expression, or for genotyping
CC of cattle and sheep, and for the identification of the 15112 bovine
CC LMPD EST sequences and the corresponding nucleic acids.
CC Note: The present sequence was not shown in the specification but
CC was obtained in electronic format from the USPTO web site:
CC seqdata.uspto.gov/sequence.html?docId=20020137139.
XX
XX Sequence 480 BP; 97 AC; 108 G; 101 G; 98 T; 0 other.
XX
Alignment Scores: 3,78e-07 Length: 404
Score: 100.00 Matches: 19
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 94.74% Mismatches: 0
Query Match: 97.09% Indels: 0
Gaps: 23
US-10-000-039a-3 (1-19) x ABX42261 (1-404)
Oy 1 AspProGluPheHrCluGluProValProHsnSerIleGlyLysSerProAspSer 19
Db 184 GATCTGATGCTCACTGAGAGACGCTCTCCCACTCCATCCGCTCCGCGAGAAC 240
RESULT 12
ABX38963
ID ABX38963 standard; cDNA: 433 BP.
AC ABX38963;
XX
XX 20-FEB-2003 (first entry)
DT 20-FEB-2003 (first entry)
DE Bovine EST associated with lactation/muscle/fat deposition #4128.
XX
XX Bovine; ss: EST; expressed sequence tag; lactation; LMPD;
XX muscle deposition; fat deposition; genome mapping; gene identification;
XX gene analysis; cattle breeding.
XX
XX Bos Taurus.
XX
XX US2002137139-A1.
XX
XX 26-SEP-2002.
XX
XX 24-SEP-2001; 2001US-0960352.
XX
XX 12-JAN-1999; 99US-115707P.
XX 11-JAN-2000; 2000US-0480902.
XX
XX (BVAT//) BYATT J C.
XX (MATH//) MATHIALAGAN N.
XX (TAON//) TAO N.
XX (WARR//) WARREN W C.
XX
XX Byatt JC, Mathialagan N, Tao N, Warren WC;
XX WPI; 2003-110599/10.
XX
XX New nucleic acid associated with lactation, and muscle and fat
XX deposition, useful for genome mapping, gene identification and
XX analysis, cattle breeding, or for genetically improving cattle
XX
XX Claim 2: SEQ ID NO 4128; 245pp: English.
XX
XX The invention relates to a purified nucleic acid molecule associated with
XX lactation or muscle and fat deposition (designated LMPD), derived to a
XX second nucleic acid molecule comprising any of 15112 nucleotide
XX sequences, appearing as ABX34836-ABX49947, or complements of them.
XX Also included are: (1) a transfected cell having a nucleic acid
XX comprising an insert nucleic acid linked to the cell to cause termination of
XX transcription and addition of polyadenylated ribonucleotides to a 3' end
XX of the mRNA molecule; and (2) determining a level or pattern of a
XX molecule in a bovine cell or tissue comprising: (a) incubating a marker
XX complement or fragment with a complementary nucleic acid molecule
XX obtained from the bovine cell or tissue, where hybridization between the
XX marker nucleic acid and the complementary nucleic acid permits the
XX detection of the molecule; and (b) detecting the level or pattern of the
XX nucleic acid is predictive of the level or pattern of the molecule.
XX The LMPD nucleic acid is used for determining a level or pattern
XX of a molecule in a bovine cell or tissue. It is useful for genome

```

of the mRNA molecule; and (2) determining a level or pattern of a molecule in a bovine cell or tissue comprising: (a) incubating a marker nucleic acid with a complementary nucleic acid sequence or its complement or fragment with complementary nucleic acid sequence obtained from the bovine cell or tissue, where hybridisation between the marker nucleic acid and the complementary nucleic acid permits the detection of the marker nucleic acid; (b) determining the level or pattern of the complementary nucleic acid, where the detection of the marker nucleic acid is predictive of the level or pattern of the molecule. The LMO nucleic acid is used for determining a level or pattern of a molecule in a bovine cell or tissue. It is useful for genome mapping and for identifying genes. The LMO nucleic acid is useful for constructs for use in cattle gene expression, or for genetically improving cattle. The present sequence is one of the 15112 bovine LMO ESTs expressed sequence tag) nucleic acids. The present sequence was obtained in electronic format from the USPTO web site: seqdata.uspto.gov/sequence.html?docID=20020137139.

XX Sequence 433 BP; 107 A; 115 C; 105 G; 106 T; 0 other;

Alignment Scores: 2.51e-06 Length: 433
Pred. No.: 100.00% Matches: 18
Score: 95.00 Mismatches: 0
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 94.74% Mismatches: 0
Query Match: 97.09% Indels: 0
DB: 25 Gaps: 0

US-10-000-039A-3 (1-19) x ABX38963 (1-433)

Qy 1 AspProGluPhnHrGluGluProvalProtnSerIrrGlySerProaspSer 19
Db 184 GATCGTGGTTCACAGAGAGCGGCGCCGACGTCATCGAGCGGTCGCGGAGCG 240

RESULT 13

XX AB199409 standard; cDNA; 431 BP.

AC AB199409;

XX 07-MAY-2002 (first entry)

XX Mouse ischaemic condition related cDNA sequence SEQ ID NO:325.

XX Mouse: ischaemic; compressive ischaemia; occlusive ischaemia; vasospastic ischaemia; ischaemic condition; ischaemic disease; ss.

XX Mus musculus.

XX W02001180188-A2.

XX 22-NOV-2001.

XX 18-MAY-2001; 2001WO-IP04192.

XX 18-MAY-2000; 2000JP-0145977.

XX (UYNH-) UNIV NIEHO SCHOOL JURIDICAL PERSON.

XX Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;

XX WPI: 2002-034773/04.

XX Examining the ischaemic condition (e.g. occlusive ischaemia) by measuring expression levels of particular genes defined in the specification or by determining the expression profile of a gene group comprising these genes.

XX Claim 2: Page 893; 2690pp; English.

XX The present invention describes a method for examining ischaemic conditions, comprising measuring the expression levels of particular

CC genes (1) in a test sample or determining the expression profile of a gene group in the sample comprising genes selected from (1). The method is useful for examining the ischaemic condition (e.g. compressive ischaemia, occlusive ischaemia, vasospastic ischaemia, ischaemic condition, ischaemic disease) expression levels of particular genes (AB199409 to AB199912) surrounding the protein sequences in AB57020 to AB57374) or by determining the expression profile of a gene group comprising these genes. The genes are used as an indicator when screening for ischaemic condition improving drugs or therapeutics for ischaemic diseases. AB199913 and AB199914 CC represent PCR primers for a mouse ischaemic condition related sequence, which are used in the present invention.

XX Sequence 431 BP; 75 A; 128 G; 115 G; 111 T; 2 other;

Alignment Scores: 2.51e-06 Length: 431
Pred. No.: 100.00% Matches: 17
Score: 95.00 Mismatches: 2
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 89.47% Mismatches: 0
DB: 24 Gaps: 0

US-10-000-039A-3 (1-19) x AB199409 (1-431)

Qy 1 AspProGluPhnHrGluGluProvalProtnSerIrrGlySerProaspSer 19
Db 15 GATCCGAGGTTTACCGAGAGCGGCGCCGACGTCATCGAGCGGTCGCGGAGCG 71

RESULT 14

XX AAA45592

ID AAA45592 standard; DNA; 2365 BP.

XX ABM46592;

XX 25-SEP-2000 (first entry)

XX DNA encoding a rat serum and glucocorticoid induced protein kinase.

XX Protein kinase; Pkl1; Pkl2; Ypk1; Yrk2; protein kinase B-alpha;

XX serum and glucocorticoid induced protein kinase; SGK; Ikbeta;

XX 3-phosphoinositide-dependent protein kinase-1; PKI; fungal infection;

XX tumor; cancer; diabetes; obesity; antifungal; Candida infection; ss.

XX Rattus sp.

XX Key

XX CDS

XX Location/Qualifiers

XX 1..288 a

XX /product= "serum and glucocorticoid induced protein

XX kinase (SGK)"

XX /transcript= "SGK"

XX /note= "The codon encoding Met at position 1 and

XX Pro at position 318 are not given"

XX W0200036135-A2.

XX 22-JUN-2000.

XX 14-DEC-1999; 99WO-0804228.

XX 14-DEC-1998; 98US-0112114.

XX (NBI-) MEDICAL RES COUNCIL.

XX (NBI-) UNIV CALIFORNIA.

XX Thorne JW, Alessi DR, Torrance PD, Casamayor A;

XX WPI: 2000-442301/38.

XX P-PSDB; MAY9550.

XX Screening method identifying compounds which modulate protein kinase activity for use in treating fungal infections and cancer.

[illegible]

GenCore version 5.1.6
Copyright (C) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: August 11, 2003, 08:24:50 ; Search time 532 Seconds

(410000 alignments)
161.958 Million cell updates/sec

Title: US-10-000-039A-3

Perfect score: 103

Sequence: 1 DRETFEEP/PNSIGSPRS 19

Scoring table:
BLOSUM62
Xgapop 10.0, Xgapext 0.5
Xgapop 6.0, Xgapext 0.5
Ygapop 6.0, Ygapext 7.0
Delop 6.0, Delxet 7.0

Searched: 288871 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DP seq length: 0

Maximum DP seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Displaying first 15 summaries

Command line parameters:
-MODEL=frame_plus_p2n_model
-DP=GenEmul -OPW=fastap -SUFFIX=rgs -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITIS-bits -START=1 -END=1 -MATRIX=BLOSUM62 -TRANS=human40.col -LIST=45
-DOCLIGN=200 -THR_SCORE=PCP -HRC=MAX=100 -HRC=MIN=PM -ALIGN=100 -MODE=LOCAL
-USER=US100000039_0CGM_1.1.5569 -runat.01082003.08518.27511 -NCPU=6 -ICPU=3
-NO_MAP -LANGQUERY -NEG_SCORES=0 -WATP -DESPLOCK=100 -XGAPEXT=0.5 -FGAPOP=6
-DESPLOCK=100 -WARM_SWEEP=0 -WARM_SWEEP=0 -WARM_SWEEP=0 -WARM_SWEEP=0
-FOLDEN=7 -FOLDOP=10 -FOLDEXT=0.5 -FOLDOP=6 -DELXET=7

Database :

GenEmul:

1: gb-ba:

2: gb-ba:

3: gb-ba:

4: gb-ba:

5: gb-ba:

6: gb-ba:

7: gb-ba:

8: gb-pl:

9: gb-pr:

10: gb-pr:

11: gb-sts:

12: gb-sts:

13: gb-sts:

14: gb-sts:

15: gb-ba:

16: gb-ba:

17: gb-ba:

18: gb-ba:

19: gb-ba:

20: gb-ba:

21: gb-ba:

22: gb-ba:

23: gb-ba:

24: gb-ba:

25: gb-ba:

26: gb-ba:

27: gb-ba:

28: gb-ba:

pred. no. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	FW	ID	Description
1	103	100.0	1296	6	AX056374	Sequence
2	103	100.0	2281	6	AX017284	Sequence
3	103	100.0	2281	6	AX017284	Sequence
4	103	100.0	2281	6	AX017284	Sequence
5	103	100.0	2311	6	AX017284	Sequence
6	103	100.0	2311	6	AX017284	Sequence
7	103	100.0	2311	6	AX017284	Sequence
8	103	100.0	2311	6	AX017284	Sequence
9	103	100.0	2311	6	AX017284	Sequence
10	103	100.0	2311	6	AX017284	Sequence
11	103	100.0	2311	6	AX017284	Sequence
12	103	100.0	2311	6	AX017284	Sequence
13	103	100.0	2311	6	AX017284	Sequence
14	103	100.0	2311	6	AX017284	Sequence
15	103	100.0	2311	6	AX017284	Sequence
16	103	100.0	2311	6	AX017284	Sequence
17	103	100.0	2311	6	AX017284	Sequence
18	103	100.0	2311	6	AX017284	Sequence
19	103	100.0	2311	6	AX017284	Sequence
20	103	100.0	2311	6	AX017284	Sequence
21	99	96.1	1417	5	AX057138	Sequence
22	97	94.2	2470	5	SAC223715	Sequence
23	97	94.2	3105	5	SAC223716	Sequence
24	97	94.2	3105	5	SAC223716	Sequence
25	95	92.2	1659	10	BC002222	Mus muscu
26	95	92.2	1920	4	AF139639	Oryctolag
27	95	92.2	2423	10	BC005720	Mus muscu
28	95	92.2	2423	10	BC005720	Mus muscu
29	95	92.2	2423	10	AF139638	Mus muscu
30	95	92.2	2423	6	AX056375	Sequence
31	95	92.2	2423	10	AF139638	Mus muscu
32	95	92.2	2423	10	AF139638	Mus muscu
33	95	92.2	2423	10	AF139638	Mus muscu
34	95	92.2	2423	10	AF139638	Mus muscu
35	95	92.2	2423	10	AF139638	Mus muscu
36	95	92.2	2423	10	AF139638	Mus muscu
37	92	89.3	2139	5	BC032831	Danio rer
38	92	89.3	180682	2	BC032831	Danio rer
39	66	64.1	151	4	AF317416	Canis fam
40	66	64.1	151	4	AF317416	Canis fam
41	64	62.1	18116	10	AX056476	Sequence
42	64	62.1	1812	6	AX056472	Sequence
43	64	62.1	1812	6	AX056472	Sequence
44	64	62.1	1812	9	AF190434	Homo sapi
45	64	62.1	1812	9	AF190434	Homo sapi

ALIGNMENTS

RESULT 1

AUTHORS	Au-Young, J. and Seilheimer, J.J.
TITLE	Composition for the detection of signaling pathway gene expression

LOCUS AK53549 2364 bp DNA linear PAT 27-NOV-2002
 DEFINITION Sequence 1 from Patent WO02014397.
 ACCESSION AK53549
 VERSION AK53549.1 GI:25997549
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Lang, F., Busjahn, A. and Luft, F. C.

TITLE Quantitative diagnostic analysis of hypertension

JOURNAL Lancet. 367:207-211, 26-Sep-2002;
 Lang, Florian (DE)

FEATURES Location/Qualifiers
 1..2354 /db_xref="taxon:9606"
 /db_type="genomic DNA"
 43..1338 /db_xref="taxon:9606"

CDS
 /codon_start=1
 /protein_id="CAD93123.1"

/db_xref="GI:25997549" /protein_id="CAD93123.1"
 NYTAKGSPKSPVQKLSQPOPELNAKQVPPSPQNLGSPNSHPAKSPQHPLEK
 VTIGSGFKVQKLVYQVINGEELVLORECELEPPRPARYDAISALQILHSLSLI
 GLHSTQAKLVYQVINGEELVLORECELEPPRPARYDAISALQILHSLSLI
 TDMKGLKLVYQVINGEELVLORECELEPPRPARYDAISALQILHSLSLI
 TDMKGLKLVYQVINGEELVLORECELEPPRPARYDAISALQILHSLSLI
 PPRNSIGKSPQVQVATSKVKEAEAFGFSYAPTPQSL
 /note="1. SNP (C in T), stumme Mutation, d.h. beide Versionen des SNPs resultieren in der AMINO ACID Asp in der AMINO ACID-Position 240"

variation
 /note="1. SNP (C in T), stumme Mutation, d.h. beide Versionen des SNPs resultieren in der AMINO ACID Asp in der AMINO ACID-Position 240"

BASE COUNT 613 a 513 c 710 t

Alignment Scores:
 Pred. No.: 1
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 100.00%
 Mismatches: 0
 Gaps: 0

US-10-000-039a-3 (1-19) x AK53549 (1-2354)
 OY 1 AsprcgluphethrclgluprovalprohnserrilcllysserProAspser 19
 DB 1198 GACCCGAGTACCGAGNACCTGTCCCNACTCCATGCGACGACCTCCGACGC 1354

RESULT 9
 LOCUS AK53549 2364 bp mRNA linear PRI 15-JUL-2002

DEFINITION Sequence 1 from Patent WO02014397. Highly similar to

SPR-PROTEIN-PROTEIN KINASE SRN (EC 2.7.1.1).

ACCESSION AK98509

VERSION AK98509.1 GI:2758535

KEYWORDS oligo cloning; fis (full insert sequence).

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Ishibashi, T., Kanehori, K., Yoshida, M., Matsunaga, S., Ishida, S.,

Ono, Y., Hotta, T., Hirokawa, S., Murakawa, K., Takiguchi, S.,

Kusano, J., Watanabe, M., Fujimori, K., Tanaka, H., Ishida, M.,

Kanashita, H., Kubota, Y., Sugita, T., Matsuda, T., Nakagawa, K., Miura, S.,

Nishikawa, T., Sugiyama, A., Kawakami, B., Nagai, K., Isoqeli, T. and Sugano, S.

TITLE NEDO human cDNA sequencing project

REFERENCE 2 (bases 1 to 2364)

AUTHORS Sugano, S. and Suzuki, Y.

JOURNAL NEDO human cDNA sequencing project supported by Ministry of

Health, Labour and Welfare, Japan (1998-2002)

TITLE NEDO human cDNA sequencing project supported by Ministry of

Health, Labour and Welfare, Japan (1998-2002)

JOURNAL NEDO human cDNA sequencing project supported by Ministry of

Health, Labour and Welfare, Japan (1998-2002)

FEATURES Location/Qualifiers
 1..2364 /db_xref="taxon:9606"
 /db_type="genomic DNA"

CDS
 /codon_start=1
 /protein_id="CAD93123.1"

/db_xref="GI:25997549" /protein_id="CAD93123.1"
 NYTAKGSPKSPVQKLSQPOPELNAKQVPPSPQNLGSPNSHPAKSPQHPLEK
 VTIGSGFKVQKLVYQVINGEELVLORECELEPPRPARYDAISALQILHSLSLI
 GLHSTQAKLVYQVINGEELVLORECELEPPRPARYDAISALQILHSLSLI
 TDMKGLKLVYQVINGEELVLORECELEPPRPARYDAISALQILHSLSLI
 TDMKGLKLVYQVINGEELVLORECELEPPRPARYDAISALQILHSLSLI
 PPRNSIGKSPQVQVATSKVKEAEAFGFSYAPTPQSL
 /note="1. SNP (C in T), stumme Mutation, d.h. beide Versionen des SNPs resultieren in der AMINO ACID Asp in der AMINO ACID-Position 240"

variation
 /note="1. SNP (C in T), stumme Mutation, d.h. beide Versionen des SNPs resultieren in der AMINO ACID Asp in der AMINO ACID-Position 240"

BASE COUNT 613 a 524 c 517 g 708 t

Alignment Scores:
 Pred. No.: 1
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 100.00%
 Mismatches: 0
 Gaps: 0

US-10-000-039a-3 (1-19) x AK98509 (1-2364)
 OY 1 AsprcgluphethrclgluprovalprohnserrilcllysserProAspser 19
 DB 1213 GACCCGAGTACCGAGNACCTGTCCCNACTCCATGCGACGACCTCCGACGC 1369

RESULT 10
 LOCUS AK98509 2370 bp DNA linear PAT 20-APR-2002

DEFINITION Sequence 1 from patent US 6,126,181.

ACCESSION AK98509

VERSION AK98509.1 GI:2020996

KEYWORDS Cell volume-regulated human kinase h-sk

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE Unclassified

AUTHORS Lang, F. and Waldegger, S.

TITLE Cell volume-regulated human kinase h-sk

JOURNAL Patent: US 6,126,181-A1 (04-Dec-2001);

FEATSEQ 1..2370 /db_xref="taxon:9606"

BASE COUNT 636 a 517 c 513 g 704 t

Alignment Scores:
 Pred. No.: 1
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 100.00%
 Mismatches: 0
 Gaps: 0

US-10-000-039a-3 (1-19) x AK98509 (1-2370)

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 11, 2003, 08:19:59 : Search time 0.86696 Seconds
(without alignments)
424.584 Million cell updates/sec

Title: US-10-000-039a-3

Perfect score: 103

Sequence: 1 DPEFTPEPPNKGSPDS 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 98705 seqs. 20044758 residues

Total number of hits satisfying chosen parameters: 98705

Maximum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%

Listing first 45 summaries

Database :

Pending_Patents_Ab_News*
1: /cgn2_5/pdata1/paa/US06_NEK_COMB_Pep.*
2: /cgn2_5/pdata1/paa/US06_NEK_COMB_Pep.*
3: /cgn2_5/pdata1/paa/US07_NEK_COMB_Pep.*
4: /cgn2_5/pdata1/paa/US07_NEK_COMB_Pep.*
5: /cgn2_5/pdata1/paa/US08_NEK_COMB_Pep.*
6: /cgn2_5/pdata1/paa/US10_NEK_COMB_Pep.*
7: /cgn2_5/pdata1/paa/US10_NEK_COMB_Pep.*

Proc. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	103	100.0	19	6	US-10-000-039a-3
2	103	100.0	431	1	PCT-US03-10142-2
3	103	100.0	431	1	US-10-000-039a-3
4	103	100.0	431	1	US-10-000-039a-3
5	64	62.1	367	6	US-10-293-177-256
6	46	44.7	414	6	US-10-603-113-1403
7	45	43.7	1706	6	US-10-293-244-5922
8	45	43.7	1706	6	US-10-293-244-5922
9	44	42.7	496	6	US-10-286-897-1979
10	44	42.7	496	6	US-10-286-897-1979
11	44	42.7	496	6	US-10-286-897-1979
12	44	42.7	1122	6	US-10-408-765a-1005
13	44	42.7	1122	6	US-10-408-765a-1005
14	43	42.7	464	6	US-10-408-765a-2991
15	43	42.7	464	6	US-10-408-765a-2991
16	43	42.7	464	6	US-10-408-765a-2991
17	42	40.8	184	6	US-10-408-765a-394
18	42	40.8	184	6	US-10-408-765a-394
19	42	40.8	228	6	US-10-613-520-1597
20	42	40.8	464	6	US-10-394-222a-13
21	41.5	40.8	464	6	US-10-394-222a-13
22	41	39.8	331	6	PCT-US03-29210-188
23	41	39.8	331	6	PCT-US03-29210-188
24	40.5	39.3	344	6	US-10-408-765a-354
25	40.5	39.3	344	6	US-10-408-765a-354
26	40.5	39.3	1130	6	US-10-326-956-2263

27 40.5 39.3 1259 7 US-60-485-450-1063
28 40.5 39.3 1259 7 US-60-485-450-1063
29 40 38.8 219 6 US-10-408-765a-1366
30 40 38.8 308 6 US-10-603-113-14349
31 40 38.8 416 6 US-10-286-897-2715
32 40 38.8 416 6 US-10-286-897-2715
33 40 38.8 670 7 US-60-485-450-973
34 40 38.8 725 6 US-10-408-765a-102
35 40 38.8 913 6 US-10-286-897-2238
36 40 38.8 913 6 US-10-286-897-2238
37 40 38.8 1121 7 US-60-485-450-972
38 40 38.8 1203 6 US-10-273-573-10232
39 40 38.8 1209 6 US-10-408-765a-1044
40 38.8 1684 6 US-10-293-244-3225
41 40 38.8 1684 6 US-10-293-244-3225
42 40 38.8 3273 6 US-10-293-244-1257
43 40 38.8 3273 6 US-10-293-244-1257
44 40 38.8 3273 6 US-10-293-244-1257
45 39.5 38.3 407 6 US-10-286-897-2760

ALIGNMENTS

RESULT 1
US-10-000-039a-3

Sequence 3 Application US/10000039A

GENERAL INFORMATION:

APPLICANT: LANG, Florian

TITLE OF INVENTION: CELL VOLUME-REGULATED HUMAN KINASE H-NSK

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: FOLEY & LAMMER

ADDRESS: 10000039A

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

SOFTWARE: PASCAL RELEASE #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10-000-039A

CLASSIFICATION: <unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/031,295

APPLICATION NUMBER: DR 157-08-173.8

FILING DATE: 28-FEB-1997

ATTORNEY/AGENT INFORMATION:

REGISTRATION NUMBER: 31,298

REFERENCE/DOCKET NUMBER: 058315/0123

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 672-5300

TELEFAX: (202) 672-5339

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 19 amino acids

STRANDEDNESS: <unknown>

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-10-000-039a-3

Query Match 100.0% Score 103; DB 6; Length 19;
Best Local Similarity 100.0%; NC-14.3e-10;
Matches 15; Conservativeness 0; Mismatches 0; Gaps 0;

```

OY      1 DPEETEEPVNSIGNSPDS 19
DB      1 DPEETEEPVNSIGNSPDS 19

RESULT 2
PCT-US03-10142-2
1 Sequence 2, Application PC/TU03010142
2 GENERAL INFORMATION: Corporation, et al.
3 TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
4 FILE REFERENCE: 21402-573C
5 CURRENT APPLICATION NUMBER: 06/070349
6 PRIOR APPLICATION NUMBER: 60/370349
7 PRIOR FILING DATE: 2002-04-05
8 PRIOR APPLICATION NUMBER: 60/284543
9 PRIOR FILING DATE: 2002-04-08
10 PRIOR APPLICATION NUMBER: 60/370969
11 PRIOR FILING DATE: 2002-04-08
12 PRIOR APPLICATION NUMBER: 60/03746
13 PRIOR FILING DATE: 2002-06-15
14 PRIOR APPLICATION NUMBER: 60/372019
15 PRIOR FILING DATE: 2002-04-12
16 PRIOR APPLICATION NUMBER: 60/374379
17 PRIOR FILING DATE: 2002-04-22
18 PRIOR APPLICATION NUMBER: 05/779679
19 PRIOR FILING DATE: 2001-02-08
20 PRIOR APPLICATION NUMBER: 60/81045
21 PRIOR FILING DATE: 2001-02-08
22 PRIOR APPLICATION NUMBER: 10/055877
23 PRIOR FILING DATE: 2002-01-22
24 PRIOR APPLICATION NUMBER: 60/262892
25 Remaining Prior Application data removed - See File Wrapper or PALM.
26 NUMBER OF SEQ ID NOS: 173
27 SOFTWARE: CutsseqList version 0.1
28 SEQ ID NO: 1
29 TYPE: PNT
30 ORGANISM: Homo sapiens
31 PCT-US03-10142-2

Query Match      100.0%; Score 103; DB 1; Length 431;
Best Local Similarity 100.0%; Pred. No. 1,4e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 DPEETEEPVNSIGNSPDS 19
DB      386 DPEETEEPVNSIGNSPDS 404

RESULT 3
PCT-US03-10142-2
1 Sequence 3, Application PC/TU03010142
2 GENERAL INFORMATION: Corporation, et al.
3 TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
4 FILE REFERENCE: 21402-573C
5 CURRENT APPLICATION NUMBER: 06/070349
6 PRIOR APPLICATION NUMBER: 60/370349
7 PRIOR FILING DATE: 2002-04-05
8 PRIOR APPLICATION NUMBER: 60/284543
9 PRIOR FILING DATE: 2002-04-08
10 PRIOR APPLICATION NUMBER: 60/370969
11 PRIOR FILING DATE: 2002-04-08
12 PRIOR APPLICATION NUMBER: 60/03746
13 PRIOR FILING DATE: 2002-06-15
14 PRIOR APPLICATION NUMBER: 60/372019
15 PRIOR FILING DATE: 2002-04-12
16 PRIOR APPLICATION NUMBER: 60/374379
17 PRIOR FILING DATE: 2002-04-22
18 PRIOR APPLICATION NUMBER: 05/779679
19 PRIOR FILING DATE: 2001-02-08
20 PRIOR APPLICATION NUMBER: 60/81045
21 PRIOR FILING DATE: 2001-02-08
22 PRIOR APPLICATION NUMBER: 10/055877
23 PRIOR FILING DATE: 2002-01-22
24 PRIOR APPLICATION NUMBER: 60/262892
25 Remaining Prior Application data removed - See File Wrapper or PALM.
26 NUMBER OF SEQ ID NOS: 173
27 SOFTWARE: CutsseqList version 0.1
28 SEQ ID NO: 2
29 TYPE: PNT
30 ORGANISM: Homo sapiens
31 PCT-US03-10142-2

Query Match      100.0%; Score 103; DB 1; Length 431;
Best Local Similarity 100.0%; Pred. No. 1,4e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

1 PRIOR FILING DATE: 2002-04-22
2 PRIOR APPLICATION NUMBER: 60/779679
3 PRIOR FILING DATE: 2001-02-08
4 PRIOR APPLICATION NUMBER: 60/181045
5 PRIOR FILING DATE: 2000-02-08
6 PRIOR APPLICATION NUMBER: 60/055877
7 PRIOR FILING DATE: 2002-01-22
8 PRIOR APPLICATION NUMBER: 60/262892
9 PRIOR FILING DATE: 2001-01-19
10 PRIOR APPLICATION NUMBER: 60/03746
11 Remaining Prior Application data removed - See File Wrapper or PALM.
12 NUMBER OF SEQ ID NOS: 173
13 SOFTWARE: CutsseqList version 0.1
14 SEQ ID NO: 431
15 TYPE: PNT
16 ORGANISM: Homo sapiens
17 PCT-US03-10142-4

Query Match      100.0%; Score 103; DB 1; Length 431;
Best Local Similarity 100.0%; Pred. No. 1,4e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 DPEETEEPVNSIGNSPDS 19
DB      386 DPEETEEPVNSIGNSPDS 404

RESULT 4
US-10-000-039a-2
1 Sequence 4, Application US/10000039a
2 GENERAL INFORMATION: Corporation, et al.
3 TITLE OF INVENTION: CELL VOLUME-REGULATED HUMAN KINASE H-SOK
4 NUMBER OF SEQUENCES: 1
5 NUMBER OF SEQUENCES: 1
6 ADDRESS: POLY & LARNER
7 CORRESPONDENCE ADDRESS:
8 POLY & LARNER, 1000 K STREET, N.W.
9 CITY: Washington
10 STATE: D.C.
11 COUNTRY: U.S.A.
12 PCT-US-03-10142-4
13 COMPUTER READABLE FORM:
14 MEDIUM TYPE: Floppy disk
15 COMPUTER: IBM PC compatible
16 SOFTWARE: PLOTTER: PLOTTER
17 SOFTWARE: PLOTTER: PLOTTER
18 CURRENT APPLICATION DATA:
19 APPLICATION NUMBER: US/10/000,039a
20 FILING DATE: 28-FEB-1997
21 APPLICATION NUMBER: DB 197-08-173.8
22 FILING DATE: 28-FEB-1997
23 PRIOR APPLICATION DATA:
24 APPLICATION NUMBER: 05/09/031,295
25 FILING DATE: 28-FEB-1997
26 APPLICATION NUMBER: DB 197-08-173.8
27 FILING DATE: 28-FEB-1997
28 ATTORNEY/AGENT INFORMATION:
29 ATTORNEY/AGENT NAME: G.
30 REGISTRATION NUMBER: 31,298
31 REFERENCE/DOCKET NUMBER: 058315/0123
32 TELECOMMUNICATION INFORMATION:
33 TELEPHONE: (202) 692-5300
34 TELEFAX: (202) 692-5399
35 INFORMATION FOR SEQ ID NO: 2:
36 SEQUENCE CHARACTERISTICS:
37 LENGTH: 431 amino acids
38 TOPOLOGY: linear
39 MOLECULE TYPE: protein
40 SEQUENCE DESCRIPTION: SMO ID NO: 2;
41 US-10-000-039a-2

Query Match      100.0%; Score 103; DB 6; Length 431;

```

Best Local Similarity 100.0%, Pred. No. 1.4e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPEETPEPVNSIGKSPDS 19
DB 386 DPEETPEPVNSIGKSPDS 404

RESULT 5
US-10-231-172-256

Sequence 15403, Application US/10291172
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc
TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
FILE REFERENCE: 21272-045
CURRENT APPLICATION NUMBER: US/10/291.172
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: 09/693,267
PRIOR FILING DATE: 2000-10-29/693,363
PRIOR APPLICATION NUMBER: 09/665,363
PRIOR FILING DATE: 2000-09-19
PRIOR APPLICATION NUMBER: 09/616,847
PRIOR FILING DATE: 2000-07-09/616,847
PRIOR APPLICATION NUMBER: 09/596,193
PRIOR FILING DATE: 2000-06-17
PRIOR APPLICATION NUMBER: 09/574,454
PRIOR FILING DATE: 2000-06-17
PRIOR APPLICATION NUMBER: 09/519,705
PRIOR FILING DATE: 2000-03-07
NUMBER OF SEQ ID NOS: 752
SOFTWARE: Custom
SEQ ID NO 15403
LENGTH: 367
TYPE: PRT
ORGANISM: Homo sapiens
US-10-231-172-256

Query Match 62.1%; Score 64; DB 6; Length 367;
Best Local Similarity 63.2%; Pred. No. 0.012;
Matches 12; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 DPEETPEPVNSIGKSPDS 19
DB 323 DPEETPEPVNSIGKSPDS 341

RESULT 6
US-10-603-113-15403

Sequence 15403, Application US/10603113
GENERAL INFORMATION:
APPLICANT: Keith Weinbeck et al
TITLE OF INVENTION: AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/10/603.113
PRIOR FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US/09/248,796
PRIOR FILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 28206
SOFTWARE: Custom
SEQ ID NO 15403
LENGTH: 414
TYPE: PRT
ORGANISM: Candida albicans
US-10-603-113-15403

Query Match 44.7%; Score 46; DB 6; Length 414;
Best Local Similarity 56.2%; Pred. No. 8;
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 3 ETEETPEPVNSIGKSPD 18
DB 214 ETEETPEPVNSIGKSPD 229

RESULT 7

US-10-293-244-1932
Sequence 1932, Application US/10293244
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc
TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
FILE REFERENCE: 21272-029
CURRENT APPLICATION NUMBER: US/10/293.244
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: 09/728,422
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: 09/693,325
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 09/663,561
PRIOR FILING DATE: 2000-09-19
PRIOR APPLICATION NUMBER: 04/654,936
PRIOR FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: 09/620,325
PRIOR FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: 04/598,075
PRIOR FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: 09/560,875
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 04/496,914
PRIOR FILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 3960
SOFTWARE: Custom
SEQ ID NO 1932
LENGTH: 1706
TYPE: PRT
ORGANISM: Homo sapiens
US-10-293-244-1932

Query Match 43.7%; Score 45; DB 6; Length 1706;
Best Local Similarity 50.0%; Pred. No. 56;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 DPEETPEPVNSIG 14
DB 494 EPEETPEPVNSIG 507

RESULT 8

US-10-273-573-5843
Sequence 5843, Application US/10273573
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 21273-066
CURRENT APPLICATION NUMBER: US/10/273.573
PRIOR FILING DATE: 2002-10-18
PRIOR APPLICATION NUMBER: 09/522,929
PRIOR FILING DATE: 2000-04-16
PRIOR APPLICATION NUMBER: 09/770,160
PRIOR FILING DATE: 2001-01-26
NUMBER OF SEQ ID NOS: 10594
SOFTWARE: Custom
SEQ ID NO 5843
LENGTH: 468
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (4)...(30)
OTHER INFORMATION: Trubshaw domain identified by pfam. Accession name US-10-273-573-5843
Trubshaw, E-value=0.066, PFAM score of 9.3
US-10-273-573-5843

Query Match 43.7%; Score 44; DB 6; Length 468;
Best Local Similarity 49.1%; Pred. No. 19;

DB 3936 NPE--EEPLPNYDKSLD 3951
 ||| ||||| |||

RESULT 13
 US-10-408-765A-2991
 : Sequence 2991, Application US/10408765A
 : GENERAL INFORMATION:
 : APPLICANT: Ghosh, Soumitra S.
 : APPLICANT: Ghosh, Soumitra S.
 : APPLICANT: Zhang, Bing
 : APPLICANT: Gibson, Bradford W.
 : APPLICANT: Taylor, Steven W.
 : APPLICANT: Gibson, Bradford W.
 : APPLICANT: Warlock, Dale E.
 : TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
 : TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
 : CURRENT APPLICATION NUMBER: US/10/408,765A
 : CURRENT FILING DATE: 2003-04-04
 : NUMBER OF SEQ ID NOS: 3077
 : SEQUENCE VERSION: 1.0
 : SEQ ID NO 394
 : LENGTH: 4624
 : TYPE: PRT Homo sapiens
 : US-10-408-765A-2991

Query Match 42.7%; Score 44; DB 6; Length 4624;
 Best Local Similarity 53.3%; Pred. No. 41;
 Matches 10; Conservative 3; Mismatches 3; Indels 2; Gaps 1;
 QY 1 DPETEEVPVNSIGKSPD 18
 ||| ||||| |||
 DB 3977 NPE--EEPLPNYDKSLD 3992

RESULT 14
 US-10-326-956-2353
 : Sequence 2353, Application US/10326956
 : GENERAL INFORMATION:
 : APPLICANT: Ghosh, Soumitra S.
 : TITLE OF INVENTION: Protein Complexes and Methods for their Use
 : FILE REFERENCE: 220615
 : CURRENT APPLICATION NUMBER: US/10/326,956
 : CURRENT FILING DATE: 2001-12-20
 : PRIOR APPLICATION NUMBER: US/01/320,253.6
 : PRIOR FILING DATE: 2001-12-20
 : NUMBER OF SEQ ID NOS: 3282
 : SEQUENCE VERSION: 1.0
 : SEQ ID NO 233
 : LENGTH: 687
 : TYPE: PRT Saccharomyces cerevisiae
 : ORGANISM: Saccharomyces cerevisiae
 : US-10-326-956-2353

Query Match 41.7%; Score 43; DB 6; Length 687;
 Best Local Similarity 53.3%; Pred. No. 41;
 Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 QY 5 TEPEVPVNSIGKSPDS 19
 ||||| |||
 DB 43 SDPEVPFSAAGAROTS 57

RESULT 15
 US-10-408-765A-394
 : Sequence 394, Application US/10408765A
 : GENERAL INFORMATION:
 : APPLICANT: Ghosh, Soumitra S.
 : APPLICANT: Zhai, Esia D.
 : APPLICANT: Taylor, Steven W.
 : APPLICANT: Gibson, Bradford W.

APPLICANT: Taylor, Steven W.
 APPLICANT: Ghosh, Soumitra S.
 APPLICANT: Warlock, Dale E.
 : TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
 : TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
 : CURRENT APPLICATION NUMBER: US/10/408,765A
 : CURRENT FILING DATE: 2003-04-04
 : NUMBER OF SEQ ID NOS: 3077
 : SEQUENCE VERSION: 1.0
 : SEQ ID NO 394
 : LENGTH: 713
 : TYPE: PRT Homo sapiens
 : US-10-408-765A-394

Query Match 41.7%; Score 43; DB 6; Length 713;
 Best Local Similarity 53.3%; Pred. No. 41;
 Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 QY 2 PFTTEEPVPSNGKSPDS 19
 ||||| |||
 DB 148 PENOQTFPRDQVNVDS 165

Search completed: August 11, 2003, 08:36:28
 Job time: 1.097 secs

Copy-right (C) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on:

August 11, 2003, 08:19:00 : search time 26.706 seconds
(without alignments)
637,216 Million cell updates/sec

Title: US-10-000-039a-3

Perfect score: 103

Sequence: 1 DPTFTFFPNKSGKSPDS 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 5580241 seqs, 870357830 residues

Total number of hits satisfying chosen parameters: 5580241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Minimum Match 100%

Listing first 45 summaries

Database : Pending statistics 00 bytes +

1:	/cgn2_5/ptodata1/paa/US06_COMB.pep.*
2:	/cgn2_5/ptodata1/paa/US07_COMB.pep.*
3:	/cgn2_5/ptodata1/paa/US08_COMB.pep.*
4:	/cgn2_5/ptodata1/paa/US09_COMB.pep.*
5:	/cgn2_5/ptodata1/paa/US10_COMB.pep.*
6:	/cgn2_5/ptodata1/paa/US082_COMB.pep.*
7:	/cgn2_5/ptodata1/paa/US083_COMB.pep.*
8:	/cgn2_5/ptodata1/paa/US084_COMB.pep.*
9:	/cgn2_5/ptodata1/paa/US085_COMB.pep.*
10:	/cgn2_5/ptodata1/paa/US086_COMB.pep.*
11:	/cgn2_5/ptodata1/paa/US087_COMB.pep.*
12:	/cgn2_5/ptodata1/paa/US088_COMB.pep.*
13:	/cgn2_5/ptodata1/paa/US089_COMB.pep.*
14:	/cgn2_5/ptodata1/paa/US090_COMB.pep.*
15:	/cgn2_5/ptodata1/paa/US091_COMB.pep.*
16:	/cgn2_5/ptodata1/paa/US092_COMB.pep.*
17:	/cgn2_5/ptodata1/paa/US093_COMB.pep.*
18:	/cgn2_5/ptodata1/paa/US094_COMB.pep.*
19:	/cgn2_5/ptodata1/paa/US095_COMB.pep.*
20:	/cgn2_5/ptodata1/paa/US096_COMB.pep.*
21:	/cgn2_5/ptodata1/paa/US097_COMB.pep.*
22:	/cgn2_5/ptodata1/paa/US098_COMB.pep.*
23:	/cgn2_5/ptodata1/paa/US099_COMB.pep.*
24:	/cgn2_5/ptodata1/paa/US100_COMB.pep.*
25:	/cgn2_5/ptodata1/paa/US101_COMB.pep.*
26:	/cgn2_5/ptodata1/paa/US102_COMB.pep.*
27:	/cgn2_5/ptodata1/paa/US103_COMB.pep.*
28:	/cgn2_5/ptodata1/paa/US104_COMB.pep.*
29:	/cgn2_5/ptodata1/paa/US105_COMB.pep.*
30:	/cgn2_5/ptodata1/paa/US106_COMB.pep.*
31:	/cgn2_5/ptodata1/paa/US107_COMB.pep.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	DB ID	Description
1	103	100.0	19	26 US-10-000-039-3
2	103	100.0	82	24 US-09-937-009a-18
				Sequence 1, Appl
				Sequence 2, Appl
				Sequence 3, Appl
				Sequence 4, Appl
				Sequence 5, Appl
				Sequence 6, Appl
				Sequence 7, Appl
				Sequence 8, Appl
				Sequence 9, Appl
				Sequence 10, Appl
				Sequence 11, Appl
				Sequence 12, Appl
				Sequence 13, Appl
				Sequence 14, Appl
				Sequence 15, Appl
				Sequence 16, Appl
				Sequence 17, Appl
				Sequence 18, Appl
				Sequence 19, Appl
				Sequence 20, Appl
				Sequence 21, Appl
				Sequence 22, Appl
				Sequence 23, Appl
				Sequence 24, Appl
				Sequence 25, Appl
				Sequence 26, Appl
				Sequence 27, Appl
				Sequence 28, Appl
				Sequence 29, Appl
				Sequence 30, Appl
				Sequence 31, Appl
				Sequence 32, Appl
				Sequence 33, Appl
				Sequence 34, Appl
				Sequence 35, Appl
				Sequence 36, Appl
				Sequence 37, Appl
				Sequence 38, Appl
				Sequence 39, Appl
				Sequence 40, Appl
				Sequence 41, Appl
				Sequence 42, Appl
				Sequence 43, Appl
				Sequence 44, Appl
				Sequence 45, Appl
				Sequence 46, Appl
				Sequence 47, Appl
				Sequence 48, Appl
				Sequence 49, Appl
				Sequence 50, Appl
				Sequence 51, Appl
				Sequence 52, Appl
				Sequence 53, Appl
				Sequence 54, Appl
				Sequence 55, Appl
				Sequence 56, Appl
				Sequence 57, Appl
				Sequence 58, Appl
				Sequence 59, Appl
				Sequence 60, Appl
				Sequence 61, Appl
				Sequence 62, Appl
				Sequence 63, Appl
				Sequence 64, Appl
				Sequence 65, Appl
				Sequence 66, Appl
				Sequence 67, Appl
				Sequence 68, Appl
				Sequence 69, Appl
				Sequence 70, Appl
				Sequence 71, Appl
				Sequence 72, Appl
				Sequence 73, Appl
				Sequence 74, Appl
				Sequence 75, Appl
				Sequence 76, Appl
				Sequence 77, Appl
				Sequence 78, Appl
				Sequence 79, Appl
				Sequence 80, Appl
				Sequence 81, Appl
				Sequence 82, Appl
				Sequence 83, Appl
				Sequence 84, Appl
				Sequence 85, Appl
				Sequence 86, Appl
				Sequence 87, Appl
				Sequence 88, Appl
				Sequence 89, Appl
				Sequence 90, Appl
				Sequence 91, Appl
				Sequence 92, Appl
				Sequence 93, Appl
				Sequence 94, Appl
				Sequence 95, Appl
				Sequence 96, Appl
				Sequence 97, Appl
				Sequence 98, Appl
				Sequence 99, Appl
				Sequence 100, Appl

ALIGNMENTS

RESULT 1

US-10-000-039-3
Sequence 1, Appl
GENERAL INFORMATION US/1000039
APPLICANT: LANG, Florian
TITLE OF INVENTION: HUMAN KINASE H-SCK
INVENTOR: MALDENBERG, Tubingen
NUMBER OF SOURCES: 1
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESS: POLEY & LAHONER
C/O: 1000 N. Street, N.W.
CITY: Washington
STATE: D. C.
COUNTRY: U.S.A.
E-MAIL: 20009-5109
COMPUTER: IBM PC compatible
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION NUMBER: US/10/000-039
FILING DATE: 04-Dec-2001
PRIORITY INFORMATION: UNKNOWN
PRIOR APPLICATION DATA:

3	103	100.0	340	US-10-217-155a-17
4	103	100.0	340	US-10-217-555-17
5	103	100.0	340	US-10-217-555a-17
6	103	100.0	340	US-10-217-555a-17
7	103	100.0	340	US-10-217-555a-17
8	103	100.0	340	US-10-217-555a-17
9	103	100.0	340	US-10-217-555a-17
10	103	100.0	340	US-10-217-555a-17
11	103	100.0	340	US-10-217-555a-17
12	103	100.0	340	US-10-217-555a-17
13	103	100.0	340	US-10-217-555a-17
14	103	100.0	340	US-10-217-555a-17
15	103	100.0	340	US-10-217-555a-17
16	103	100.0	340	US-10-217-555a-17
17	103	100.0	340	US-10-217-555a-17
18	103	100.0	340	US-10-217-555a-17
19	103	100.0	340	US-10-217-555a-17
20	103	100.0	340	US-10-217-555a-17
21	103	100.0	340	US-10-217-555a-17
22	103	100.0	340	US-10-217-555a-17
23	103	100.0	340	US-10-217-555a-17
24	103	100.0	340	US-10-217-555a-17
25	103	100.0	340	US-10-217-555a-17
26	103	100.0	340	US-10-217-555a-17
27	103	100.0	340	US-10-217-555a-17
28	103	100.0	340	US-10-217-555a-17
29	103	100.0	340	US-10-217-555a-17
30	103	100.0	340	US-10-217-555a-17
31	103	100.0	340	US-10-217-555a-17
32	103	100.0	340	US-10-217-555a-17
33	103	100.0	340	US-10-217-555a-17
34	103	100.0	340	US-10-217-555a-17
35	103	100.0	340	US-10-217-555a-17
36	103	100.0	340	US-10-217-555a-17
37	103	100.0	340	US-10-217-555a-17
38	97	94.2	433	US-09-791-537-26034
39	97	94.2	433	US-09-791-537-64803
40	97	94.2	433	US-09-791-537-64803
41	95	92.2	433	US-09-791-537-64803
42	95	92.2	433	US-09-791-537-64803
43	95	92.2	433	US-09-791-537-64803
44	95	92.2	433	US-09-791-537-64803
45	64	62.1	52	31 US-09-162-245-2469

APPLICANT: Yang, Jing

; GENERAL
; APPLIC

! GENERAL INFORMATION:
; APPLICANT: Barford, David

PRIOR APPLICATION NUMBER: 00/216,290
 PRIOR FILING DATE: 2000-07-14
 PRIOR APPLICATION NUMBER: 00/225,757
 PRIOR FILING DATE: 2000-08-14
 PRIOR APPLICATION NUMBER: 00/236,868
 PRIOR FILING DATE: 2000-08-22
 PRIOR APPLICATION NUMBER: 00/216,647
 PRIOR FILING DATE: 2000-07-07

PRIOR APPLICATION NUMBER: 60/216,880
 PRIOR FILING DATE: 2000-07-07
 PRIOR APPLICATION NUMBER: 60/225,270
 PRIOR FILING DATE: 2000-08-14
 PRIOR APPLICATION NUMBER: 60/231,869
 PRIOR FILING DATE: 2000-12-06
 PRIOR APPLICATION NUMBER: 60/235,834
 PRIOR FILING DATE: 2000-09-27
 PRIOR APPLICATION NUMBER: 60/234,274

PRIOR APPLICATION NUMBER: 60/234,223
 PRIOR FILING DATE: 2000-09-21
 PRIOR APPLICATION NUMBER: 60/228,924
 PRIOR FILING DATE: 2000-08-14
 PRIOR APPLICATION NUMBER: 60/234,518
 PRIOR FILING DATE: 2000-08-14
 PRIOR APPLICATION NUMBER: 60/216,369
 PRIOR FILING DATE: 2000-09-29
 PRIOR APPLICATION NUMBER: 60/234,519
 PRIOR FILING DATE: 2000-08-14

;; PRIOR APPLICATION NUMBER: 60/241,809
;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/249,299
;; PRIOR FILING DATE: 2000-11-17
;; PRIOR APPLICATION NUMBER: 60/236,327
;; PRIOR FILING DATE: 2000-06-26

PRIOR APPLICATION NUMBER: 60/241,785
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/244,617
PRIOR FILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 60/225,268
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/236,368
PRIOR FILING DATE: 2000-09-29

;; PRIOR FILING DATE: 2000-12-08
;; PRIOR APPLICATION NUMBER: 60/251,868
;; PRIOR FILING DATE: 2000-12-08
;; PRIOR APPLICATION NUMBER: 60/229,344

;; PRIOR APPLICATION NUMBER: 60/251,868
;; PRIOR FILING DATE: 2000-12-08
;; PRIOR APPLICATION NUMBER: 60/229,344

```

1 PRIOR FILING DATE: 2000-09-01
2 PRIOR APPLICATION NUMBER: 60/234,997
3 PRIOR FILING DATE: 2000-09-01
4 PRIOR APPLICATION NUMBER: 60/229,343
5 PRIOR FILING DATE: 2000-09-01
6 PRIOR APPLICATION NUMBER: 60/229,345
7 PRIOR FILING DATE: 2000-09-01
8 PRIOR APPLICATION NUMBER: 60/229,345
9 PRIOR FILING DATE: 2000-09-01
10 PRIOR APPLICATION NUMBER: 60/229,345
11 PRIOR FILING DATE: 2000-09-01
12 PRIOR APPLICATION NUMBER: 60/229,345
13 PRIOR FILING DATE: 2000-09-01
14 PRIOR APPLICATION NUMBER: 60/229,345
15 PRIOR FILING DATE: 2000-09-01
16 PRIOR APPLICATION NUMBER: 60/229,345
17 PRIOR FILING DATE: 2000-09-01
18 PRIOR APPLICATION NUMBER: 60/229,345
19 PRIOR FILING DATE: 2000-09-01
20 PRIOR APPLICATION NUMBER: 60/229,345
21 PRIOR FILING DATE: 2000-09-01
22 PRIOR APPLICATION NUMBER: 60/229,345
23 PRIOR FILING DATE: 2000-09-01
24 PRIOR APPLICATION NUMBER: 60/229,345
25 PRIOR FILING DATE: 2000-09-01
26 PRIOR APPLICATION NUMBER: 60/229,345
27 PRIOR FILING DATE: 2000-09-01
28 PRIOR APPLICATION NUMBER: 60/229,345
29 PRIOR FILING DATE: 2000-09-01
30 PRIOR APPLICATION NUMBER: 60/229,345
31 PRIOR FILING DATE: 2000-09-01
32 PRIOR APPLICATION NUMBER: 60/229,345
33 PRIOR FILING DATE: 2000-09-01
34 PRIOR APPLICATION NUMBER: 60/229,345
35 PRIOR FILING DATE: 2000-09-01
36 PRIOR APPLICATION NUMBER: 60/229,345
37 PRIOR FILING DATE: 2000-09-01
38 PRIOR APPLICATION NUMBER: 60/229,345
39 PRIOR FILING DATE: 2000-09-01
40 PRIOR APPLICATION NUMBER: 60/229,345
41 PRIOR FILING DATE: 2000-09-01
42 PRIOR APPLICATION NUMBER: 60/229,345
43 PRIOR FILING DATE: 2000-09-01
44 PRIOR APPLICATION NUMBER: 60/229,345
45 PRIOR FILING DATE: 2000-09-01
46 PRIOR APPLICATION NUMBER: 60/229,345
47 PRIOR FILING DATE: 2000-09-01
48 PRIOR APPLICATION NUMBER: 60/229,345
49 PRIOR FILING DATE: 2000-09-01
50 PRIOR APPLICATION NUMBER: 60/229,345
51 PRIOR FILING DATE: 2000-09-01
52 PRIOR APPLICATION NUMBER: 60/229,345
53 PRIOR FILING DATE: 2000-09-01
54 PRIOR APPLICATION NUMBER: 60/229,345
55 PRIOR FILING DATE: 2000-09-01
56 PRIOR APPLICATION NUMBER: 60/229,345
57 PRIOR FILING DATE: 2000-09-01
58 PRIOR APPLICATION NUMBER: 60/229,345
59 PRIOR FILING DATE: 2000-09-01
60 PRIOR APPLICATION NUMBER: 60/229,345
61 PRIOR FILING DATE: 2000-09-01
62 PRIOR APPLICATION NUMBER: 60/229,345
63 PRIOR FILING DATE: 2000-09-01
64 PRIOR APPLICATION NUMBER: 60/229,345
65 PRIOR FILING DATE: 2000-09-01
66 PRIOR APPLICATION NUMBER: 60/229,345
67 PRIOR FILING DATE: 2000-09-01
68 PRIOR APPLICATION NUMBER: 60/229,345
69 PRIOR FILING DATE: 2000-09-01
70 PRIOR APPLICATION NUMBER: 60/229,345
71 PRIOR FILING DATE: 2000-09-01
72 PRIOR APPLICATION NUMBER: 60/229,345
73 PRIOR FILING DATE: 2000-09-01
74 PRIOR APPLICATION NUMBER: 60/229,345
75 PRIOR FILING DATE: 2000-09-01
76 PRIOR APPLICATION NUMBER: 60/229,345
77 PRIOR FILING DATE: 2000-09-01
78 PRIOR APPLICATION NUMBER: 60/229,345
79 PRIOR FILING DATE: 2000-09-01
80 PRIOR APPLICATION NUMBER: 60/229,345
81 PRIOR FILING DATE: 2000-09-01
82 PRIOR APPLICATION NUMBER: 60/229,345
83 PRIOR FILING DATE: 2000-09-01
84 PRIOR APPLICATION NUMBER: 60/229,345
85 PRIOR FILING DATE: 2000-09-01
86 PRIOR APPLICATION NUMBER: 60/229,345
87 PRIOR FILING DATE: 2000-09-01
88 PRIOR APPLICATION NUMBER: 60/229,345
89 PRIOR FILING DATE: 2000-09-01
90 PRIOR APPLICATION NUMBER: 60/229,345
91 PRIOR FILING DATE: 2000-09-01
92 PRIOR APPLICATION NUMBER: 60/229,345
93 PRIOR FILING DATE: 2000-09-01
94 PRIOR APPLICATION NUMBER: 60/229,345
95 PRIOR FILING DATE: 2000-09-01
96 PRIOR APPLICATION NUMBER: 60/229,345
97 PRIOR FILING DATE: 2000-09-01
98 PRIOR APPLICATION NUMBER: 60/229,345
99 PRIOR FILING DATE: 2000-09-01
100 PRIOR APPLICATION NUMBER: 60/229,345

```

```

1 PRIOR APPLICATION NUMBER: 60/249,245
2 PRIOR FILING DATE: 2000-11-17
3 PRIOR APPLICATION NUMBER: 60/249,244
4 PRIOR FILING DATE: 2000-11-17
5 PRIOR APPLICATION NUMBER: 60/249,217
6 PRIOR FILING DATE: 2000-11-17
7 PRIOR APPLICATION NUMBER: 60/249,211
8 PRIOR FILING DATE: 2000-11-17
9 PRIOR APPLICATION NUMBER: 60/249,215
10 PRIOR FILING DATE: 2000-11-17
11 PRIOR APPLICATION NUMBER: 60/249,264
12 PRIOR FILING DATE: 2000-11-17
13 PRIOR APPLICATION NUMBER: 60/249,214
14 PRIOR FILING DATE: 2000-11-17
15 PRIOR APPLICATION NUMBER: 60/249,297
16 PRIOR FILING DATE: 2000-11-17
17 PRIOR APPLICATION NUMBER: 60/232,400
18 PRIOR FILING DATE: 2000-09-14
19 PRIOR APPLICATION NUMBER: 60/231,242
20 PRIOR FILING DATE: 2000-09-06
21 PRIOR APPLICATION NUMBER: 60/232,081
22 PRIOR FILING DATE: 2000-09-06
23 PRIOR APPLICATION NUMBER: 60/232,080
24 PRIOR FILING DATE: 2000-09-06
25 PRIOR APPLICATION NUMBER: 60/231,414
26 PRIOR FILING DATE: 2000-09-06
27 PRIOR APPLICATION NUMBER: 60/231,244
28 PRIOR FILING DATE: 2000-09-06
29 PRIOR APPLICATION NUMBER: 60/233,064
30 PRIOR FILING DATE: 2000-09-14
31 PRIOR APPLICATION NUMBER: 60/233,063
32 PRIOR FILING DATE: 2000-09-14
33 PRIOR APPLICATION NUMBER: 60/232,397
34 PRIOR FILING DATE: 2000-09-14
35 PRIOR APPLICATION NUMBER: 60/232,399
36 PRIOR FILING DATE: 2000-09-14
37 PRIOR APPLICATION NUMBER: 60/232,401
38 PRIOR FILING DATE: 2000-09-14
39 PRIOR APPLICATION NUMBER: 60/241,808
40 PRIOR FILING DATE: 2000-10-20
41 PRIOR APPLICATION NUMBER: 60/241,826
42 PRIOR FILING DATE: 2000-10-20
43 PRIOR APPLICATION NUMBER: 60/241,786
44 PRIOR FILING DATE: 2000-10-20
45 PRIOR APPLICATION NUMBER: 60/241,221
46 PRIOR FILING DATE: 2000-10-20
47 PRIOR APPLICATION NUMBER: 60/246,475
48 PRIOR FILING DATE: 2000-11-08
49 PRIOR APPLICATION NUMBER: 60/241,243
50 PRIOR FILING DATE: 2000-09-08
51 PRIOR APPLICATION NUMBER: 60/233,065
52 PRIOR FILING DATE: 2000-09-14
53 PRIOR APPLICATION NUMBER: 60/232,398
54 PRIOR FILING DATE: 2000-09-14
55 PRIOR APPLICATION NUMBER: 60/232,398
56 PRIOR FILING DATE: 2000-09-14
57 PRIOR APPLICATION NUMBER: 60/232,398
58 PRIOR FILING DATE: 2000-09-14
59 PRIOR APPLICATION NUMBER: 60/232,398
60 PRIOR FILING DATE: 2000-09-14
61 PRIOR APPLICATION NUMBER: 60/232,398
62 PRIOR FILING DATE: 2000-09-14
63 PRIOR APPLICATION NUMBER: 60/232,398
64 PRIOR FILING DATE: 2000-09-14
65 PRIOR APPLICATION NUMBER: 60/232,398
66 PRIOR FILING DATE: 2000-09-14
67 PRIOR APPLICATION NUMBER: 60/232,398
68 PRIOR FILING DATE: 2000-09-14
69 PRIOR APPLICATION NUMBER: 60/232,398
70 PRIOR FILING DATE: 2000-09-14
71 PRIOR APPLICATION NUMBER: 60/232,398
72 PRIOR FILING DATE: 2000-09-14
73 PRIOR APPLICATION NUMBER: 60/232,398
74 PRIOR FILING DATE: 2000-09-14
75 PRIOR APPLICATION NUMBER: 60/232,398
76 PRIOR FILING DATE: 2000-09-14
77 PRIOR APPLICATION NUMBER: 60/232,398
78 PRIOR FILING DATE: 2000-09-14
79 PRIOR APPLICATION NUMBER: 60/232,398
80 PRIOR FILING DATE: 2000-09-14
81 PRIOR APPLICATION NUMBER: 60/232,398
82 PRIOR FILING DATE: 2000-09-14
83 PRIOR APPLICATION NUMBER: 60/232,398
84 PRIOR FILING DATE: 2000-09-14
85 PRIOR APPLICATION NUMBER: 60/232,398
86 PRIOR FILING DATE: 2000-09-14
87 PRIOR APPLICATION NUMBER: 60/232,398
88 PRIOR FILING DATE: 2000-09-14
89 PRIOR APPLICATION NUMBER: 60/232,398
90 PRIOR FILING DATE: 2000-09-14
91 PRIOR APPLICATION NUMBER: 60/232,398
92 PRIOR FILING DATE: 2000-09-14
93 PRIOR APPLICATION NUMBER: 60/232,398
94 PRIOR FILING DATE: 2000-09-14
95 PRIOR APPLICATION NUMBER: 60/232,398
96 PRIOR FILING DATE: 2000-09-14
97 PRIOR APPLICATION NUMBER: 60/232,398
98 PRIOR FILING DATE: 2000-09-14
99 PRIOR APPLICATION NUMBER: 60/232,398
100 PRIOR APPLICATION NUMBER: 60/232,398

```

Query Match 100.0% Score 103; DB 22; Length 341;
 Best Local Similarity 100.0%; Pred. No. 9, 2e-07;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DPEETPEVPNSIGKSPIS 19
 Db 296 DPEETPEVPNSIGKSPIS 314
 |||||

RESULT 8
 US-10-206-664-1611 Application US/10206664
 TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 APPLICANT: Rosen et al.
 TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 REFERENCE: PTZ68CIN
 CURRENT FILING DATE: 2000-07-29
 PRIOR APPLICATION REMOVED - See File Wrapper or Palm

```

; NUMBER OF SEQ ID NOS: 2628
; Accession: GenBank Ver. 2.0
; SEQ ID NO 1611
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-205-664-1611

Query Match 100.0%; Score 103; DB 28; Length 341;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPFTTEPVPNSICKSPUS 19
DB 296 DPFTTEPVPNSICKSPUS 314

RESULT 9
PCT-US03-03967-4
; Sequence 104, Application US/09646673A
; GENERAL INFORMATION:
; APPLICANT: NOVARTIS
; APPLICANT: HINGZMANN, BERND
; APPLICANT: SCHMITT, ARMIN
; APPLICANT: PILARSKY, CHRISTIAN
; APPLICANT: ROSENTHAL, ANDRE
; APPLICANT: ROSENTHAL, ANDRE
; TITLE OF INVENTION: HUMAN NUCLEIC ACID SEQUENCES FROM TISSUE OF BREAST
; FILE REFERENCE: SCH 1765
; CURRENT FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/09/646,673A
; PRIOR FILING DATE: 1999-03-19
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 104
; LENGTH: 388
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-646-673A-104

Query Match 100.0%; Score 103; DB 20; Length 388;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPFTTEPVPNSICKSPUS 19
DB 343 DPFTTEPVPNSICKSPUS 361

RESULT 10
US-10-131-410-104
; Sequence 104, Application US/10131410
; GENERAL INFORMATION:
; APPLICANT: SPECIFIC, THOMAS
; APPLICANT: HINGZMANN, BERND
; APPLICANT: SCHMITT, ARMIN
; APPLICANT: ROSENTHAL, ANDRE
; APPLICANT: DAHL, EDGAR
; APPLICANT: ROSENTHAL, ANDRE
; TITLE OF INVENTION: HUMAN NUCLEIC ACID SEQUENCES FROM TISSUE OF BREAST
; FILE REFERENCE: SCH 1765
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: 09/646,673
; PRIOR APPLICATION NUMBER: PCT/0899/00908
; PRIOR FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 202
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 104

; NUMBER OF SEQ ID NOS: 2628
; Accession: GenBank Ver. 2.1
; SEQ ID NO 1611
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-205-664-1611

Query Match 100.0%; Score 103; DB 27; Length 388;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPFTTEPVPNSICKSPUS 19
DB 343 DPFTTEPVPNSICKSPUS 361

RESULT 11
PCT-US03-03967-4
; Sequence 4, Application PC/TUS0303967
; GENERAL INFORMATION:
; APPLICANT: NOVARTIS
; APPLICANT: NOVARTIS CORPORATION et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL001313PCT
; CURRENT APPLICATION NUMBER: PCT/US03/03967
; CURRENT FILING DATE: 2003-02-10
; NUMBER OF SEQ NOS: 4
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 407
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-03967-4

Query Match Similarity 100.0%; Score 103; DB 1; Length 407;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPFTTEPVPNSICKSPUS 19
DB 362 DPFTTEPVPNSICKSPUS 380

RESULT 12
US-10-067-977-4
; Sequence 4, Application US/10067977
; GENERAL INFORMATION:
; APPLICANT: NOVARTIS
; APPLICANT: NOVARTIS PHARMA and KIC, ZHANG
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL001313PCT
; CURRENT APPLICATION NUMBER: US/10/067,977
; CURRENT FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 407
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-067-977-4

Query Match Similarity 100.0%; Score 103; DB 26; Length 407;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPFTTEPVPNSICKSPUS 19
DB 362 DPFTTEPVPNSICKSPUS 380

RESULT 13
PCT-US03-01981-363
; Sequence 363, Application PC/TUS0303967

```

```

1 GENERAL INFORMATION:
2 APPLICANT: Genzyme, Shingon Company.
3 TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES AND POLYPEPTIDE FOR PREDICTING
4 TITLE OF INVENTION: ACTIVITY OF COMPOUNDS THAT INTERACT WITH PROTEIN TYROSINE KINASE
5 TITLE OF INVENTION: AND/OR PROTEIN TYROSINE KINASE PATHWAYS
6 FILE REFERENCE: PCT/US03/01981
7 CURRENT FILING DATE: 2003-05-22
8 PRIOR APPLICATION NUMBER: US 60/350,061
9 PRIOR FILING DATE: 2003-01-18
10 SOFTWARE: Patent version 3.2
11 SEQ ID NO 363
12 LENGTH: 431
13 ORGANISM: Homo sapiens
14 PCT-US03-01981-363

Query Match 100.0%; Score 103; DB 1; Length 431;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DPEETPEVPNSIGKSPDS 19
| | | | | | | | | | | | | | | | | | | | | |
Db 386 DPEETPEVPNSIGKSPDS 404

RESULT 14
PCT-US03-02571-12 Collection PC/US0302571
1 GENERAL INFORMATION:
2 APPLICANT: Millennium Pharmaceuticals, Inc.
3 TITLE OF INVENTION:
4 APPLICANT: Logan, Thomas Joseph
5 APPLICANT: Galvin, Katherine M.
6 APPLICANT: Healy, Aileen
7 APPLICANT: Acton, Susan L.
8 APPLICANT: Scaglione, Nancy
9 APPLICANT: Perodini, Jacqueline
10 APPLICANT: Rodriguez-Way, Aerialle
11 TITLE OF INVENTION: cardiovascular disease using 1682, 6169, 6193, 7771, 14395.
12 TITLE OF INVENTION: 29002, 33216, 43726, 69292, 26156, 32427, 2402, 7747, 1730.
13 TITLE OF INVENTION: 9151, 60491, 13710, 7077, 32076, 1419, 18036, 16105, 38650.
14 TITLE OF INVENTION: 10632, 18610, 8165, 2448, 2445, 64524, 84237, 8512, 2866.
15 TITLE OF INVENTION: 283, 2554, 9461, 17799, 26686, 43848, 32135, 12108, 2914,
16 TITLE OF INVENTION: 51130, 19489, 18133, 2917, 59590, 15992, 2094, 2252, 3474,
17 FILE REFERENCE: WP02-018, 15409, 1452 or 6395 molecules
18 CURRENT APPLICATION NUMBER: PCT/US03/02571
19 CURRENT FILING DATE: 2003-01-29
20 PRIOR FILING DATE: 2002-02-29
21 PRIOR FILING DATE: 2002-02-01
22 PRIOR FILING DATE: 2002-03-15
23 PRIOR FILING DATE: 2002-03-15
24 PRIOR FILING DATE: 2002-04-19
25 PRIOR FILING DATE: 2002-04-19
26 PRIOR FILING DATE: 2002-04-39
27 PRIOR FILING DATE: 2002-06-12
28 PRIOR FILING DATE: 2002-06-24
29 PRIOR FILING DATE: 2002-07-03
30 PRIOR FILING DATE: 2002-07-10
31 PRIOR FILING DATE: 2002-07-10
32 PRIOR FILING DATE: 2002-08-21
33 PRIOR FILING DATE: 2002-08-21
34 PRIOR FILING DATE: 2002-08-23

```

```

1 Remaining Prior Application data removed - See file Wrapper or PALM.
2 SOFTWARE: PARSEQ for Windows Version 4.0
3 SEQ ID NO 12
4 LENGTH: 431
5 ORGANISM: Homo sapiens
6 PCT-US03-02571-12

Query Match 100.0%; Score 103; DB 1; Length 431;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DPEETPEVPNSIGKSPDS 19
| | | | | | | | | | | | | | | | | | | | | |
Db 386 DPEETPEVPNSIGKSPDS 404

RESULT 15
US-09-064-253-2
1 Sequence 2, Application US/09064253
2 GENERAL INFORMATION:
3 APPLICANT:
4 TITLE OF INVENTION: Human Serum Glucocorticoid
5 TITLE OF INVENTION: Regulated Kinase, A Target For Chronic Renal Disease
6 FILE REFERENCE:
7 CORRESPONDENCE ADDRESS:
8 ADDRESSEE: Smithline Beecham Corporation
9 STREET: 709 Swedeland Road
10 CITY: King of Prussia
11 STATE: PA
12 COUNTRY: USA
13 ZIP: 19406
14 CONTACT:
15 COMMERCIAL:
16 MEDIUM TYPE: Diskette
17 COMPUTER: IBM Compatible
18 OPERATING SYSTEM: DOS
19 APPLICATION:
20 CURRENT APPLICATION DATA: Windows Version 2.0
21 CURRENT APPLICATION NUMBER: US/09/064,253
22 FILING DATE:
23 FILING DATE: Herewith
24 PRIOR APPLICATION DATA:
25 APPLICATION NUMBER: 60/051,125
26 FILING DATE: 27-JUN-1997
27 APPLICANT:
28 NAME: HALL, WILLIAM
29 REGISTRATION NUMBER: 34,144
30 REFERENCE/DOCKET NUMBER: 0950002
31 TELEPHONE: (610)270-5219
32 TELEFAX: (610)270-5090
33 TRLEX:
34 INVENTOR: FOR SEQ ID NO: 2:
35 SEQUENCE CHARACTERISTICS:
36 LENGTH: 431 amino acids
37 TYPE: amino acid
38 COMPLETENESS: single
39 TOPOLOGY: linear
40 US-09-064-253-2

Query Match 100.0%; Score 103; DB 14; Length 431;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DPEETPEVPNSIGKSPDS 19
| | | | | | | | | | | | | | | | | | | | | |
Db 386 DPEETPEVPNSIGKSPDS 404

Search completed: August 11, 2003, 08:35:53
Job time : 26.70 secs

```

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OX protein - protein search, using sv model

Run on: August 11, 2003, 08:22:25 : Search time 15.412 seconds
(without alignments)
150,930 Million cell updates/sec

Title: US-10-000-039a-3

Perfect score: 103

Sequence: 1 DFFETPEVPSIGNSPDS 19

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searchid: 479057 seqs, 127295195 residues

Total number of hits satisfying chosen parameters: 479057

Maximum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 100

Listing first 43 summaries

Database : Published Applications, NA: * /US07_PUBCOMB pep.*
1: /cgn2_6/pdata1/pubpa/US06_PUB pep.*
2: /cgn2_6/pdata1/pubpa/US06_PUB pep.*
3: /cgn2_6/pdata1/pubpa/US06_PUB pep.*
4: /cgn2_6/pdata1/pubpa/US06_PUB pep.*
5: /cgn2_6/pdata1/pubpa/US06_PUB pep.*
6: /cgn2_6/pdata1/pubpa/US06_PUB pep.*
7: /cgn2_6/pdata1/pubpa/US06_PUB pep.*
8: /cgn2_6/pdata1/pubpa/US06_PUB pep.*
9: /cgn2_6/pdata1/pubpa/US06_PUB pep.*
10: /cgn2_6/pdata1/pubpa/US06_PUB pep.*
11: /cgn2_6/pdata1/pubpa/US06_PUB pep.*
12: /cgn2_6/pdata1/pubpa/US06_PUB pep.*
13: /cgn2_6/pdata1/pubpa/US06_PUB pep.*
14: /cgn2_6/pdata1/pubpa/US06_PUB pep.*
15: /cgn2_6/pdata1/pubpa/US06_PUB pep.*
16: /cgn2_6/pdata1/pubpa/US06_PUB pep.*
17: /cgn2_6/pdata1/pubpa/US06_PUB pep.*
18: /cgn2_6/pdata1/pubpa/US06_PUB pep.*

pred. No. is the number of results predicted by chance to have a
score of 103 or higher. The results are sorted by descending p-value,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	103	100.0	431	15	Sequence 3, Appl 1
2	103	100.0	431	15	Sequence 3, Appl 1
3	103	100.0	431	15	Sequence 7, Appl 1
4	103	100.0	431	15	Sequence 2, Appl 1
5	95	92.2	430	9	Sequence 9, Appl 1
6	95	92.2	430	9	Sequence 9, Appl 1
7	46	44.7	193	11	Sequence 1638, Ap
8	46	44.7	193	11	Sequence 3889, Ap
9	44	42.7	194	9	Sequence 4, Appl 1
10	44	42.7	194	9	Sequence 4, Appl 1
11	44	42.7	194	9	Sequence 4, Appl 1
12	43	41.7	111	15	Sequence 21, Appl 1
13	43	41.7	111	15	Sequence 1658, A
14	43	41.7	600	11	Sequence 71, Appl 1
15	43	41.7	600	11	Sequence 14, Appl 1

Sequence 14, Appl 1
Sequence 74, Appl 1
Sequence 58, Appl 1
Sequence 104, Appl 1
Sequence 42, Appl 1
Sequence 142, Appl 1
Sequence 50, Appl 1
Sequence 46, Appl 1
Sequence 48, Appl 1
Sequence 40, Appl 1
Sequence 52, Appl 1
Sequence 62, Appl 1
Sequence 59, Appl 1
Sequence 2, Appl 1
Sequence 2, Appl 1
Sequence 3, Appl 1
Sequence 3, Appl 1
Sequence 20, Appl 1
Sequence 12514, A
Sequence 8, Appl 1
Sequence 16, Appl 1
Sequence 11834, A
Sequence 5, Appl 1
Sequence 211, Appl 1
Sequence 213, Appl 1

US-10-124-557-84
US-10-124-557-74
US-10-124-557-58
US-10-124-557-104
US-10-124-557-42
US-10-124-557-42
US-10-124-557-142
US-10-124-557-50
US-10-124-557-66
US-10-124-557-66
US-10-124-557-48
US-10-124-557-40
US-10-124-557-52
US-10-124-557-52
US-10-124-557-62
US-10-106-698-5932
US-10-1028-245-2
US-10-1028-245-2
US-10-246-354-3
US-10-246-354-3
US-09-801-574-20068
US-10-156-761-12514
US-10-126-279-48
US-10-160-865-16
US-10-156-761-1834
US-10-1024-368-5
US-10-1024-368-5
US-10-108-605-211
US-10-108-605-211

ALIGNMENTS

RESULT 1
US-10-000-039-3

Sequence 3, Application US/10000039
Publication No. US/0300035591
GENERAL INFORMATION

APPLICANT: Wald, Florian

TITLE OP INVENTION: SMALL VOLUME-REGULATED HUMAN KINASE II-SKK

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: FOLEY & LARKNER

CITIZENSHIP: UNITED STATES OF AMERICA

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

COMPUTER: IBM PC compatible

MEDIUM TYPE: Floppy disk

SOFTWARE: IBM PC DOS/MS-DOS

SOFTWARE RELEASE: Release 11.0, Version 11.30

CURRENT APPLICATION NUMBER: US/10/000,039

FILING DATE: 04-Dec-2001

PRIOR APPLICATION DATA

APPLICATION NUMBER: US/09/031,295

FILING DATE: 26-FEB-1998

FILING DATE: 29-FEB-1997

ATTORNEY/AGENT INFORMATION:

NAME: Sandercock, Colin G.

REGISTRATION NUMBER: 31,298

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 672-5300

TELEFAX: (202) 672-5399

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:
 LENGTH: 431 amino acids
 STRANDEDNESS: Unknown
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 SEQUENCE DESCRIPTION: SEQ ID NO: 3:
 US-10-000-039a-3

Query Match 100.0% Score 103; DB 15; Length 19;
 Best Local 100.0% Pred No. 7, 5e-09;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DPFTFEPVNSIGKSPDS 19
 DB 1 DPFTEFVNSIGKSPDS 19

RESULT 2
 US-09-810-808-5
 Sequence 5, Application US/09810089
 Patent Local 100.0% Pred No. 7, 5e-09;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 GENERAL INFORMATION:
 APPLICANT: Au-Young, Janice
 Guebler, Karl J., R.
 TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES
 NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:
 AU-YOUNG, JANICE
 STREET: 3174 Porter drive
 CITY: Palo Alto
 STATE: CA
 COUNTRY: U.S.A.
 ZIP: 94304, S.

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq Version 1.5
 CURRENT APPLICATION DATA: US/09/810,808
 FILING DATE: 15-Mar-2001
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/541,228
 FILING DATE: 15-Mar-2001
 ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy J.
 RESIDENCE NUMBER: 740
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-855-0555
 INFORMATION FOR SEQ ID NO: 5:
 LENGTH: 431 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 IMMEDIATE SOURCE:
 CLONE: Consensus
 SEQUENCE DESCRIPTION: SEQ ID NO: 5:
 US-09-810-808-5

Query Match 100.0% Score 103; DB 9; Length 431;
 Best Local 100.0% Pred. No. 2, 3e-07;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DPFTFEPVNSIGKSPDS 19
 DB 386 DPFTEFVNSIGKSPDS 404

RESULT 3

US-09-981-353-7
 Sequence 7, Application US/09981353
 Patent Local 100.0% Pred No. 2, 3e-07;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 GENERAL INFORMATION:
 APPLICANT: Lasek, Amy W.
 Jones, David A.
 TITLE OF INVENTION: EXPRESSED IN COLON CANCER
 FILE REFERENCE: PA-0038 US
 CURRENT APPLICATION NUMBER: US/09/981,353
 CURRENT FILING DATE: 2001-10-11
 FILING DATE: 04-Dec-2001
 SOFTWARE: PERL Program
 SEQ ID NO: 7
 LENGTH: 431
 TYPE: amino acid
 TOPOLOGY: linear
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: misc.feature
 LOCATION: 1..431
 ORGANIZATION: INCLYTE ID NO. US20020160382A1 3819039CD1
 US-09-981-353-7

Query Match 100.0% Score 103; DB 10; Length 411;
 Best Local 100.0% Pred. No. 2, 3e-06;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DPFTFEPVNSIGKSPDS 19
 DB 386 DPFTEFVNSIGKSPDS 404

RESULT 4

US-10-000-039-2
 Sequence 2, Application US/10000039
 Publication No. US20030003559A1
 GENERAL INFORMATION:
 APPLICANT: LANG, Florian
 WALDEGGER, Tullingen
 TITLE OF INVENTION: CELL VOLUME-REGULATED HUMAN KINASE H-SOX
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: FOLEY & LARUNER
 STREET: 3000 K Street, N.W.
 CITY: Washington
 STATE: D.C.
 COUNTRY: U.S.A.
 ZIP: 20007-5109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: FASTA Release 1.0, Version 1.30
 CURRENT APPLICATION NUMBER: US/10/000,039
 FILING DATE: 04-Dec-2001
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/031,295
 FILING DATE: 26-Feb-1998
 FILING DATE: 28-Feb-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Sandercock, Collin G.
 RESIDENCE NUMBER: 100
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 472-5300
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 431 amino acids


```

; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-000-039-2

Query Match
Best Local Similarity 100.0%; Score 103; DB 15; Length 431;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DPFTTEPVPNSIGKSPDS 19
Db 386 DPFTTEPVPNSIGKSPDS 404

RESULT 5
US-09-810-808-9
; Sequence 9, Application US/09810808
; Patent No. US2002004211A1
; GENERAL INFORMATION:
; APPLICANT: Guejuey, Janice
; INVENTOR: Guejuey, Karl J
; TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES
; ADDRESSES: Icyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; FILE NAME: 09-810-808-9
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 1.5
; CURRENT APPLICATION NUMBER: US/09/810,808
; FILING DATE: 15-Mar-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/541,228
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J
; REGISTRATION NUMBER: 36,749
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION SOURCE:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 430 amino acids
; TYPE: amino acid
; STRAND: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-810-808-9

Query Match
Best Local Similarity 92.2%; Score 95; DB 9; Length 430;
Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DPFTTEPVPNSIGKSPDS 19
Db 385 DPFTTEPVPNSIGKSPDS 403

RESULT 6

```

```

US-09-971-118-2
; Sequence 2, Application US/09971118
; Patent No. US2002012036A1
; GENERAL INFORMATION: ALLEN
; APPLICANT: YOGANATHAN, THILLAINATHAN
; TITLE OF INVENTION: SGK2 AND ITS USES
; FILE REFERENCE: KINGD25CIP
; CURRENT APPLICATION NUMBER: US/09/971,118
; PRIOR APPLICATION NUMBER: PCT/US01/21479
; PRIOR FILING DATE: 2001-09-20
; PRIOR PCT APPLICATION NUMBER: PCT/02/237,419
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO: 2
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-971-118-2

Query Match
Best Local Similarity 62.1%; Score 64; DB 10; Length 367;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DPFTTEPVPNSIGKSPDS 19
Db 323 DPFTTEPVPNSIGKSPDS 341

RESULT 7
US-09-925-300-1638
; Sequence 1638, Application US/09925300
; Patent No. US20020015168A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PCT/US01/001638
; CURRENT APPLICATION NUMBER: US/09/925,300
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: PCT/96/0174,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: SeqScribe Ver. 2.0
; SEQ ID NO: 1638
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: SITE
; LOCATION: (90)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-300-1638

Query Match
Best Local Similarity 44.7%; Score 46; DB 10; Length 93;
Matches 8; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 DPFTTEPVPNSIGKSP 17
Db 42 DPKEFVEVPSLLPQP 58

RESULT 8
US-09-764-891-3889
; Sequence 3889, Application US/09764891
; Patent No. US20030077808A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.

```


US-10-006-869-21

Query Match 41.7% Score 43; DB 15; Length 111;
Best Local Similarity 53.3%; Pred. No. 2; Mismatches 8; Indels 0; Gaps 0;
Matches 8; Conservative 2;

QY 2 PFTPEPVNSIKSPDS 19
DB 14 PBNQRQFFPRDGNKYDS 31

RESULT 13
US-10-136-761-11658

; Sequence 11658, Application US/10156761
; Publication No. US03030119018A1
; GENERAL INFORMATION: Saccharomyces cerevisiae
; APPLICANT: TERA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SAKAI, YOSHIYUKI
; APPLICANT: SAKAI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA

; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR FILING DATE: 2001-05-30
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 11658
; LENGTH: 146

; ORGANISM: Streptomyces avermitilis
US-10-136-761-11658

Query Match 41.7% Score 43; DB 15; Length 146;
Best Local Similarity 57.1%; Pred. No. 55;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 5 TPEPVNSIKSPDS 18
DB 118 TPEPVNSIKSPDS 131

RESULT 14

; US-09-893-519A-71
; Sequence 71, Application US/09893519A
; Publication No. US0303027243A1
; GENERAL INFORMATION: ANADYS PHARMACEUTICALS, INC.
; APPLICANT: THOMPSON, Craig
; APPLICANT: MOORE, Jeffrey
; APPLICANT: BRADLEY, John
; APPLICANT: DESILVA, Tamara
; APPLICANT: HARRIS, Sandra
; APPLICANT: KUMARITSKY, Svetlana
; APPLICANT: MOORE, Daniel
; APPLICANT: MCCOY, Melissa
; APPLICANT: SANDERSON, Karen
; APPLICANT: SHIBUO
; APPLICANT: ZHU, Fan
; APPLICANT: LONG, Fan
; APPLICANT: DAYDOV, Eugene
; TITLE OF INVENTION: ANTICANCER COMPOUNDS AND METHODS OF USE
; FILE REFERENCE: 141-051892
; CURRENT APPLICATION NUMBER: US/09/893,519A
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 60/215,164

; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 60/224,457
; PRIOR FILING DATE: 2000-08-10
; SEQ ID NOS: 146
; SOFTWARE: Patentin Version 3.1
; SEQ ID NO 71
; LENGTH: 600
; TITLE: PFT
; ORGANISM: Saccharomyces cerevisiae
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Corresponds to SEQ ID NO: 144
US-09-893-519A-71

Query Match 41.7% Score 43; DB 11; Length 600;
Best Local Similarity 53.3%; Pred. No. 2.6e+02;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 5 TPEPVNSIKSPDS 19
DB 43 SDPEVNSAGNAUTS 57

RESULT 15

; US-10-124-557-14
; Sequence 14, Application US/10124557
; Publication No. US0303011789A1
; GENERAL INFORMATION:
; APPLICANT: Turner, Katherine
; Clark, Stephen C.
; Jackson, Kenneth M.
; Hewick, Rodney M.
; Giesner, Thomas G.
; TITLE OF INVENTION: Megakaryocyte Stimulating Factors
; NUMBER OF SEQUENCES: 43
; CONSERVATION: 100%
; ADDRESSEE: Genelabs Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140

; COMPUTER READABLE FORM:
; FILED: 10/12/2002
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/10/124,557
; FILING DATE: 16-Apr-2002
; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/643,562
; FILING DATE: 18-JUN-1991
; APPLICATION NUMBER: US 07/546,114
; FILING DATE: 29-JUN-1990
; APPLICATION NUMBER: US 07/457,196
; FILING DATE: 08-AUG-1989
; APPLICATION NUMBER: US 07/390,901
; FILING DATE: 08-AUG-1989

; ATTORNEY/AGENT INFORMATION:
; NAME: Genelabs
; REGISTRATION NUMBER: 31,422
; REFERENCE/DOCKET NUMBER: G1 5190
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)876-1170
; TELEFAX: (617)876-1170

; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 941 amino acids
; TOPOLOGY: linear
; MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-124-557-14

Query Match 41.7%; Score 43; DB 14; Length 941;
Best Local Similarity 43.8%; Pred. No. 4, 2e-02;
Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 2 PFTEEPVNSIGKSP 17

Db 11 : 11 : 11

679 PELSAEPTKALENSP 694

Search completed: August 11, 2003, 08:42:59
Job time : 16.412 secs

DR	EHLB: AJ232716; CAAL1528.1; "
DR	HSSP: P00517; 1YDR.
DR	InterPro: IPR000190; Pfam: C1.
DR	InterPro: IPR000719; SCF_Pk.kinase.
DR	InterPro: IPR002290; Src_Thr-Pk.kinase.
DR	Pfam: PF00069; pfkinase_1.
DR	Pfam: PF00069; pfkinase_C1.
DR	Pfam: PF00069; pfkinase_C1.
DR	Pfam: PF00069; pfkinase_C1.
DR	SMART: SMO0220; S_TKc_1.kinase.1.
DR	SMART: SMO0133; S_TKc_X:1.kinase.
DR	PROSITE: PS00107; PROTEIN_KINASE_ASP: 1.
DR	PROSITE: PS00107; PROTEIN_KINASE_ASP: 1.
DR	PROSITE: PS00108; PROTEIN_KINASE_ST: 1.
DR	ATP-binding; Kinase; Serine/threonine-protein kinase; Translucose
KW	SEQUENCE 594 Aa; 66857 Mw; 40153EC180578767 CRC64;
QV	Query Match 94.2%; Score 97; DB 13; Length 594;
DG	Best Local Similarity 89.5%; Pred.No. 3.9e-07;
	Matches 17; Conservative 2; Mismatches 0; Indels 0;
	1 DPETEEFPVNSIGSGPS 19
	EEEEEEEEEEEEEEEE
	549 DPETEEFPVNSIGSGPS 567
RESULTS 4	
Q95U9L	PRELIMINARY:
O39JUA	PMT: J85 AA.
DT	01-JUN-2001 (TrEMBLrel. 17, Created)
DT	01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT	01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
GN	S-HAR-2 setum/glucoctoid-regulated kinase (fragment).
OS	Sak.
OC	Mus musculus (Mouse).
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Eumetazoa; Vertebrata; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI	NCBI TaxID: 10090.
RP	SEQUENCE FROM N.A.
RP	Submitted 9 JAN-2001 to the ENBL/Genebank/DBSJ databases.
MD	MGI: BC002223; AAH02222.1; "
MD	MGI: MG1:1340062; Sak.
DR	InterPro: IPR000761; Pfkinase_C.
DR	InterPro: IPR000761; Pfkinase_C.
DR	Pfam: PF00069; pfkinase_1.
DR	Pfam: PF00433; pfkinase_C: 1.
DR	Problem: PR000001; Prot_Kinase: 1.
DR	Problem: PR000001; Prot_Kinase: 1.
KW	ATP-binding; Kinase; Transferase.
KW	ATP-binding; Kinase; Transferase.
FT	NOM_TERM
FT	SEQUENCE 185 Aa; 20921 Mw; EDN4244ABF03945 CRC64;
QV	Query Match 92.2%; Score 95; DB 11; Length 185;
DG	Best Local Similarity 89.5%; Pred. No. 2.3e-07;
	Matches 17; Conservative 2; Mismatches 0; Indels 0;
	1 DPETEEFPVNSIGSGPS 19
	EEEEEEEEEEEEEEEE
	140 DPETEEFPVNSIGSGPS 158
RESULTS 5	
Q95U9L	PRELIMINARY:
O39JUA	PMT: 40 AA.
DT	01-DEC-2001 (TrEMBLrel. 19, Created)
DT	01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
GN	S-HAR-2 setum/glucoctoid-regulated kinase 1 (fragment).
OS	Sak.

OS *Capra hircus* (Capra)
OC Mammalia: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
OC Mammalia: Buthera: Carnivora: Fissipedia: Canidae: Canis.
OC NCBI_TaxID=9615;
OC SEQUENCE FROM N.A.
EX MEDLINE-2116084; PubMed-11266509;
RA MICK V.E., Itani O.A., Loftus R.N., Rusted R.F., Schmidt T.J.,
RA Thomas G.C. Subunit of the Epithelial Sodium Channel Is an Aldosterone-
RA Induced Transcript in Mammalian Collecting Ducts, and This
RA Transcriptional Response Is Mediated via Distinct cis-Elements in the
RA 5'-Flanking Region
RA PubMed-11266509; PubMed-11266509;
RA EMBL: AF217416; AKS41444.1; -;
RA Kinase.
RA NON-TER
FT SEQUENCE 40 AA; 4189 MW; E54EB1867622586 CRC64;
SQ
Query Match 64.1%; Score 66; DB 6; Length 40;
Best Local Similarity 92.3%; Pred. No. 0.0021;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 7 EBPVNSIGKSPDS 19
DB 1 EBPVNSIGKSPDS 13
RESULT 6
OY 1 EBPVNSIGKSPDS 19
AC OY4559; PRELIMINARY; PRT; 448 AA.
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TRENBLrel. 15, Last annotation update)
DR Hypothetical 50.9 kDa protein.
GN FAM19.70.
OS Arabidopsis thaliana (Mouse-ear cress). Embryophyta; Tracheophyta;
OC Eukaryota: Viridiplantae: Streptophyta; Eudicotyledons: Core eudicot; Rosidae;
OC Eudicotyledons: Magnoliophyta: Eudicotyledons: Core eudicot; Rosidae;
OC Eudicotyledons: Brassicales; Brassicaceae; Arabidopsis.
OC NCBI_TaxID=3702;
RN [1]
RN SEQUENCE FROM N.A.
RA Vitale D., Liquori R., Flores M., Argiriou A., De Simone V.,
RA Mevas H.W., Rudd S., Lemcke K., Mayer K.P.X., Quetier P.,
RA Salanubart M.; 2000. The EMBL/Genbank/DBJ databases.
RN [2]
RN SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RA Submitted(2000-03-13); CAB91592.1;
RA InterPro: IPR003871; DUF223.
DR Pfam: PF02721; DUF223.1.
DR Hypothetical protein.
SQ SEQUENCE 448 AA; 50924 MW; 5421BFB84778F1FB CRC64;
Query Match 46.6%; Score 48; DB 10; Length 448;
Best Local Similarity 62.5%; Pred. No. 24;
Matches 10; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
OY 1 DPETPEPVPNIGKSTK 16
DB 315 DPENPEPVPNIGKSTK 330
RESULT 7
OY 1 DPETPEPVPNIGKSTK 16
AC OY4545; PRELIMINARY; PRT; 490 AA.
DT 01-JUN-2002 (TRENBLrel. 21, Created)
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)

DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Hamitot hydrolytic
GN OY4539; PRELIMINARY; PRT; 2404.
OC Bacteria: Proteobacteria: Alphaproteobacteria: Rhizobiales:
OC Rhizobiales: Rhizobium.
OC NCBI_TaxID=176299;
RN [1]
RN SEQUENCE FROM N.A.
EX MEDLINE-21160850; PubMed-11743193;
RA WOOD D.W., Setubal J.C., Kuhl R., Weeks D.E., Kitajima J.P.,
RA Churruarín V., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D., Sr.,
RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
RA Kutyavin T., Levy R., Li M.-J., McLelland E., Palmeri A., Gordon B.,
Raymond C., Rose T., Tiedje J.M., Biddle P., Jung M., Krespan M., Perry M.,
Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Bolan M.,
Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
Mester E.W.; 2003. The genome of the natural genetic engineer *Agrobacterium tumefaciens* C58.
FT C58.
RL Science 294:2317-2323(2001).
RN [2]
RN SEQUENCE FROM N.A.
EX MEDLINE-21160851; PubMed-11743194;
RA Goodner B., Hinkle G., Gattling S., Miller N., Blanchard M.,
RA Quirillo B., Goldman B.S., Cho Y., Akenazi M., Halling C., Mullin L.,
RA Roumelis K., Gordon J., Vaudin M., Jaspard M., D. Scott C., Lappes C., Markis B.,
RA Flanagan C., Crowell C., Gursion J., Lomo C., Sear C., Strub C.,
Cielo C., Slater S.;
RA Genome sequence of the plant pathogen and biotechnology agent
RA *Symbiobacterium meliloti* 252.
RL Science 294:2323-2328(2001).
DR EMBL: AB009282; AAL44342.1; -;
DR EMBL: AB008330; AAM9867.1; -;
DR InterPro: IPR0000659; HAMITOT_10.
DR Pfam: PF01233; HAMITOT_10.
DR PRINTS; PR00084; HTLDHGRNASE.
DR Complete proteome.
SQ SEQUENCE 490 AA; 53904 MW; 374627989CADD07 CRC64;
Query Match 46.6%; Score 48; DB 16; Length 490;
Best Local Similarity 47.4%; Pred. No. 26;
Matches 9; Conservative 2; Mismatches 8; Indels 0; Gaps 0;
OY 1 DPETPEPVPNIGKSPDS 19
DB 423 DPENPEPVPNIGKSPDS 441
RESULT 8
OY 1 DPETPEPVPNIGKSPDS 19
AC OY4525; PRELIMINARY; PRT; 165 AA.
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE A205840 protein.
DE A205840 protein.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota: Viridiplantae: Streptophyta; Eudicotyledons: Core eudicot; Rosidae;
OC Eukaryota: Magnoliophyta: Eudicotyledons: Core eudicot; Rosidae;
OC Eudicotyledons: Brassicales; Brassicaceae; Arabidopsis.
OC NCBI_TaxID=3702;
RN [1]
RN SEQUENCE FROM N.A.
RA STRATHEV, Columbia.
RA Lin X., Kuhl S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Fuji C.Y., Mason T.M., Boyman C.L., Barnstead M.E., Feldblum T.V.,
Buell C.R., Hestum K.A., Luo J.J., Roming C.M., Rhee H., Moffat K.S.,

[illegible]


```

Db      1 DPFEETPVNSIGKSPDS 19

RESULT 2
US-08-712-709-5
; Sequence 5, Application US/08712709
; Patent No. 5863780
; GENE: NOVEL HUMAN PROTEIN KINASES
; APPLICANT: Au-Young, Janice
; APPLICANT: Guegler, Karl J.
; TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
SOFTWARE: FASTSQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/111,444
PRIORITY NUMBER: 08/712,709
PRIOR APPLICATION DATA:
FILING DATE: INFORMATION:
ATTORNEY/AGENT INFORMATION:
NAME: REGILL, LUCY
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0118 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-845-4166
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 100.00
TYPE: amino acids
STRANDEDNESS: single
TOPOLOGY: linear
MULTIPLY: 1
IMMEDIATE SOURCE:
LIBRARY:
CLONE: Consensus
US-08-111-444-5
Query Match      100.00; Score 103; Length 431:
Best Local Similarity 100.00; Pred. No. 7.1e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 DPFEETPVNSIGKSPIS 19
Db      386 DPFEETPVNSIGKSPUS 404

RESULT 4
US-09-541-228-5
; Sequence 5, Application US/09541228
; Patent No. 6207007
; GENE: NOVEL HUMAN PROTEIN KINASES
; APPLICANT: Au-Young, Janice
; APPLICANT: Guegler, Karl J.
; TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
SOFTWARE: FASTSQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/541,228
PRIORITY NUMBER: 08/712,709
PRIOR APPLICATION DATA:
FILING DATE: INFORMATION:
ATTORNEY/AGENT INFORMATION:
NAME: REGILL, LUCY
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0118 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555

```



```

1  COMPUTER: IBM Compatible
2  OPERATING SYSTEM: DOS
3  SOFTWARE: FAST320 Version 1.5
4  COUNTRY: UNITED STATES
5  APPLICATION NUMBER: US/09/111,444
6  FILING DATE:
7  PRIOR APPLICATION DATA: 08/712,709
8  CURRENT APPLICATION NUMBER:
9  FILING DATE:
10 ATTORNEY/AGENT INFORMATION:
11 NAME: Billings, Lucy J
12 RESIDENCE: New York, NY 10016
13 REGISTRATION NUMBER: 66,710
14 TELECOMMUNICATION INFORMATION:
15 TELEPHONE: 415-855-0555
16 TELEFAX: 415-845-4166
17 INFORMATION FOR SEQ ID NO: 9:
18 SEQUENCE CHARACTERISTICS:
19 LENGTH: 430 amino acids
20 TYPE: amino acid
21 STRAND: single
22 TOPOLOGY: linear
23 IMMEDIATE SOURCE:
24 ORGANISM: Yeast
25 CLONE: 294637
26 US-09-111-444-9
27
28 Query Match 92.28; Score 95; DB 3; Length 430;
29 Best Local Similarity 89.5%; Pred. No. 1,2e-06;
30 Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
31
32 Y 1 DPEETPEVPSNIGSPDS 19
33 DB 385 DPEETPEVPSNIGSPDS 403
34
35 RESULT 9
36 US-09-541-228-9
37 Sequence 9, Application US/09541228
38 Patent No. 6232077
39 GENE: HUMAN C-MYC
40 APPLICANT: AL-UQUY, Janice
41 APPLICANT: Guegler, Karl J.
42 APPLICANT: Hawkins, Phillip R.
43 APPLICANT: HAWKINS, PHILLIP R.
44 NUMBER OF SEQUENCES: 9
45 CORRESPONDENCE ADDRESS:
46 ADDRESSEE: Incyte Pharmaceuticals, Inc.
47 STREET: 177A Porter Drive
48 CITY: Palo Alto
49 STATE: CA
50 COUNTRY: U.S.
51 ZIP: 94304
52 COMPUTER: IBM Compatible
53 OPERATING SYSTEM: DOS
54 CURRENT APPLICATION NUMBER: 09/541,228
55 APPLICATION NUMBER: US/09/541,228
56 FILING DATE:
57 PRIOR APPLICATION DATA: 08/712,709
58 CURRENT APPLICATION NUMBER:
59 FILING DATE:
60 ATTORNEY/AGENT INFORMATION:
61 NAME: Billings, Lucy J
62 RESIDENCE: New York, NY 10016
63 REGISTRATION NUMBER: 66,710
64 TELECOMMUNICATION INFORMATION:
65 TELEPHONE: 415-855-0555
66 TELEFAX: 415-845-4166
67 INFORMATION FOR SEQ ID NO: 9:

```

```

1  SEQUENCE CHARACTERISTICS:
2  LENGTH: 430 amino acids
3  STRAND: single
4  TOPOLOGY: linear
5  MOLECULE TYPE: peptide
6  IMMEDIATE SOURCE:
7  ORGANISM: Yeast
8  CLONE: 294637
9  US-09-541-228-9
10
11 Query Match 92.28; Score 95; DB 3; Length 430;
12 Best Local Similarity 89.5%; Pred. No. 1,2e-06;
13 Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
14
15 Y 1 DPEETPEVPSNIGSPDS 19
16 DB 385 DPEETPEVPSNIGSPDS 403
17
18 RESULT 9
19 US-09-134-001C-4705
20 Sequence 4705, Application US/09134001C
21 Patent No. 6380370
22 GENE: HUMAN C-MYC
23 APPLICANT: LYNN DOUCETTE-SLAMM et al
24 APPLICANT: DOUCETTE-SLAMM, LYNN
25 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
26 TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
27 CURRENT APPLICATION NUMBER: US/09/134,001C
28 CURRENT FILING DATE: 1998-08-13
29 PRIOR APPLICATION NUMBER: US 60/064,964
30 PRIOR FILING DATE: 1998-08-13
31 PRIOR APPLICATION NUMBER: US 60/055,779
32 PRIOR FILING DATE: 1997-08-14
33 NUMBER OF SEQ ID NOS: 5674
34 SEQ ID NO: 4705
35 SEQ ID NO: 4706
36 TYPE: PRT
37 ORGANISM: Staphylococcus epidermidis
38 US-09-134-001C-4705
39
40 Query Match 42.74; Score 44; DB 4; Length 540;
41 Best Local Similarity 47.1%; Pred. No. 76;
42 Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
43
44 Y 1 DPEETPEVPSNIGSP 17
45 DB 356 DSEFDKREKATITSLQKLP 372
46
47 RESULT 10
48 US-09-187-859-21
49 Sequence 21, Application US/09187859A
50 Patent No. 6380370
51 GENE: HUMAN C-MYC
52 GENERAL INFORMATION:
53 APPLICANT: Blaschuk, Orest W.
54 APPLICANT: Gour, Barbara J.
55 TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
56 TITLE OF INVENTION: TRANSPORT AND MODULATED FUNCTIONS
57 FILE REFERENCE: 100086 407C1
58 CURRENT APPLICATION NUMBER: US/09/187,859A
59 CURRENT FILING DATE: 1998-11-06
60 NUMBER OF SEQ ID NOS: 2
61 SOFTWARE: PatentIn Ver. 2.0
62 SEQ ID NO 21
63 LENGTH: 111
64 STRAND: single
65 TOPOLOGY: linear
66 ORGANISM: Homo sapiens
67 CLONING VECT:
68 US-09-187-859-21
69
70 Query Match 41.74; Score 43; DB 4; Length 111;
71 Best Local Similarity 44.44; Pred. No. 19;

```



```

RESULT 14
US-08-218-265-4
: Sequence 4, Application US/08218265
: Patent No. 5922585
: GENERAL INFORMATION: Richard A. Thompson, Craig M.
: APPLICANT: Koleske, Anthony J.
: TITLE OF INVENTION: No. 5922585el Factors Which Modify Gene
: DESCRIPTION OF INVENTION: Description and Methods of Use Thereof
: NUMBER OF SEQUENCES: 35
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
: CITY: Lexington
: STATE: MA
: COUNTRY: US
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: CURRENT APPLICATION DATA: Release #1.0, Version #1.25
: APPLICATION NUMBER: US/08/218,265
: FILING DATE: 25-MAR-1994
: PRIORITY INFORMATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: Granahan, Patricia
: REGISTRATION NUMBER: 32,227
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 617-861-6240
: TELEFAX: 617-861-9540
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 687 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-218-265-4
: Query Match 41.7%; Score 43; DB 2; Length 687;
: Best Local Similarity 53.3%; Pred. No. 1.4e+02;
: Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
OY 5 TEEPVPNSGNKSPDS 19
DB 43 SDEPVPESNKAUTS 57
Search completed: August 11, 2003, 08:24:44
Job time : 3.69099 secs

```

```

RESULT 15
US-08-521-477-4
: Sequence 4, Application US/08521872
: Patent No. 6015682
: GENERAL INFORMATION: Richard A. Thompson, Craig M.
: APPLICANT: Koleske, Anthony J.
: TITLE OF INVENTION: No. 6015682el Factors Which Modify Gene
: DESCRIPTION OF INVENTION: Description and Methods of Use Thereof
: NUMBER OF SEQUENCES: 37
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
: CITY: Lexington
: STATE: Massachusetts
: COUNTRY: USA
: ZIP: 02173
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: CURRENT APPLICATION DATA: Release #1.0, Version #1.30
: APPLICATION NUMBER: US/08/521,872
: FILING DATE: 31-AUG-1995
: PRIORITY INFORMATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/218,265
: FILING DATE: 25-MAR-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Granahan, Patricia
: REGISTRATION NUMBER: 32,227
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 617-861-6240
: TELEFAX: 617-861-9540
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 687 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-218-265-4
: Query Match 41.7%; Score 43; DB 3; Length 687;
: Best Local Similarity 53.3%; Pred. No. 1.4e+02;
: Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
OY 5 TEEPVPNSGNKSPDS 19
DB 43 SDEPVPESNKAUTS 57

```


CC	or send an email to tlcmuser@isu-sib.ch .	
DR	ENBL: Y10012; CAY1138.1;	
DR	ENBL: X10003; CAY1139.1;	
DR	ENBL: X10004; CAY1140.1;	
DR	ENBL: X10005; CAY1141.1;	
DR	ENBL: X10006; CAY1142.1;	
DR	ENBL: X10007; CAY1143.1;	
DR	ENBL: X10008; CAY1144.1;	
DR	ENBL: X10009; CAY1145.1;	
DR	ENBL: X10010; CAY1146.1;	
DR	ENBL: X10011; CAY1147.1;	
DR	ENBL: X10012; CAY1148.1;	
DR	ENBL: X10013; CAY1149.1;	
DR	ENBL: X10014; CAY1150.1;	
DR	ENBL: X10015; CAY1151.1;	
DR	ENBL: X10016; CAY1152.1;	
DR	ENBL: X10017; CAY1153.1;	
DR	ENBL: X10018; CAY1154.1;	
DR	ENBL: X10019; CAY1155.1;	
DR	ENBL: X10020; CAY1156.1;	
DR	ENBL: X10021; CAY1157.1;	
DR	ENBL: X10022; CAY1158.1;	
DR	ENBL: X10023; CAY1159.1;	
DR	ENBL: X10024; CAY1160.1;	
DR	ENBL: X10025; CAY1161.1;	
DR	ENBL: X10026; CAY1162.1;	
DR	ENBL: X10027; CAY1163.1;	
DR	ENBL: X10028; CAY1164.1;	
DR	ENBL: X10029; CAY1165.1;	
DR	ENBL: X10030; CAY1166.1;	
DR	ENBL: X10031; CAY1167.1;	
DR	ENBL: X10032; CAY1168.1;	
DR	ENBL: X10033; CAY1169.1;	
DR	ENBL: X10034; CAY1170.1;	
DR	ENBL: X10035; CAY1171.1;	
DR	ENBL: X10036; CAY1172.1;	
DR	ENBL: X10037; CAY1173.1;	
DR	ENBL: X10038; CAY1174.1;	
DR	ENBL: X10039; CAY1175.1;	
DR	ENBL: X10040; CAY1176.1;	
DR	ENBL: X10041; CAY1177.1;	
DR	ENBL: X10042; CAY1178.1;	
DR	ENBL: X10043; CAY1179.1;	
DR	ENBL: X10044; CAY1180.1;	
DR	ENBL: X10045; CAY1181.1;	
DR	ENBL: X10046; CAY1182.1;	
DR	ENBL: X10047; CAY1183.1;	
DR	ENBL: X10048; CAY1184.1;	
DR	ENBL: X10049; CAY1185.1;	
DR	ENBL: X10050; CAY1186.1;	
DR	ENBL: X10051; CAY1187.1;	
DR	ENBL: X10052; CAY1188.1;	
DR	ENBL: X10053; CAY1189.1;	
DR	ENBL: X10054; CAY1190.1;	
DR	ENBL: X10055; CAY1191.1;	
DR	ENBL: X10056; CAY1192.1;	
DR	ENBL: X10057; CAY1193.1;	
DR	ENBL: X10058; CAY1194.1;	
DR	ENBL: X10059; CAY1195.1;	
DR	ENBL: X10060; CAY1196.1;	
DR	ENBL: X10061; CAY1197.1;	
DR	ENBL: X10062; CAY1198.1;	
DR	ENBL: X10063; CAY1199.1;	
DR	ENBL: X10064; CAY1200.1;	
DR	ENBL: X10065; CAY1201.1;	
DR	ENBL: X10066; CAY1202.1;	
DR	ENBL: X10067; CAY1203.1;	
DR	ENBL: X10068; CAY1204.1;	
DR	ENBL: X10069; CAY1205.1;	
DR	ENBL: X10070; CAY1206.1;	
DR	ENBL: X10071; CAY1207.1;	
DR	ENBL: X10072; CAY1208.1;	
DR	ENBL: X10073; CAY1209.1;	
DR	ENBL: X10074; CAY1210.1;	
DR	ENBL: X10075; CAY1211.1;	
DR	ENBL: X10076; CAY1212.1;	
DR	ENBL: X10077; CAY1213.1;	
DR	ENBL: X10078; CAY1214.1;	
DR	ENBL: X10079; CAY1215.1;	
DR	ENBL: X10080; CAY1216.1;	
DR	ENBL: X10081; CAY1217.1;	
DR	ENBL: X10082; CAY1218.1;	
DR	ENBL: X10083; CAY1219.1;	
DR	ENBL: X10084; CAY1220.1;	
DR	ENBL: X10085; CAY1221.1;	
DR	ENBL: X10086; CAY1222.1;	
DR	ENBL: X10087; CAY1223.1;	
DR	ENBL: X10088; CAY1224.1;	
DR	ENBL: X10089; CAY1225.1;	
DR	ENBL: X10090; CAY1226.1;	
DR	ENBL: X10091; CAY1227.1;	
DR	ENBL: X10092; CAY1228.1;	
DR	ENBL: X10093; CAY1229.1;	
DR	ENBL: X10094; CAY1230.1;	
DR	ENBL: X10095; CAY1231.1;	
DR	ENBL: X10096; CAY1232.1;	
DR	ENBL: X10097; CAY1233.1;	
DR	ENBL: X10098; CAY1234.1;	
DR	ENBL: X10099; CAY1235.1;	
DR	ENBL: X10100; CAY1236.1;	
DR	ENBL: X10101; CAY1237.1;	
DR	ENBL: X10102; CAY1238.1;	
DR	ENBL: X10103; CAY1239.1;	
DR	ENBL: X10104; CAY1240.1;	
DR	ENBL: X10105; C	

RP INDUCTION BY CNS INJURY.
RA MEDLINE=92517173; PubMed=785047;
RA Imatsumi K., Teuda M., Manaka A., Tobiya M., Takagi T.;
RA "Differential expression of sgk mRNA, a member of the Ser/Thr protein
RA kinase family, in the brain after injury.";
RA Brain Res. Mol. Brain Res. 26:189-196(1994).
RN [3]
RP INDUCTION BY FSH. PubMed=7740159;
RA MEDLINE=9252535; PubMed=7740159;
RA Allison T., Sirois J.;
RA "Ovarian cell differentiation: a cascade of multiple hormones,
RA cellular signals, and regulated genes";
RA Endocrinol. Rev. 15:233-244(1994).
RN [4]
RP INDUCTION BY P53.
RA TISSUE=Memory epithelium;
RA PubMed=774846;
RA MEDLINE=9252191; PubMed=774846;
RA Malvar A.C., Huang A.J., Phu P.T., Cha H.H., Firestone G.L.;
RA "p53 stimulates promoter activity of the sgk.
RA serum/glucocorticoid-inducible serine/threonine protein kinase gene
RA in rodent mammary epithelial cells";
RA J. Biol. Chem. 271:12474-12482(1996).
RN [5]
RP PHOSPHORYLATION ON THR-256 BY PDKP1.
RA MEDLINE=9256246; PubMed=10357815;
RA Huang A.J., Buse P., Malvar A.C., Firestone G.L.,
RA Hemmings B.A.;
RA "Serum and glucocorticoid-inducible kinase (SGK) is a target of the PI
RA 3-kinase-stimulated signaling pathway";
RA J. Biol. Chem. 271:12474-12482(1996).
RN [6]
CC -1- FUNCTION: Protein kinase that plays an important role in
CC suggesting an involvement in the regulation of processes such as
CC cell survival, neuronal excitability and renal sodium excretion.
CC Similarity: May also play an important role in the development of
CC particular groups of neurons in the postnatal brain.
CC -1- SUBUNIT: A heterodimer of protein A and a phosphoprotein.
CC -1- SIMILARITY: (By similarity).
CC -1- TISSUE SPECIFICITY: Expressed in most tissues with highest levels
CC in the ovary, thymus and lung serum. By tumor suppressor p53 in
CC mammary epithelial tumor cells. By FSH in granulosa cells. By
CC injury to the central nervous system.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use. However, the copyright notice and the EMBL logo must be present in any
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@sib-sib.ch).
DR EMBL: P00124; AA042137.1
DR EMBL: P00131; IYDR
DR InterPro: IPR000961; Pkinase.C
DR InterPro: IPR000726; Ser_Thr_Kinase
DR Pfam: P00069; pkinase; 1.
DR Pfam: P00433; pkinase.C; 1.
DR ProDom: P000001; Prot_kinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR PROSITE: P500107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: P500109; PROTEIN_KINASE_ST; 1.
DR PROSITE: P500111; PROTEIN_KINASE_DOM; 1.
DR PROSITE: P500112; Serine/threonine protein kinase; ATP-binding;
KW Phosphorylation.
DR DOMAIN 98 354 PROTEIN KINASE.
FT NP_BIND 104 112 ATP (BY SIMILARITY).

FT BINDING 127 127 ATP (BY SIMILARITY).
FT ACT_SITE 222 222 BY SIMILARITY.
FT MOD_RES 256 256 BY SIMILARITY.
SQ SEQUENCE 430 AA: 48927 MW: 005615801506246 CRC64;
Query Match 92.2%; Score 95; DB 1; Length 430;
Best Local Similarity 89.5%; Pred. No. 2.9e-07;
Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 DPEETPEVPSNGISKPUS 19
DB 385 DPEETPEVPSNGISPD 403
RESULT 3
ID SGK_MOUSE STANDARD: PRT; 431 AA.
DC 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Serine/threonine-protein kinase SGK1 (EC 2.7.1.37)
DE SGK OR SGK1, glucocorticoid-regulated kinase 1).
GN SGK_MOUSE (Mouse)
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
ON NCBI_TaxID=10090.
RP SEQUENCE FROM N.A. PubMed=10358046;
RA Nary-Fejes-Toth A., Canessa C., Cleveland E.S., Aldrich G.,
RA Fejes-Toth G.;
RA "sgk is an aldosterone-induced kinase in the renal collecting duct.
RA Effects on epithelial Na+ channels";
RA J. Biol. Chem. 274:16575-16579(1999).
RN [2]
RP SEQUENCE FROM N.A. PubMed=10751222;
RA Seldin M., Garty H., Heuvely E.;
RA "Regulation of sgk by aldosterone and its effects on the epithelial
RA Na(+) channel";
RA Am. J. Physiol. 278:F613-F619(2000).
RN [3]
RP SEQUENCE FROM N.A.
RA STRAIN=FVB/N;
RX MEDLINE=12477932; PubMed=12477932;
RA Struhsberg B., Felingso E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Altshul S.P., Zeeberg B.S., Bueckow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan B., Moore T., Max S.I., Wang J., Hsieh P.,
RA Stachenko K., Marusik B., Garner A.A., Rubin G.M., Hong L.T., E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano M.A., Peters G.J., Abrahamson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gauratane P.H.,
RA Villalon D.K., Mazny D.W., Sodergren E.J., Lu X., Gibbs R.A., Kiyajima S.W.,
RA Fahy J., Helton E., Keteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shcherbenko Y., Bouffard G.G.,
RA Butlerfer A.C., Gramwood J.W., Schmidt R., Peterson M.C.,
RA Butterfield Y.S.M., Krywinski M.I., Skalska U., Smalish D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length
RA human cDNA sequences and their organization in genomic DNA";
RA Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP REGULATION BY P53.
RA MEDLINE=9252163; PubMed=8647846;
RA Malvar A.C., Huang A.J., Phu P.T., Cha H.H., Firestone G.L.;
RA "p53 stimulates promoter activity of the sgk."

serum/glucocorticoid-inducible serine/threonine protein kinase gene
in rodent mammary epithelial cells.*;
[5] Biol. Chem. 271:12414-12422(1996).

FUNCTION:
RC MEDLINE:22477005; Pubmed:12483118;
RA -song M.L.L., Malyar A.C., Kim B., O'Keefe B.A., Firestone G.L.;
RC "The serine/threonine protein kinase, Sdk, is a cell survival response to multiple types of environmental stress stimuli in mammary epithelial cells".
RT J. Biol. Chem. 278:5971-5982(2003).
RC
CC -1- Sdk is an estrogen-induced kinase in mammary epithelial cells,
CC suggesting an involvement in the regulation of processes such as
CC cell survival, neuronal excitability, and renal sodium excretion.
CC
CC -1- Sdk is a stress response protein.
CC
CC -1- CATALYTIC ACTIVITY: ATP + a protein -> ADP + a phosphorylated protein.
CC
CC -1- PHOSPHORYLATION LOCATION: Cytoplasmic and nuclear, upon
CC phosphorylation (by similarity).
CC
CC -1- EPITHELIAL TUMOR CELLS: The tumor suppressor p53 in mammary
CC epithelial tumor cells by ser/thr protein kinases.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the European Bioinformatics Institute and the EMBL outstation
CC at the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announcement/>
CC or send an email to license@isb-sib.ch).

CC EMBL: AF139639; AA043302.1;
CC EMBL: BC005720; AH05740.1;
CC EMBL: P00517; IYDR.

CC MD: MGI:1340652; Sgk.
CC InterPro: IPR000961; Pkinase.C.
CC InterPro: IPR002490; Ser_thr_Pkinase.
CC Pfam: PF00069; pkinase.1.
CC PRODOM: PD000001; pkinase.C.1.
CC SMART: SM00133; S_TK_X.1.
CC SMART: SM00220; S_TK_1.
CC PROSITE: PS0107; PROTEIN_KINASE_ATP.1.
CC PROSITE: PS0108; PROTEIN_KINASE_DOM.1.
CC PROSITE: PS0108; PROTEIN_KINASE_SF1.
CC Apoptosis: Transferrase; Serine/threonine-protein kinase; ATP-binding;
CC Phosphorylation. 355 PROTEIN KINASE
CC NP_BIND 104 112 ATP (BY SIMILARITY).
CC BINDING 127 137 ATP (BY SIMILARITY).
CC ACT_SITE 222 222 BY SIMILARITY.
CC MOD_RES 256 256 BY SIMILARITY.

CC ACT_SITE 222 222 BY SIMILARITY. (BY PDKP1) (BY
CC SIMILARITY).
CC MOD_RES 256 256 BY SIMILARITY.
CC
CC SEQUENCE 431 AA: 48928 MW: 50F59846A6C2754 CRC64;

Query Match 92.2%; Score 95; DB 1; Length 431;
Best Local Similarity 82.5%; Pred. No. 2.9e-07;
Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPFEETPVPNSICKSPDS 19

Db 386 DPFEETPVPNSICKSPDS 404

RESULT 4
ID SSKL_RABIT STANDARD; PRT; 431 AA.
AC QX918;
AC 16-OCT-2001 (Rel. 40, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)

serine/threonine-protein kinase Sgk1 (EC 3.7.1.37)
(Serum/glucocorticoid-regulated kinase 1).
CC SKK OR SKK1.
CC NCBI: 22477005; Pubmed: 12483118;
CC NCBI: 22477005; Pubmed: 12483118;
CC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
CC NCBI_TaxId=9986;
CC
CC SOURCE FROM N.A.
CC MEDLINE:9267894; Pubmed:10358046;
CC Nary-Rejes-Toth A., Canessa C., Cleaveland E.S., Aldrich G.,
CC "Sgk is an estrogen-induced kinase in the renal collecting duct.
CC Effects on epithelial Na⁺ channels".
CC J. Biol. Chem. 274:11697-11698(1999).
CC -1- Sgk is an estrogen-induced kinase in the renal collecting duct,
CC suggesting an involvement in the regulation of processes such as
CC cell survival, neuronal excitability, and renal sodium excretion.
CC
CC -1- Sgk is a stress response protein.
CC
CC -1- CATALYTIC ACTIVITY: ATP + a protein -> ADP + a phosphorylated protein.
CC
CC -1- PHOSPHORYLATION LOCATION: Cytoplasmic and nuclear, upon
CC phosphorylation (by similarity).
CC
CC -1- EPITHELIAL TUMOR CELLS: The tumor suppressor p53 in mammary
CC epithelial tumor cells by ser/thr protein kinases.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC at the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announcement/>
CC or send an email to license@isb-sib.ch).

CC EMBL: AF139639; AA043303.1;
CC EMBL: P00517; IYDR.
CC InterPro: IPR000961; Pkinase.C.
CC InterPro: IPR002490; Ser_thr_Pkinase.
CC Pfam: PF00069; pkinase.1.
CC PRODOM: PD000001; pkinase.C.1.
CC SMART: SM00133; S_TK_X.1.
CC SMART: SM00220; S_TK_1.
CC PROSITE: PS0107; PROTEIN_KINASE_ATP.1.
CC PROSITE: PS0108; PROTEIN_KINASE_DOM.1.
CC PROSITE: PS0108; PROTEIN_KINASE_SF1.

CC Apoptosis: Transferrase; Serine/threonine-protein kinase; ATP-binding;
CC Phosphorylation. 355 PROTEIN KINASE
CC NP_BIND 104 112 ATP (BY SIMILARITY).
CC BINDING 127 137 ATP (BY SIMILARITY).
CC ACT_SITE 222 222 BY SIMILARITY.
CC MOD_RES 256 256 BY SIMILARITY.

CC ACT_SITE 222 222 BY SIMILARITY. (BY PDKP1) (BY
CC SIMILARITY).
CC MOD_RES 256 256 BY SIMILARITY.
CC
CC SEQUENCE 431 AA: 48990 MW: 5548368775838FD CRC64;

Query Match 92.2%; Score 95; DB 1; Length 431;
Best Local Similarity 82.5%; Pred. No. 2.9e-07;
Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPFEETPVPNSICKSPDS 19

Db 386 DPFEETPVPNSICKSPDS 404

RESULT 5
ID SSKL_MOUSE STANDARD; PRT; 367 AA.
AC QX925; OR00P6;
AC 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC at the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is not modified
CC and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
CC or send an email to license@sib-sib.ch)
CC EMBL: U11791; AA79483.1; ;
DR InterPro: IPRO00784; Late_L2;
KW Casein; Casein; Casein; Late; Protein; L2; 1;
SQ SEQUENCE 460 AA; 56 38; Score 58; DB 1; Length 460;
Best Local Similarity 56 38; Pred No 3;
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
OY Query Match 56 38; Score 58; DB 1; Length 460;
Best Local Similarity 56 38; Pred No 3;
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
DB 356 DDPFTPEVPVPSIS 371
RESULT 8
ID EXTN_TOBAC STANDARD; PRT; 620 AA;
AC P13983; 1990 (rel. 13, Created)
DT 01-JAN-1990 (rel. 13, Last sequence update)
DT 16-OCT-2001 (rel. 40, Last annotation update)
DE Extensin precursor (Cell wall hydroxyproline-rich glycoprotein).
GN HRPNPT3; tabacum (Common tobacco)
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; Lamiales; Solanales; Solanaceae; Nicotiana.
RN 111-1; txid0-1097;
SQ SEQUENCE FROM N.A.
RP STRAIN-cv. Xanthi; TISSUE-Leaf;
RA Kellen, Lamb C. J. (Unpub-261350);
RT "Specific expression of a novel cell wall hydroxyproline-rich
RT glycoprotein gene in lateral root initiation."
RL [J. J. Cancer Res. 59:1879-882(1998).
CC -!- FUNCTION: HAS A SPECIFIED STRUCTURAL FUNCTION. POSSIBLY IN
CC THE MECHANICAL PENETRATION OF THE CORTEX AND EPIDERMIS OF THE
CC MAIN ROOT.
CC -!- SUBCELLULAR LOCATION: Extracellular matrix (secreted through a
CC COLLAGEN-DEPENDENT SECRETORY PATHWAY). THE PROLINE RESIDUE IS HYDROXYLATED AND THEN
CC GLYCOSYLATED.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL
CC outstation at the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is not modified
CC and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
CC or send an email to license@sib-sib.ch)
CC EMBL: X13883; CA32090.1; ;
DR InterPro: IPRO00480; Glutelin.
DR InterPro: IPRO02965; P-rich_extensin.
DR PRINTS: PR00211; GLUTELIN.
DR PRINTS: PR01217; PRICHEXTENSIN.
KW Hydroxylation; 1 20 POTENTIAL.
FT SIGNAL 21 620 EXTENSIN.
FT CHAIN 70 73 H-A-P-P.
FT REPEAT

FT REPEAT 148 151 H-A-P-P.
FT DOMAIN 229 242 2 X 7 AA TANDEN REPEATS OF T-H-H-H-A-P-P.
FT REPEAT 229 235 1.
FT REPEAT 235 242 1.
FT REPEAT 242 255 2.
FT DOMAIN 499 600 3 X APPROXIMATE TANDEN REPEATS.
SQ SEQUENCE 620 AA; 65406 MW; 64102278A28554 CRC64;
Query Match 49 51; Score 51; DB 1; Length 620;
Best Local Similarity 55 48; Pred No 3;
Matches 10; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
OY 2 PFTPEVPVPSISGSPG 19
DB 36 PFTSPPSSISGLSPSS 53
RESULT 9
ID UPK3_HUMAN STANDARD; PRT; 287 AA.
AC O75631; O60061; 39, Created)
DT 30-MAY-2000 (rel. 39, Last sequence update)
DT 16-OCT-2001 (rel. 40, Last annotation update)
DE Uroplakin III precursor (UPIII).
OS UPK3; sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OM NCBI_TxId-9606;
RP SEQUENCE FROM N.A.
RC TISSUE-Ureter;
RA Geall K., Hall G., Smith B., Southgate J.;
RN [2] submitted (AUG-1998) to the EMBL/Genbank/DBJ databases.
SQ SEQUENCE FROM N.A.
RP TISSUE-Bladder; urothelium;
RA VEDLING-9903581; Pubmed-9818021; Kim C.-J., Ilegro T., Okada Y.;
RT "Expression of uroplakin Ib and uroplakin III genes in tissues and
RT peripheral blood of patients with transitional cell carcinoma."
RL [J. J. Cancer Res. 59:1879-882(1998).
CC -!- FUNCTION: COMPONENT OF THE ASYMMETRIC UNIT BY TERMINALLY
CC HIGHLY SPECIALIZED BIOMEMBRANE ELABORATED BY TERMINALLY
CC DIFFERENTIATED UROTHELIAL CELLS. MAY PLAY AN IMPORTANT ROLE
CC IN CELL-CELL INTERACTION IN TEMPORALLY DIFFERENTIATED
CC UROTHELIAL CELLS OF THE BLADDER AND URETER.
CC UROTHELIAL GLYCOCALYX WHICH MAY PLAY AN IMPORTANT ROLE IN
CC PREVENTING BACTERIAL ADHERENCE (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC at the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is not modified
CC and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
CC or send an email to license@sib-sib.ch)
CC EMBL: X202560; BAA31480.1; ;
DR EMBL: AB010637; BAA325678.1; ;
DR EMBL: AB010116; BAA25678.1; ;
DR Genes; HMC12580; UPK3.
KW Uroplakin III; Transmembrane; Signal.
FT SIGNAL 19 287 UROPLAKIN III.
FT CHAIN 19 207 LUMENAL (POTENTIAL).
FT DOMAIN 19 207

DR EMBL: X97238; CAA65877.1; -.
 DR InterPro: IPR003760; Bmp.
 DR Pfam: PF02508; Bmp.
 DR KEGG: 04500; Bmp.
 KW Antigen; Membrane; Lipoprotein; Signal.
 FT SIGNAL 1
 FT NON_TER 1
 FT VARIANT 3
 FT VARIANT 4 325
 FT LIPID 4
 FT VARIANT 8
 FT VARIANT 12
 FT VARIANT 13
 FT VARIANT 113
 FT VARIANT 180
 FT VARIANT 205
 FT VARIANT 239
 FT VARIANT 250
 FT VARIANT 257
 SQ SEQUENCE 325 AA; 35480 MW; D192BIAZM4IC158 CRC64;
 Query Match 43.7%; Score 45; DB 1: Length 325;
 Best Local Similarity 46.2%; Prod. No. 13;
 Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
 OY 1 DREFTESPVNSI 13
 II::IIII:::
 DU 101 DPVWSEEPITNL 113

Search completed: August 11, 2003, 08:19:54
 Job time : 3.87554 secs

Result No.	Score	Query	Length	ID	Description
1	95	92.2	431	A80094	serum and glucocor
2	51	93.5	620	S06733	hydroxyproline-ric
3	48	46.6	448	T48966	hypothetical prote
4	48	46.6	490	A29290	hypothetical prote
5	48	46.6	490	A29290	mammalian dehydr
6	47.5	46.1	163	U84488	hypothetical prote
7	47.5	46.1	4006	T09070	probable tenascin
8	46.5	45.1	1660	T18362	hypothetical prote
9	46.5	45.1	1660	T18362	S-layer protein
10	46	44.7	287	T15986	cytochrome c
11	46	44.7	764	T38356	serpin homolog sp
12	46	44.7	764	T38356	serpin homolog sp
13	46	44.7	764	T38356	serpin homolog sp
14	46	44.7	837	T15925	tepa protein U6140
15	45	43.7	339	A84596	hypothetical prote
16	45	43.7	339	A84596	probable replicat
17	45	43.7	548	T32686	hypothetical prote
18	44	42.7	144	T01290	hypothetical prote
19	44	42.7	323	T00248	peroxidase GC
20	44	42.7	323	T00248	peroxidase GC
21	44	42.7	539	T50368	hypothetical prote
22	44	42.7	539	T50368	palmi Crase protei
23	44	42.7	539	T50368	palmi hypothetical
24	44	42.7	1040	S06737	homophilic protein A
25	43.5	42.2	1089	T31583	hypothetical prote
26	43	41.7	162	F84880	hypothetical prote
27	43	41.7	170	S01233	etipha-crystallin
28	43	41.7	274	T05509	hypothetical prote
29	43	41.7	274	T05509	hypothetical prote

100

Qy 2 PEFTPEPVNSICKSPUS 19

[illegible]

PT Inflammation, infections etc.

XX Claim 7; Page 9; 15pp; German.

CC The human cell-volume regulating kinase h-suk is inhibited by the

CC swelling of cells (or presence of urea), whereas cell shrinkage

CC stimulates its expression. The nucleic acid h-suk, and fragments, are

CC used for the diagnosis and treatment of diseases, specifically for

CC diagnosis of conditions that involve such changes as hypertension,

CC natriuretic, diabetes mellitus, renal insufficiency, hypercatabolism, and

CC hepatic encephalopathy. Inflammation, microbial/viral infection, fructose

CC intolerance, peripheral hypoglycemia and Alzheimer's disease.

CC Inhibitors of acid-proteinase and proteinase receptors that bind

CC h-suk, can be used to treat these disorders.

XX Sequence 19 AA:

Query Match 100.0%; Score 103; DB 19; Length 19;

Best Local Similarity 100.0%; Fred. No. 4.2e-09;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPEFTPEVPVNSGKSPDS 19

DB 1 DPEFTPEVPVNSGKSPDS 19

RESULT 2

AA959836

AA959836 standard; Protein: 321 AA.

AC AA959836;

XX 20-SEP-2001 (first entry)

DE AGC protein kinase family member SGK1 protein sequence.

XX Protein Kinase; Identification; hydrophobic pocket; Interacting:

KW cancer; diabetes; inhibition; apoptosis; tissue injury;

KW Ischaemic injury; stroke.

OS Homo sapiens.

OS Synthetic.

XX WO200114497-A2.

XX 21-JUN-2001.

XX 04-DEC-2000; 2000WO-GB04598.

XX 02-DEC-1999; 99US-0168559.

XX (UTDU-) UNIV DUNDRE.

PA Alessi D, Blondi R;

XX WPI: 2001-390252/41.

XX Identifying modulators of protein kinase (PK) activity, useful in

XX developing drugs for treating cancer or diabetes, by measuring the

PT interacting polypeptides - modulate or mimic the interaction of PK with

PT interacting polypeptides -

XX Disclosure; Fig 16; 180pp; English.

XX The present invention describes a method for identifying a compound that

XX modulates protein kinase activity. The method comprises measuring the

XX ability of the compound to inhibit, promote or mimic the interaction of

XX a hydrophobic pocket-containing protein kinase with an interacting

XX polypeptide. The interacting polypeptide interacts with the hydrophobic

XX pocket of the protein kinase and/or comprises the amino acid sequence

XX Phe/Tyr-Xaa-Xaa-Phe/Tyr (1). The method is useful in screening assays

XX for developing pharmaceutical compounds or drugs. Compounds, polypeptides

XX or polynucleotides from the present invention are useful in medicine,

XX particularly in the manufacture of a medicament for treating a patient

XX in need of modulation of signaling by a hydrophobic pocket-containing

XX protein kinase. Specifically, the patient has cancer or diabetes or is

XX in need of modulation of apoptosis or is a patient suffering from tissue

XX injury or a condition that involves such changes as hypertension, and

XX composition is also useful for inhibiting the degree or rate of

XX phosphorylation by the protein kinase. The interacting polypeptide or

XX compound is useful in methods of stabilising a hydrophobic pocket-

XX containing protein kinase. AA959836 to AA959847 represent amino acid

XX sequences, and AA94210 and AA94211 represent oligonucleotide sequences,

XX used in the exemplification of the present invention.

XX Sequence 321 AA:

Query Match 100.0%; Score 103; DB 22; Length 321;

Best Local Similarity 100.0%; Fred. No. 9.6e-08;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPEFTPEVPVNSGKSPDS 19

DB 276 DPEFTPEVPVNSGKSPDS 294

RESULT 3

AA959831

AA959831 standard; Protein: 173 AA.

AC AA959815;

XX 20-SEP-2001 (first entry)

DE AGC protein kinase family member SGK1 protein sequence.

XX Protein Kinase; Identification; hydrophobic pocket; Interacting:

KW cancer; diabetes; inhibition; apoptosis; tissue injury;

KW Ischaemic injury; stroke.

OS Homo sapiens.

OS Synthetic.

XX WO200114497-A2.

XX 21-JUN-2001.

XX 04-DEC-2000; 2000WO-GB04598.

XX 02-DEC-1999; 99US-0168559.

XX (UTDU-) UNIV DUNDRE.

PA Alessi D, Blondi R;

XX WPI: 2001-390252/41.

XX Identifying modulators of protein kinase (PK) activity, useful in

XX developing drugs for treating cancer or diabetes, by measuring the

PT ability of the compound to modulate or mimic the interaction of PK with

PT interacting polypeptides -

XX Disclosure; Fig 15; 180pp; English.

XX The present invention describes a method for identifying a compound that

XX modulates protein kinase activity. The method comprises measuring the

XX ability of the compound to inhibit, promote or mimic the interaction of

XX a hydrophobic pocket-containing protein kinase with an interacting

XX polypeptide. The interacting polypeptide interacts with the hydrophobic

XX pocket of the protein kinase and/or comprises the amino acid sequence

XX Phe/Tyr-Xaa-Xaa-Phe/Tyr (1). The method is useful in screening assays

XX for developing pharmaceutical compounds or drugs. Compounds, polypeptides

XX or polynucleotides from the present invention are useful in medicine,

XX particularly in the manufacture of a medicament for treating a patient

XX in need of modulation of signaling by a hydrophobic pocket-containing

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPRTPEPVNSIGSPDS 13
DB 385 DPRTPEPVNSIGSPDS 404

RESULT 11
AAB55614
ID AAB55614 standard; Protein; 430 AA.
XX XX
XX AAB55614;
XX XX
XX 27-MAR-2001 (first entry)
XX XX
XX Novel protein kinase, SEQ ID NO: 140.
XX XX
XX Human; mouse; protein kinase; antihistaminic; antisclerotic; osteopathic;
XX XX immunosuppressive; cardiac; renal; inflammatory; tumor; viral;
XX XX immune disorder; cardiovascular disease; neurodegenerative disease;
XX XX cancer; autoimmune disorder; stroke; inflammatory bowel disease;
XX XX inflammatory pelvic disease; multiple sclerosis; psoriasis;
XX OS NUS musculus.
XX XX WO200073459-A2.
XX XX
XX PD 07-DIC-2000.
XX XX
XX 26-MAY-2000; 2000WO-0514842.
XX XX
XX 28-MAY-1999; 99US-0136503.
XX XX
XX (SUGC) SUGEN INC.
XX XX
XX Plowman GD, Martinez R, Whyte D, Sudersanam S;
XX XX WP: 2001-032161/04.
XX DR N-FSDB; AAF44640.
XX XX
XX Nucleic acids encoding kinase polypeptides, useful for diagnosing and
XX XX treating immune-related diseases and disorders, cardiovascular disease,
XX XX neurodegenerative diseases and/or cancers.
XX XX
XX Claim 10; Fig 1: 310pp; English.

QY 3 DPRTPEPVNSIGSPDS 19
DB 386 DPRTPEPVNSIGSPDS 404

Query Match 92.24; Score 95; DN 22; Length 430;
Best Local Similarity 89.54; Pred. No. 2.3e-06;
Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPRTPEPVNSIGSPDS 19
DB 386 DPRTPEPVNSIGSPDS 404

RESULT 13
AAT93530
ID AAT93530 standard; Protein; 431 AA.
XX XX
XX AAT93530
XX XX
XX 25-SEP-2000 (first entry)
XX XX
XX DE A rat serum and glucocorticoid induced protein kinase.
XX XX
XX Protein kinase; p38 β ; p38 γ ; p38 δ ; p38 ϵ ; p38 ζ ; p38 η ; p38 θ ; p38 ι ; p38 κ ; p38 λ ; p38 μ ;
XX XX serum and glucocorticoid induced protein kinase; SGK; PKA; p38 α ;
XX XX 3-phosphoinositide-dependent protein kinase-1; PKP1; fungal infection;
XX XX thrush; cancer; diabetes; obesity; antifungal; Candida infection.
XX OS Rattus sp.
XX XX
XX PN WO200036135-A2.

DB 385 DPRTPEPVNSIGSPDS 403

RESULT 12
AAB24116
ID AAB24116 standard; Protein; 431 AA.
XX XX
XX AAB24116;
XX XX
XX 29-JAN-2001 (first entry)
XX XX
XX Rat serum and glucocorticoid regulated kinase protein (RSGK).
XX XX Human; SGK3; serine threonine kinase; HSK3; FSK;
XX XX serum and glucocorticoid regulated kinase.
XX OS Rattus sp.
XX XX
XX CNI259573-A.
XX XX
XX 12-JUN-2000.
XX XX
XX 29-OCT-1998; 98CN-0123822.
XX XX
XX 29-OCT-1998; 98CN-0123822.
XX XX
XX (UYFU) UNIV PUDAM.
XX XX
XX Yu L, Fu Q, Zhao Y;
XX XX
XX WP: 2000-587991/56.
XX XX
XX New human serine threonine protein kinase, its code sequence,
XX XX preparation, and use -
XX XX
XX Example 3; Fig 4: 29pp; Chinese.
XX XX
XX The present invention describes human serine threonine kinase SGK3.
XX XX human SGK3 shares homology with human serine threonine kinase family.
XX XX regulated kinase (HSGK) and rat SGK (RSGK). The present sequence
XX XX represents the rat RSGK protein sequence from the present invention.
XX XX
XX Sequence 431 AA;

Query Match 92.24; Score 95; DN 21; Length 431;
Best Local Similarity 89.54; Pred. No. 2.3e-06;
Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPRTPEPVNSIGSPDS 19
DB 386 DPRTPEPVNSIGSPDS 404

RESULT 13
AAT93530
ID AAT93530 standard; Protein; 431 AA.
XX XX
XX AAT93530
XX XX
XX 25-SEP-2000 (first entry)
XX XX
XX DE A rat serum and glucocorticoid induced protein kinase.
XX XX
XX Protein kinase; p38 β ; p38 γ ; p38 δ ; p38 ϵ ; p38 ζ ; p38 η ; p38 θ ; p38 ι ; p38 κ ; p38 λ ;
XX XX serum and glucocorticoid induced protein kinase; SGK; PKA; p38 α ;
XX XX 3-phosphoinositide-dependent protein kinase-1; PKP1; fungal infection;
XX XX thrush; cancer; diabetes; obesity; antifungal; Candida infection.
XX OS Rattus sp.
XX XX
XX PN WO200036135-A2.

xy

Identifying modulators of protein kinase (PK) activity, useful in developing drugs for treating cancer or diabetes, by measuring the ability of the compound to modulate or mimic the interaction of PK with interacting polypeptides -

XX

Disclosure: Fig 16: 180op: English.

XX

[illegible]

XY

Sequence 319 AA;

Query Match 62.1%; Score 64; DB 22; Length 319;
Best Local Similarity 63.2%; Pred. No. 0.11;
Matches 12; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

by

1 DPEETEEPVPNSIGKSPDS 19

3

276 DPFTQEA VSKSIGCTPDT 294

Search completed: August 11, 2003, 08:18:52
Job time : 7.03433 secs

1

No.	Score	Match length	ID	Description
1	85	100	16	Human cell
2	85	100	19	Human cell
3	85	100	32	Human cell
4	85	100	38	Human cell
5	85	100	43	Human cell
6	85	100	43	Human cell
7	85	100	43	Human cell
8	85	100	43	Human cell
9	85	100	43	Human cell
10	85	100	43	Human cell
11	85	100	43	Human cell
12	85	100	43	Human cell
13	85	100	43	Human cell
14	85	100	43	Human cell
15	85	100	43	Human cell
16	85	100	43	Human cell
17	85	100	43	Human cell
18	85	100	43	Human cell
19	85	100	43	Human cell
20	85	100	43	Human cell
21	85	100	43	Human cell
22	85	100	43	Human cell
23	85	100	43	Human cell
24	85	100	43	Human cell
25	85	100	43	Human cell
26	85	100	43	Human cell
27	85	100	43	Human cell
28	85	100	43	Human cell
29	85	100	43	Human cell
30	85	100	43	Human cell
31	85	100	43	Human cell
32	85	100	43	Human cell
33	85	100	43	Human cell
34	85	100	43	Human cell
35	85	100	43	Human cell
36	85	100	43	Human cell
37	85	100	43	Human cell
38	85	100	43	Human cell
39	85	100	43	Human cell
40	85	100	43	Human cell
41	85	100	43	Human cell
42	85	100	43	Human cell
43	85	100	43	Human cell
44	85	100	43	Human cell
45	85	100	43	Human cell
46	85	100	43	Human cell
47	85	100	43	Human cell
48	85	100	43	Human cell
49	85	100	43	Human cell
50	85	100	43	Human cell
51	85	100	43	Human cell
52	85	100	43	Human cell
53	85	100	43	Human cell
54	85	100	43	Human cell
55	85	100	43	Human cell
56	85	100	43	Human cell
57	85	100	43	Human cell
58	85	100	43	Human cell
59	85	100	43	Human cell
60	85	100	43	Human cell
61	85	100	43	Human cell
62	85	100	43	Human cell
63	85	100	43	Human cell
64	85	100	43	Human cell
65	85	100	43	Human cell
66	85	100	43	Human cell
67	85	100	43	Human cell
68	85	100	43	Human cell
69	85	100	43	Human cell
70	85	100	43	Human cell
71	85	100	43	Human cell
72	85	100	43	Human cell
73	85	100	43	Human cell
74	85	100	43	Human cell
75	85	100	43	Human cell
76	85	100	43	Human cell
77	85	100	43	Human cell
78	85	100	43	Human cell
79	85	100	43	Human cell
80	85	100	43	Human cell
81	85	100	43	Human cell
82	85	100	43	Human cell
83	85	100	43	Human cell
84	85	100	43	Human cell
85	85	100	43	Human cell
86	85	100	43	Human cell
87	85	100	43	Human cell
88	85	100	43	Human cell
89	85	100	43	Human cell
90	85	100	43	Human cell
91	85	100	43	Human cell
92	85	100	43	Human cell
93	85	100	43	Human cell
94	85	100	43	Human cell
95	85	100	43	Human cell
96	85	100	43	Human cell
97	85	100</		

CC protein kinase. Specifically, the patient has cancer or diabetes or is
 CC in need of inhibition of apoptosis, e.g. a patient suffering from tissue
 CC injury or ischemic injury, including stroke. The compound or
 CC composition of the present invention is useful for the treatment of
 CC phosphorylation by the protein kinase. The interacting polypeptide or
 CC compound is useful in methods of stabilising a hydrophobic pocket-
 CC containing protein kinase, where the protein kinase is exposed to the
 CC compound or composition of the present invention. The compound or
 CC composition of the present invention is useful for the treatment of
 CC diseases and AHA4210 and AHA4211 represent oligonucleotide sequences,
 CC used in the exemplification of the present invention.

XX Sequence 373 AA;

Query Match 100.0%; Score 85; DB 22; Length 373;

Best Local Similarity 100.0%; Pred. No. 28-05; 0; Indels 0; Gaps 0;
 Matches 16; Conservative 0; Mismatches 0;

QY 1 ENLFGSVAPPTDSFL 16

DB 373 ENLFGSVAPPTDSFL 373

RESULT 4

ID AYA48573 standard; Protein; 388 AA.

XX Sequence 388 AA;

Query Match 100.0%; Score 85; DB 20; Length 388;

Best Local Similarity 100.0%; Pred. No. 28-05; 0; Indels 0; Gaps 0;
 Matches 16; Conservative 0; Mismatches 0;

QY 08-DSC-1999 (first entry)

XX Human breast tumour-associated protein 34.

XX Expressed sequence tag; EST; human; breast; cancer; gene therapy;

XX treatment; tumour; cytostatic; medicament.

XX Homo sapiens.

XX DE1981839-A1.

XX P0 23-SEP-1999.

XX 20-MAR-1998; 980E-1013839.

XX 20-MAR-1998; 980E-1013839.

XX (META-) METAGEN GES GENOMFORSCHUNG MBH.

XX Specht T, Hinzmann B, Schmitt A, Pillarsky G, Dahl E, Rosenthal A;

XX WPI; 1999-23298/45.

XX N-PS09; AAV45311.

XX Human nucleic acid sequences and protein products from tumor breast

XX tissue, useful for breast cancer therapy

XX Claim 22; 157-158; 186pp; German.

XX This invention describes novel human nucleic acid sequences from tumor
 CC breast tissue which have cytostatic activity. The nucleic acid sequences
 CC can be used to produce and isolate full-length gene sequences. They can
 CC be used to express proteins, which can be used as tools to find an
 CC activity against breast cancer cells. The sequences can be used to sense or
 CC detect the presence of breast cancer cells. The sequences can be used for
 CC therapy to treat breast cancer. AYA48573-748617 represent protein
 CC fragments encoded by the expressed sequence tags described in the method
 CC of the invention.

XX Sequence 388 AA;

Query Match 100.0%; Score 85; DB 20; Length 388;

Best Local Similarity 100.0%; Pred. No. 28-05; 0; Indels 0; Gaps 0;
 Matches 16; Conservative 0; Mismatches 0;

QY 1 ENLFGSVAPPTDSFL 16

DB 373 ENLFGSVAPPTDSFL 388

RESULT 5

ID AAM7217 standard; Protein; 431 AA.

XX Sequence 431 AA;

Query Match 100.0%; Score 85; DB 19; Length 431;

Best Local Similarity 100.0%; Pred. No. 23e-05; 0; Indels 0; Gaps 0;
 Matches 16; Conservative 0; Mismatches 0;

QY 1 ENLFGSVAPPTDSFL 16

DB 416 ENLFGSVAPPTDSFL 431

RESULT 6

ID AAM54025 standard; Protein; 431 AA.

XX Sequence 431 AA;

Query Match 100.0%; Score 85; DB 19; Length 431;

Best Local Similarity 100.0%; Pred. No. 23e-05; 0; Indels 0; Gaps 0;
 Matches 16; Conservative 0; Mismatches 0;

QY 1 ENLFGSVAPPTDSFL 16

DB 416 ENLFGSVAPPTDSFL 431

RESULT 6

ID AAM54025 standard; Protein; 431 AA.

XX Sequence 431 AA;

Query Match 100.0%; Score 85; DB 19; Length 431;

Best Local Similarity 100.0%; Pred. No. 23e-05; 0; Indels 0; Gaps 0;
 Matches 16; Conservative 0; Mismatches 0;

QY 1 ENLFGSVAPPTDSFL 16

DB 416 ENLFGSVAPPTDSFL 431

XX The human cell-volume regulating kinase h-segk is inhibited by the
 CC swelling of cells (or presence of urea), whereas cell shrinkage
 CC stimulates its expression. The nucleic acid h-segk, and fragment, are
 CC particularly used to detect changes in cell volume, specifically for
 CC diagnosis of diseases such as diabetes mellitus, renal insufficiency, hypo-
 CC natremia, diabetes mellitus, renal insufficiency, hypercatabolism,
 CC hepatic encephalopathy, inflammation, microbial/viral infection, fructose
 CC intolerance, hyper- and hypo-glycaemia and Alzheimer's disease.
 CC The nucleic acid encoding h-segk and its binding receptors that bind
 CC h-segk, can be used to treat these disorders.

XX Sequence 431 AA;

Query Match 100.0%; Score 85; DB 19; Length 431;

Best Local Similarity 100.0%; Pred. No. 23e-05; 0; Indels 0; Gaps 0;
 Matches 16; Conservative 0; Mismatches 0;

QY 1 ENLFGSVAPPTDSFL 16

DB 416 ENLFGSVAPPTDSFL 431

RESULT 6

ID AAM54025 standard; Protein; 431 AA.

XX Sequence 431 AA;

Query Match 100.0%; Score 85; DB 19; Length 431;

Best Local Similarity 100.0%; Pred. No. 23e-05; 0; Indels 0; Gaps 0;
 Matches 16; Conservative 0; Mismatches 0;

QY 1 ENLFGSVAPPTDSFL 16

DB 416 ENLFGSVAPPTDSFL 431

RESULT 6

ID AAM54025 standard; Protein; 431 AA.

XX Sequence 431 AA;

Query Match 100.0%; Score 85; DB 19; Length 431;

Best Local Similarity 100.0%; Pred. No. 23e-05; 0; Indels 0; Gaps 0;
 Matches 16; Conservative 0; Mismatches 0;

QY 1 ENLFGSVAPPTDSFL 16

DB 416 ENLFGSVAPPTDSFL 431

29-SEP-2000; 2000US-0236369.
 PR 29-SEP-2000; 2000US-0236370.
 PR 02-OCT-2000; 2000US-0237031.
 PR 02-OCT-2000; 2000US-0237038.
 PR 02-OCT-2000; 2000US-0237039.
 PR 13-OCT-2000; 2000US-0239935.
 PR 13-OCT-2000; 2000US-0239937.
 PR 20-OCT-2000; 2000US-0240960.
 PR 20-OCT-2000; 2000US-0241765.
 PR 20-OCT-2000; 2000US-0241785.
 PR 20-OCT-2000; 2000US-0241787.
 PR 20-OCT-2000; 2000US-0241789.
 PR 20-OCT-2000; 2000US-0241826.
 PR 20-OCT-2000; 2000US-0244571.
 PR 08-NOV-2000; 2000US-0246475.
 PR 08-NOV-2000; 2000US-0246476.
 PR 08-NOV-2000; 2000US-0246477.
 PR 08-NOV-2000; 2000US-0246771.
 PR 08-NOV-2000; 2000US-0246824.
 PR 08-NOV-2000; 2000US-0246825.
 PR 08-NOV-2000; 2000US-0246826.
 PR 08-NOV-2000; 2000US-0246828.
 PR 08-NOV-2000; 2000US-0246829.
 PR 08-NOV-2000; 2000US-0246910.
 PR 08-NOV-2000; 2000US-0246911.
 PR 17-NOV-2000; 2000US-0249207.
 PR 17-NOV-2000; 2000US-0249208.
 PR 17-NOV-2000; 2000US-0249209.
 PR 17-NOV-2000; 2000US-0249211.
 PR 17-NOV-2000; 2000US-0249212.
 PR 17-NOV-2000; 2000US-0249213.
 PR 17-NOV-2000; 2000US-0249215.
 PR 17-NOV-2000; 2000US-0249216.
 PR 17-NOV-2000; 2000US-0249217.
 PR 17-NOV-2000; 2000US-0249218.
 PR 17-NOV-2000; 2000US-0249245.
 PR 17-NOV-2000; 2000US-0249246.
 PR 17-NOV-2000; 2000US-0249264.
 PR 17-NOV-2000; 2000US-0249267.
 PR 17-NOV-2000; 2000US-0249298.
 PR 17-NOV-2000; 2000US-0249300.
 PR 05-DEC-2000; 2000US-0250391.
 PR 05-DEC-2000; 2000US-0251030.
 PR 05-DEC-2000; 2000US-0251988.
 PR 06-DEC-2000; 2000US-0251989.
 PR 06-DEC-2000; 2000US-0251779.
 PR 08-DEC-2000; 2000US-0251856.
 PR 08-DEC-2000; 2000US-0251868.
 PR 08-DEC-2000; 2000US-0251889.
 PR 08-DEC-2000; 2000US-0251989.
 PR 11-DEC-2000; 2000US-0254097.
 PR 03-JAN-2001; 2000US-0255976.
 XX
 PR (HUMA-1) HUMAN GENOME SCI INC.
 XX Rosen Ch, Barazh SC, Ruban SM;
 XX WPI; 2001-581633/45.
 XX N-PSDB; ABM43988.
 DR

XX New isolated nucleic acid encoding a protein for diagnosing
 PT (1), are used to treat a medical condition and in diagnosis of a
 PT food additives or preservatives .
 XX Claim 9; SEQ ID NO 1176; 837bp; English.
 CC The invention describes an isolated nucleic acid molecule (1) encoding a
 CC novel central nervous system protein. (1) and polypeptides (11) encoded
 CC by (1), are used to treat a medical condition and in diagnosis of a
 CC disease. The invention also describes a method for identifying and
 CC autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative
 CC disorders e.g. neoplasms of the breast or liver, cardiovascular disorders
 CC e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischemia,
 CC amyotrophic lateral sclerosis, infections caused by bacteria, viruses
 CC e.g. acquired immunodeficiency virus (AIDS) and fungi, ocular disorders
 CC e.g. corneal infection, gastrointestinal disorders e.g. Crohn's disease,
 CC disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes
 CC and pituitary dwarfism, cancers and disorders at the cellular level e.g.
 CC leukemias and disorders involving hyperproliferation e.g. myeloid leu-
 CC acute kidney failure and blood related disorders e.g. myocardial
 CC infection. The polypeptides can also be used to aid wound healing and
 CC to regenerate tissues and blood. The invention also describes a method to
 CC maintain organs before transplantation, for supporting cell culture of
 CC primary tissues, to regenerate tissues and in chemotaxis. The
 CC polypeptides can also be used as a food additive or preservative to
 CC increase or decrease storage capabilities, fat content, lipid, protein,
 Query Match 68.8%; Score 58.5; UB 22; Length 276;
 Best Local Similarity 70.6%; Pred. No. 0.24; 1: Indels 1: Gaps 1:
 Matches 12: Conservative 3; Mismatches 1;
 Oy 1 EAFIGSYAPPT-DSyl 16
 Db 260 DAFVGSYAPPSNH-L 276
 RESULT 15
 XX ADU17104 standard; Protein; 276 AA.
 XX AC ADU17104;
 XX ADU17104;
 XX 07-NOV-2001 (first entry)
 XX Novel signal transduction pathway protein, Seq ID 669.
 DE Neuroprotective; cytoskeletal; dermatological; immunosuppressive; tumour;
 KW antiinflammatory; anti-HIV; anti-bacterial; antiinflammatory; cancer;
 KW immune system disorder; rheumatoid arthritis; inflammatory condition;
 KW neurodegenerative disorder; Parkinson's disease; Alzheimer's disease;
 KW sickle cell anemia; hyperproliferative disease; Crohn's disease;
 KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
 KW chromosomal abnormality; Down syndrome; ischaemia; renal disorder;
 KW irregular respiration; wound healing; endocrine; Addison's disease;
 KW acquired immunodeficiency virus (AIDS); liver disorder; AIDS;
 KW acquired immune deficiency syndrome.
 XX Homo sapiens.
 XX ADU17104 standard; Protein; 276 AA.
 XX MO200154733-A1.
 XX 02-AUG-2001.
 XX 02-AUG-2001.
 XX 31-JAN-2000; 2000US-0170665.
 XX 04-FEB-2000; 2000US-0180628.
 XX 24-FEB-2000; 2000US-0184654.
 XX 02-MAR-2000; 2000US-0186350.

PR 16-MAR-2000; 2000US-0189874.
 PR 17-MAR-2000; 2000US-0190076.
 PR 18-MAR-2000; 2000US-0200000.
 PR 19-MAY-2000; 2000US-0205515.
 PR 20-OCT-2000; 2000US-0209467.
 PR 28-JUN-2000; 2000US-0214986.
 PR 29-JUN-2000; 2000US-0215647.
 PR 07-JUL-2000; 2000US-0216880.
 PR 07-JUL-2000; 2000US-0217487.
 PR 11-JUL-2000; 2000US-0218290.
 PR 14-JUL-2000; 2000US-0220963.
 PR 26-JUL-2000; 2000US-0220964.
 PR 26-JUL-2000; 2000US-0224519.
 PR 14-AUG-2000; 2000US-0225113.
 PR 14-AUG-2000; 2000US-0225214.
 PR 14-AUG-2000; 2000US-0225267.
 PR 14-AUG-2000; 2000US-0225268.
 PR 14-AUG-2000; 2000US-0225270.
 PR 14-AUG-2000; 2000US-0225271.
 PR 14-AUG-2000; 2000US-0225757.
 PR 14-AUG-2000; 2000US-0225758.
 PR 14-AUG-2000; 2000US-0225779.
 PR 22-AUG-2000; 2000US-0236681.
 PR 22-AUG-2000; 2000US-0236688.
 PR 22-AUG-2000; 2000US-0237082.
 PR 30-AUG-2000; 2000US-0238924.
 PR 01-SEP-2000; 2000US-0239287.
 PR 01-SEP-2000; 2000US-0239343.
 PR 01-SEP-2000; 2000US-0239344.
 PR 01-SEP-2000; 2000US-0239345.
 PR 05-SEP-2000; 2000US-0239509.
 PR 05-SEP-2000; 2000US-0239510.
 PR 05-SEP-2000; 2000US-0239637.
 PR 06-SEP-2000; 2000US-0239638.
 PR 08-SEP-2000; 2000US-02311242.
 PR 08-SEP-2000; 2000US-02311243.
 PR 08-SEP-2000; 2000US-02311244.
 PR 08-SEP-2000; 2000US-02311413.
 PR 08-SEP-2000; 2000US-02311414.
 PR 08-SEP-2000; 2000US-0232080.
 PR 12-SEP-2000; 2000US-0232081.
 PR 12-SEP-2000; 2000US-0231968.
 PR 14-SEP-2000; 2000US-0232397.
 PR 14-SEP-2000; 2000US-0232398.
 PR 14-SEP-2000; 2000US-0232399.
 PR 14-SEP-2000; 2000US-0232400.
 PR 14-SEP-2000; 2000US-0232401.
 PR 14-SEP-2000; 2000US-0233062.
 PR 14-SEP-2000; 2000US-0233063.
 PR 14-SEP-2000; 2000US-0233064.
 PR 21-SEP-2000; 2000US-0234223.
 PR 21-SEP-2000; 2000US-0234224.
 PR 25-SEP-2000; 2000US-0234397.
 PR 25-SEP-2000; 2000US-0234398.
 PR 25-SEP-2000; 2000US-0234399.
 PR 25-SEP-2000; 2000US-0234584.
 PR 27-SEP-2000; 2000US-0235834.
 PR 29-SEP-2000; 2000US-0236327.
 PR 29-SEP-2000; 2000US-0236367.
 PR 29-SEP-2000; 2000US-0236368.
 PR 29-SEP-2000; 2000US-0236370.
 PR 02-OCT-2000; 2000US-0236802.
 PR 02-OCT-2000; 2000US-0237037.
 PR 02-OCT-2000; 2000US-0237038.
 PR 02-OCT-2000; 2000US-0237039.
 PR 02-OCT-2000; 2000US-0237040.
 PR 13-OCT-2000; 2000US-0239935.
 PR 13-OCT-2000; 2000US-0239936.
 PR 13-OCT-2000; 2000US-0239940.
 PR 20-OCT-2000; 2000US-0241221.
 PR 20-OCT-2000; 2000US-0241785.
 PR 20-OCT-2000; 2000US-0241786.
 PR 20-OCT-2000; 2000US-0241789.
 PR 20-OCT-2000; 2000US-0241808.
 PR 20-OCT-2000; 2000US-0241809.
 PR 20-OCT-2000; 2000US-0241825.
 PR 20-OCT-2000; 2000US-0241826.
 PR 08-NOV-2000; 2000US-0246474.
 PR 08-NOV-2000; 2000US-0246475.
 PR 08-NOV-2000; 2000US-0246476.
 PR 08-NOV-2000; 2000US-0246478.
 PR 08-NOV-2000; 2000US-0246523.
 PR 08-NOV-2000; 2000US-0246524.
 PR 08-NOV-2000; 2000US-0246525.
 PR 08-NOV-2000; 2000US-0246526.
 PR 08-NOV-2000; 2000US-0246527.
 PR 08-NOV-2000; 2000US-0246528.
 PR 08-NOV-2000; 2000US-0246529.
 PR 08-NOV-2000; 2000US-0246530.
 PR 08-NOV-2000; 2000US-0246610.
 PR 08-NOV-2000; 2000US-0246611.
 PR 17-NOV-2000; 2000US-0249207.
 PR 17-NOV-2000; 2000US-0249208.
 PR 17-NOV-2000; 2000US-0249209.
 PR 17-NOV-2000; 2000US-0249210.
 PR 17-NOV-2000; 2000US-0249211.
 PR 17-NOV-2000; 2000US-0249212.
 PR 17-NOV-2000; 2000US-0249213.
 PR 17-NOV-2000; 2000US-0249214.
 PR 17-NOV-2000; 2000US-0249215.
 PR 17-NOV-2000; 2000US-0249216.
 PR 17-NOV-2000; 2000US-0249217.
 PR 17-NOV-2000; 2000US-0249218.
 PR 17-NOV-2000; 2000US-0249244.
 PR 17-NOV-2000; 2000US-0249245.
 PR 17-NOV-2000; 2000US-0249264.
 PR 17-NOV-2000; 2000US-0249265.
 PR 17-NOV-2000; 2000US-0249267.
 PR 17-NOV-2000; 2000US-0249269.
 PR 17-NOV-2000; 2000US-0249300.
 PR 17-NOV-2000; 2000US-0249301.
 PR 01-DEC-2000; 2000US-0250191.
 PR 05-DEC-2000; 2000US-0251030.
 PR 05-DEC-2000; 2000US-0251088.
 PR 06-DEC-2000; 2000US-0251179.
 PR 06-DEC-2000; 2000US-0251856.
 PR 08-DEC-2000; 2000US-0251868.
 PR 08-DEC-2000; 2000US-0251869.
 PR 08-DEC-2000; 2000US-0251890.
 PR 08-DEC-2000; 2000US-0251990.
 PR 11-DEC-2000; 2000US-0254097.
 PR 03-JAN-2001; 2001US-0255978.
 PR (HUMA.) HUMAN GENOME SCI INC.
 PR Rosen CA, Barash SC, Ruben SM.
 PR WPI; 2001-465450/50.
 PR N-PDB; AAS27021.
 PR Novel polypeptides useful for diagnosing, treating, preventing and/or
 PR proposing disorders related to the proteins, including cancers, immune
 PR disorders and neuronal disorders.
 PR Claim 1, SEQ ID No 669; 880pp; English.
 PR

CC The invention relates to novel isolated polypeptides (1), and
 CC antibodies (2) which are useful for diagnosing, preventing and
 CC treating diseases including immune system
 CC disorders (e.g. congenital and acquired immunodeficiencies, autoimmune
 CC disorders (e.g. rheumatoid arthritis), inflammatory conditions, organ
 CC transplantation rejection, infectious diseases, autoimmune diseases
 CC (e.g. hepatitis C), bleeding disorders, haemoglobin abnormalities and
 CC other blood-related disorders (sickle cell anaemia), myeloproliferative
 CC disorders, primary haematopoietic disorders, hyperproliferative
 CC disorders (e.g. myeloid leukaemia), neurodegenerative disorders
 CC disorders (e.g. Alzheimer's disease, Parkinson's disease), chromosomal
 CC abnormalities (Down syndrome), ischaemic injury (e.g. stroke), renal
 CC disorders (e.g. glomerulonephritis), cardiovascular disorders
 CC (e.g. atherosclerosis), endocrine disorders (e.g. diabetes), disorders in
 CC wound healing, epithelial cell proliferation, endocrine disorders (e.g.
 CC Addison's disease), reproductive system disorders, gastrointestinal
 CC disorder (inflammatory disorders), liver disorders (cirrhosis),
 CC disorders (e.g. hepatitis C), infectious diseases, autoimmune diseases
 CC T-cells, to induce higher affinity antibodies, and as a means to induce
 CC tumour proliferation in pathologies e.g. acquired immune deficiency
 CC syndrome (AIDS). AM17059-AM17683 represent novel signal transduction
 CC pathway protein, amino acid sequences of the invention.
 CC

Query Match 58 84; Score 98.5; 08 22; Length 276;
 Matches 12; Conservative 3; Mismatches 1; Indels 1; Gaps 1;

Qy 1 EAFVGFSAFFT-DSEFL 16
 Db 260 DAFVGFSAFFTSDFL 276

Search completed: August 11, 2003, 08:18:52
 Job time : 5.08154 sec

DNA Res. 8, 11-22, 2001
 A: Complete genome sequence of enterohemorrhagic *Escherichia coli* O157:H7 and a
 A: Reference number: A95629; MID:21156231; PMID:11258756
 A:Accession: G90734
 A>Status: preliminary
 A:Local name: Y330-4AY>
 A:Molecule type: DNA
 A:Cross-references: CB:BA330007; PID:BA330006; GSUHR:GN00154
 A:Experimental source: strain 0157:H7, substrain RMD 050952
 A:Gene: ES0847

Query Match 52.98; Score 45; DB 2; Length 330;
 Best Local Similarity 53.34; Pred. No. 0.4;
 Matches 12; Conservative 1; Mismatches 3; Indels 4; Gaps 0;
 QY 1 EAFUGSFAPPTDSFL 15
 DB 158 ERYVGSFVAPPTDSFL 172

RESULT 6
 738904
 conserved hypothetical protein SPAC5684.02c - fission yeast (*Schizosaccharomyces pombe*)
 C:Species: *Schizosaccharomyces pombe*
 C:Accession: 738904
 C:Cross-references: EMBL:Z99261; PID:CA16193.1; GSPDB:GN00056; SWH:SPAC5684.02c
 A:Experimental source: strain 972h-; cosmid c5684
 A:Gene: SPAC5684.02c

Query Match 50.64; Score 43; DB 2; Length 162;
 Best Local Similarity 51.87; Pred. No. 0.4;
 Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY 4 LGFVAPPTDSFL 16
 DB 59 LGFVAPPTDSFL 71

RESULT 7
 873523
 probable lipoprotein R09-ori283a - *Mycoplasma pneumoniae* (strain ATCC 29342)
 A:Alternate names: R09-ori283a
 A:Accession: 873523
 A:Cross-references: ATCC 29342
 A:Variety: ATCC 29342
 C:Date: 27-Feb-1997
 C:Accession: 873523
 A:Local name: Y330-4AY>
 A:Molecule type: DNA
 A:Cross-references: GR:AE005174; MID:g12513756; PID:AA055141.1; GSPDB:GN00145; UNGP:Z09
 A:Experimental source: strain 0157:H7, substrain EDL533
 A:Gene: Z0986

Query Match 52.98; Score 45; DB 2; Length 330;
 Best Local Similarity 53.34; Pred. No. 0.4;
 Matches 12; Conservative 1; Mismatches 3; Indels 4; Gaps 0;
 QY 1 EAFUGSFAPPTDSFL 15
 DB 158 ERYVGSFVAPPTDSFL 172

RESULT 5
 G90734
 hypothetical protein EC50847 [imported] - *Escherichia coli* (strain 0157:H7, substrain RMD
 C:Species: *Escherichia coli*
 C:Accession: G90734
 C:Cross-references: EMBL:Z99261; PID:CA16193.1; GSPDB:GN00056; SWH:SPAC5684.02c
 A:Experimental source: strain 0157:H7, substrain RMD 050952
 A:Gene: ES0847

Query Match 52.98; Score 45; DB 2; Length 330;
 Best Local Similarity 53.34; Pred. No. 0.4;
 Matches 12; Conservative 1; Mismatches 3; Indels 4; Gaps 0;
 QY 1 EAFUGSFAPPTDSFL 15
 DB 158 ERYVGSFVAPPTDSFL 172

RESULT 4
 A85585
 protein encoded by prophage CP-933X [imported] - *Escherichia coli* (strain 0157:H7)
 C:Species: *Escherichia coli*
 C:Accession: A85585
 C:Cross-references: GR:AE005174; MID:g12513756; PID:AA055141.1; GSPDB:GN00145; UNGP:Z09
 A:Experimental source: strain 0157:H7, substrain EDL533
 A:Gene: Z0986

Query Match 52.98; Score 45; DB 2; Length 330;
 Best Local Similarity 53.34; Pred. No. 0.4;
 Matches 12; Conservative 1; Mismatches 3; Indels 4; Gaps 0;
 QY 1 EAFUGSFAPPTDSFL 15
 DB 158 ERYVGSFVAPPTDSFL 172

RESULT 3
 930361
 transport membrane protein (permease) [imported] - *Sulfolobus solfataricus*
 C:Species: *Sulfolobus solfataricus*
 C:Accession: 930361
 C:Cross-references: EMBL:Z99261; PID:CA16193.1; GSPDB:GN00056; SWH:SPAC5684.02c
 A:Experimental source: strain 0157:H7, substrain RMD 050952
 A:Gene: ES0847

Query Match 52.98; Score 45; DB 2; Length 330;
 Best Local Similarity 53.34; Pred. No. 0.4;
 Matches 12; Conservative 1; Mismatches 3; Indels 4; Gaps 0;
 QY 1 EAFUGSFAPPTDSFL 15
 DB 158 ERYVGSFVAPPTDSFL 172

RESULT 2
 930361
 transport membrane protein (permease) [imported] - *Sulfolobus solfataricus*
 C:Species: *Sulfolobus solfataricus*
 C:Accession: 930361
 C:Cross-references: EMBL:Z99261; PID:CA16193.1; GSPDB:GN00056; SWH:SPAC5684.02c
 A:Experimental source: strain 0157:H7, substrain RMD 050952
 A:Gene: ES0847

Query Match 52.98; Score 45; DB 2; Length 330;
 Best Local Similarity 53.34; Pred. No. 0.4;
 Matches 12; Conservative 1; Mismatches 3; Indels 4; Gaps 0;
 QY 1 EAFUGSFAPPTDSFL 15
 DB 158 ERYVGSFVAPPTDSFL 172

RESULT 1
 930361
 transport membrane protein (permease) [imported] - *Sulfolobus solfataricus*
 C:Species: *Sulfolobus solfataricus*
 C:Accession: 930361
 C:Cross-references: EMBL:Z99261; PID:CA16193.1; GSPDB:GN00056; SWH:SPAC5684.02c
 A:Experimental source: strain 0157:H7, substrain RMD 050952
 A:Gene: ES0847

Query Match 52.98; Score 45; DB 2; Length 330;
 Best Local Similarity 53.34; Pred. No. 0.4;
 Matches 12; Conservative 1; Mismatches 3; Indels 4; Gaps 0;
 QY 1 EAFUGSFAPPTDSFL 15
 DB 158 ERYVGSFVAPPTDSFL 172

Matches 7: Conservative 2: Mismatches 5: Indels 0: Gaps 0;
 QY 1 ENLPGSYAPRDS 14
 DB 204 DQFFTYTPPTQS 217

RESULT 8
 1397557
 major facilitator family transporter OC2485 [imported] - Caulobacter crescentus
 C:Accession: D87557
 C:Date: 20-Apr-2000
 C:Sequence_revision 20-Apr-2001
 C:Text_change 20-Apr-2001
 R:Neuman, W.C.; Feldblum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.A.; Heidelberg, J.F.; B. J. Lau, M.; J. M. White, O. Salzberg, S.L. Shapiro, L. Ventner, J.C.; Fraser, C.M.
 Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
 A>Title: Complete Genome Sequence of *Caulobacter crescentus*.
 A:Reference number: AB7245; NID:21173698; PMID:11259647
 A:Status: Preliminary
 A:Molecule type: DNA
 A:Residues: 1444 <S>C>
 C:Genetic: GC2485

Query Match 50.6%; Score 43; DB 2: Length 444;
 Best Local Similarity 60.0%; Pred. No. 30;
 Matches 8: Conservative 3: Mismatches 4: Indels 0: Gaps 0;
 QY 1 ENLPGSYAPRDS 15
 DB 241 KAPDTGTAPPTAS 255

RESULT 9
 970 837
 kinases (RC 2.7.2.1) - human
 C:Accession: J03777
 C:Date: 23-Jul-1999
 C:Sequence_revision 23-Jul-1999
 C:Text_change 21-Jul-2000
 R:Salton, J.; Kohn, J.P.; Miyagawa, Y.; Ishijima, H.
 J. Biol. Chem. 273, 470-476, 1998
 A>Title: Cloning and characterization of p70s6kbeta defines a novel family of p70 s6 kinases.
 A:Reference number: J03777; NID:59097259; PMID:9878960
 A:Status: Preliminary
 A:Molecule type: mRNA
 A:Residues: 1481 <S>M>
 C:Cross-references: NID:4165310; PMID:58037145; 1; PMID:94165311
 C:Keywords: phosphotransferase

Query Match 50.6%; Score 43; DB 2: Length 481;
 Best Local Similarity 58.3%; Pred. No. 32;
 Matches 7: Conservative 3: Mismatches 2: Indels 0: Gaps 0;
 QY 1 ENLPGSYAPRPT 12
 DB 381 QALGTIVAFSS 392

RESULT 10
 754642
 rib metallopeptidase-like protein - Arabidopsis thaliana
 C:Accession: J03777
 C:Date: 04-Feb-2000
 C:Sequence_revision 04-Feb-2000
 C:Text_change 04-Mar-2000
 R:Chen, N.; Koppert, C.; Brottler, P.; Winkler, P.; Gattolico, L.; Artiguenave, F.; S. Artiguenave, F.
 A:Reference number: 22310

A:Accession: 745642
 A:Status: Preliminary
 A:Residues: 1-802 <C>
 A:Cross-references: EMBL:AL133492
 A:Experimental source: cultivar Columbia; BAC clone F13112
 A:Map position: 3
 A:Introns: 275/3; 296/3; 341/3; 363/3; 425/3; 454/3; 492/3; 534/3; 570/3; 612/3; 719/3
 A:Notes: F13112.110

Query Match 50.6%; Score 43; DB 2: Length 802;
 Best Local Similarity 60.0%; Pred. No. 56;
 Matches 9: Conservative 2: Mismatches 2: Indels 2: Gaps 1;
 QY 4 LGFSYAPPT--DSFL 16
 DB 624 LGSTYTPHSDRFL 638

RESULT 11
 C82437
 Atolase 1 VCA0624 [imported] - Vibrio cholerae (strain N1696) serogroup O1
 C:Accession: J03777
 C:Date: 18-Aug-2000
 C:Sequence_revision 20-Aug-2000
 C:Text_change 02-Feb-2001
 R:Chardon, D.; Emolove, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Bradol, L.; Sellers
 L. R.R.; Mekalanos, J.J.; Ventner, J.C.; Fraser, C.M.
 Nature 406, 477-483, 2000
 A>Title: The Vibrio cholerae pathogen proteome.
 A:Reference number: A02035; NID:20406833; PMID:10952301
 A:Accession: C82437
 A:Status: Preliminary
 A:Residues: 1-680 <E>
 A:Cross-references: GB:AE004392; NID:9658031; PMID:9658031; PMID:AAFW6525; 1; GSUBJUG
 A:Experimental source: serogroup O1; strain N1696; biotype El Tor
 A:Map position: 2
 C:Superfamily: transketolase; thiamin pyrophosphate-binding domain homology

Query Match 50.0%; Score 42.5; DB 2: Length 680;
 Best Local Similarity 56.2%; Pred. No. 56;
 Matches 9: Conservative 2: Mismatches 2: Indels 3: Gaps 1;
 QY 3 PLGTSYAP--PTDSF 15
 DB 291 FLGNTAFPEIPDIY 306

RESULT 12
 T26528
 ribosomal protein Y18D10A.3 - Caenorhabditis elegans
 C:Accession: J03777
 C:Date: 15-Oct-1999
 C:Sequence_revision 15-Oct-1999
 C:Text_change 15-Oct-1999
 R:Kittling, J.
 A>Title: The *Caenorhabditis elegans* ribosomal protein Y18D10A.
 A:Reference number: 220226
 A:Status: Preliminary
 A:Residues: 1-348 <M>
 A:Cross-references: EMBL:AL034393; PMID:CA22319.1; CESP:Y18D10A.3
 A:Experimental source: clone Y18D10A
 A:Gene: CESP:Y18D10A.3
 A:Introns: 10/2; 109/1; 168/1; 193/3

Query Match 49.4%; Score 42; DB 2: Length 348;
 Best Local Similarity 58.3%; Pred. No. 32;
 Matches 9: Conservative 2: Mismatches 2: Indels 3: Gaps 1;
 QY 3 PLGTSYAP--PTDSF 15
 DB 291 FLGNTAFPEIPDIY 306

RESULT 13
 T26528
 ribosomal protein Y18D10A.3 - Caenorhabditis elegans
 C:Accession: J03777
 C:Date: 15-Oct-1999
 C:Sequence_revision 15-Oct-1999
 C:Text_change 15-Oct-1999
 R:Kittling, J.
 A>Title: The *Caenorhabditis elegans* ribosomal protein Y18D10A.
 A:Reference number: 220226
 A:Status: Preliminary
 A:Residues: 1-348 <M>
 A:Cross-references: EMBL:AL034393; PMID:CA22319.1; CESP:Y18D10A.3
 A:Experimental source: clone Y18D10A
 A:Gene: CESP:Y18D10A.3
 A:Introns: 10/2; 109/1; 168/1; 193/3

Query Match 49.4%; Score 42; DB 2: Length 348;
 Best Local Similarity 58.3%; Pred. No. 32;
 Matches 9: Conservative 2: Mismatches 2: Indels 3: Gaps 1;
 QY 3 PLGTSYAP--PTDSF 15
 DB 291 FLGNTAFPEIPDIY 306

Matches 7: Conservative 2: Mismatches 3: Indels 0: Gaps 0:

QY 1 PAFGSGVAPPT 12
 1 ||||| |||

DB 240 DAIRGSEPHPT 251

RESULT 13

Hypothetical protein glr1610 - Synchocystis sp. (strain PCC 6803)

A:Variety: PCC 6803

C:Date: 25-Apr-1997 sequence_revision 25-Apr-1997 text_change 20-Jun-2000

C:Accession: S74753 S.: Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, M.;

O. K.; Okumura, S.; Shiepo, S.; Takeuchi, C.; Wada, T.; Watanabe, M.; Yasuda

DAIR Res. 3, 109-136, 1996

Article: Sequence analysis of the genome of the unicellular cyanobacterium Synchocystis

A:Reference number: S74322; MUID:97061201; PMID:8905231

A:Accession: S74753

A>Status: nucleic acid sequence not shown; translation not shown

A:Residues: 1-433 <RAN>

A:Cross-references: EMBL:D90901; GB:AB001339; NID:g1651897; PIDN:BAI16904.1; PTD:g165197

A:Note: The nucleotide sequence was submitted to the EMBL Data Library, June 1996

A:Start codon: GTG

C:Superfamily: Mnycolatopsis orientalis hypothetical protein PCZA361.22

Query Match 49.4%; Score 42; DB 2: Length 433;

Best Local Similarity 37.5%; Pred. No. 42;

Matches 6: Conservative 6: Mismatches 4: Indels 0: Gaps 0:

QY 1 PAFGSGVAPPTDSFL 16

5 ||||| ||||| |||

DB 39 OTFLDLGFAPPSNAYL 54

RESULT 14

Inter-alpha-inhibitor H2 chain - mouse

A:Variety: Mus musculus

C:Date: 15-Jul-1995 sequence_revision 01-Sep-1995 text_change 20-Aug-1999

C:Accession: S43354

R.Chan, P.; Risler, J.L.; Raguenez, G.; Saller, J.P.

Article: The three heavy-chain precursors for the inter-alpha-inhibitor family in mouse

A:Reference number: S43353; MUID:95194326; PMID:7534067

A:Accession: S43354

A>Status: nucleic acid sequence not shown

A:Residues: 1-946 <CH>

A:Cross-references: EMBL:X70322; NID:g9595633; PIDN:CAA49842.1; PTD:g9595634

C:Superfamily: Inter-alpha-trypsin inhibitor complex component 11

Query Match 48.8%; Score 41.5; DB 2: Length 946;

Best Local Similarity 69.2%; Pred. No. 1.2e+02;

Matches 9: Conservative 0: Mismatches 3: Indels 1: Gaps 1:

QY 3 FLGSGVAPPTDSF 15

||||| ||||| ||

DB 841 FLGI-YAPPIDMF 852

RESULT 15

Hypothetical protein TP0708 - syphilis spirochete

C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)

C:Date: 24-Jul-1998 sequence_revision 24-Jul-1998 text_change 05-Nov-1999

C:Accession: H71289

A:Reference number: S43353; MUID:95194326; PMID:7534067

A:Status: nucleic acid sequence not shown

A:Residues: 1-946 <CH>

A:Cross-references: EMBL:X70322; NID:g9595633; PIDN:CAA49842.1; PTD:g9595634

C:Superfamily: Inter-alpha-trypsin inhibitor complex component 11

Query Match 48.8%; Score 41.5; DB 2: Length 946;

Best Local Similarity 69.2%; Pred. No. 1.2e+02;

Matches 9: Conservative 0: Mismatches 3: Indels 1: Gaps 1:

they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.

Article: Complete genome sequence of Treponema pallidum, the syphilis spirochete.

A:Reference number: H71289; MUID:98332770; PMID:9665876

A:Accession: H71289

A>Status: Preliminary; nucleic acid sequence not shown; translation not shown

A:Residues: 1-171 <COL>

A:Cross-references: GB:AB001244; GB:AB0000520; NID:g3223005; PIDN:AA05645.1; PTD:g333

A:Experimental source: strain Nichols

C:Accession: TP0708

A:Gene: TP0708

Query Match 48.2%; Score 41; DB 2: Length 171;

Best Local Similarity 58.2%; Pred. No. 23;

Matches 3: Conservative 3: Mismatches 2: Indels 0: Gaps 0:

QY 4 LQSVIAPPTDSF 15

||||| ||||| |||

DB 127 LQSVIAPPTDSF 138

Search completed: August 11, 2003, 08:23:29

Job Line: 4.12876 secs

OR	InterPro: IPRO002290; Ser_Thr_kinase.
OR	Pfam: PF00049; Pkinase_1.
OR	SMART: SMT0133; S_TK_1.
OR	Problem: PRO00001; PRO_Kinase: 1.
OR	SMART: SMT0133; S_TK_1.
OR	SMART: SH00220; S_TKc_1.
OR	PROSITE: PS00101; KINASE_ATP_1.
OR	PROSITE: PS00101; PROTEIN_KINASE_SF_1.
OR	APoptosis: Transferase: Serine/threonine-protein kinase; ATP-binding;
OR	Phosphorylation. 355
OR	PROSITE: PS00101; KINASE_ATP_1.
OR	NP_BIND 104 112
OR	ATP (BY SIMILARITY).
OR	BINDING 127 127
OR	FT SITE 222 222
OR	FT SITE 222 222
OR	MOLRES 436 436
OR	MOLECULAR WEIGHTS 431 AA; 48928 MW; 6DF5B846AAC2754 CRC64;
OR	Seq
OR	Query Match 94.1%; Score 80; D/B 1; Length 431;
OR	Best Local Similarity 93.8%; Proc No. 7,2e-06;
OR	Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY	1 EAFGSGYAPPVPSFL 16
OD	416 EAFGSGYAPPVDSFL 431
RESULT 3	
ID	SGKL_RAT STANDARD; PRF: 430 AA.
AC	Q06256.1 g95 (Ref. 31, Created)
CD	01-FEB-1995 (Ref. 31, Last sequence update)
DT	15-SEP-2003 (Ref. 42, Last annotation update)
DB	Serine/threonine-protein kinase sgkl (PC 2.7.1.37)
DE	(Serine/threonine-specific protein kinase) [EC 2.7.1.37]
OS	Rattus norvegicus (Rat).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC	Mammalia; Eutheria; Rodentia; Sciurognatha; Muridae; Rattus;
LN	L3_Taxidiv-10116;
RP	SEQUENCE FROM N.A.
RC	SRPIN-Pischaer 34;
RA	Heuber M.C., Roys L., Ge Y., Malvar A.C., Firestone G.L.;
RT	"Characterization of sgk, a novel member of the serine/threonine
RF	protein kinase gene family which is transcriptionally induced by
RI	cAMP and growth factors in rat brain after CNS injury";
RN	Mol. Cell. Biol. 13:2031-2040(1993).
EX	[2]
RA	INDUCTION BY CNS INJURY
RE	137,135-137; PubMed=7654007;
RP	Izumi K., Tada M., Watabe A., Toyama M., Takai T.
RF	"Differential expression of sgk mRNA, a member of the Ser/Thr protein
RI	kinase gene family, in rat brain after CNS injury";
RN	Brain Res. Mol. Brain Res. 26:189-196(1994).
EX	INDUCTION BY FSH
RE	MEDLINE=9525863;
RP	Richard J.S., Fitzpatrick S.L., Clemens J.H., Morris J.K.,
RF	"Ovarian cell differentiation: a cascade of multiple hormones,
RI	cellular signals, and regulated genes";
RN	Recent Prog. Horm. Res. 50:233-254(1995).
EX	INDUCTION BY P53
RE	TISSUE-Mammary epithelium;
RP	MEDLINE=9621813;
RA	Malvar A.C., Huang A.J., Bu P.T., Cha H.H., Firestone G.L.;
RF	Regulation of p53-inducible serine/threonine protein kinase gene
RI	family in mammary epithelial cells";
RN	Cancer Res. Clin. Oncol. 109:103-111(1999).

Tue Aug 12 10:56:10 2003

us-10-000-039a-4.rsp

Page 12

OY 4 LOFSXAPPTDSE 15
DB 127 LOFSXSTPSP 138

Search completed: August 11, 2003, 08:19:56
Job time : 3.594 secs

[illegible]

Tue Aug 12 10:56:10 2003

us-10-000-039a-4.rspt

Page 7

Search completed: August 11, 2003, 08:22:16
Job time : 6.29165 secs

DB 1 EAFGFSVAPPTDSFL 16

RESULT 2

US-08-712-709-5 Application US/08712709

Patent No. 5663780

GENERAL INFORMATION:

APPLICANT: Au-Young, Janice

INVENTOR: Au-Young, Janice

APPLICANT: Hawkins, Phillip R.

APPLICANT: Hawkins, Phillip R.

TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES

NUMBER OF SEQUENCES: 9

ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive

CITY: Palo Alto

COUNTRY: U.S.

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSQ Version 1.5

TELEPHONE: 415-855-4155

TELEFAX: 415-845-4156

APPLICATION NUMBER: US/08/712,709

FILING DATE: Filed herewith

ATTORNEY/AGENT INFORMATION:

REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0118 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-855-4155

TELEFAX: 415-845-4156

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 331 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLSCULE TYPE: Peptide

IMMEDIATE SOURCE:

LIBRARY:

CLONE: Consensus

US-08-712-709-5

Query Match 100.0%; Score 85; DB 2; Length 431;

Best Local Similarity 100.0%; Pred. No. 8.8e-06;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EAFGFSVAPPTDSFL 16

DB 416 EAFGFSVAPPTDSFL 431

RESULT 3

US-09-111-444-5 Application US/09111444

Patent No. 6045792

GENERAL INFORMATION:

APPLICANT: Au-Young, Janice

INVENTOR: Au-Young, Janice

APPLICANT: Hawkins, Phillip R.

APPLICANT: Hawkins, Phillip R.

TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES

NUMBER OF SEQUENCES: 9

ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive

CITY: Palo Alto

COUNTRY: U.S.

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSQ Version 1.5

TELEPHONE: 415-855-4155

TELEFAX: 415-845-4156

APPLICATION NUMBER: US/09/111,444

FILING DATE: Filed herewith

PRIOR APPLICATION DATA:

ATTORNEY/AGENT INFORMATION:

REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0118 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-855-4155

TELEFAX: 415-845-4156

APPLICATION NUMBER: 08/712,709

NAME: Billings, Lucy J

REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0118 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-855-4155

TELEFAX: 415-845-4156

APPLICATION NUMBER: 08/712,709

NAME: Billings, Lucy J

REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0118 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-855-4155

TELEFAX: 415-845-4156

APPLICATION NUMBER: 08/712,709

NAME: Billings, Lucy J

REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0118 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-855-4155

TELEFAX: 415-845-4156

APPLICATION NUMBER: 08/712,709

NAME: Billings, Lucy J

REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0118 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-855-4155

TELEFAX: 415-845-4156

APPLICATION NUMBER: 08/712,709

NAME: Billings, Lucy J

REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0118 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-855-4155

TELEFAX: 415-845-4156

APPLICATION NUMBER: 08/712,709

NAME: Billings, Lucy J

REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0118 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-855-4155

TELEFAX: 415-845-4156

APPLICATION NUMBER: 08/712,709

NAME: Billings, Lucy J

REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0118 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-855-4155

TELEFAX: 415-845-4156

APPLICATION NUMBER: 08/712,709

NAME: Billings, Lucy J

REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0118 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-855-4155

TELEFAX: 415-845-4156

APPLICATION NUMBER: 08/712,709

NAME: Billings, Lucy J

REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0118 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-855-4155

TELEFAX: 415-845-4156

APPLICATION NUMBER: 08/712,709

NAME: Billings, Lucy J

REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0118 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-855-4155

TELEFAX: 415-845-4156

APPLICATION NUMBER: 08/712,709

NAME: Billings, Lucy J

REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0118 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-855-4155

TELEFAX: 415-845-4156

APPLICATION NUMBER: 08/712,709

NAME: Billings, Lucy J

REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0118 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-855-4155

TELEFAX: 415-845-4156

APPLICATION NUMBER: 08/712,709

NAME: Billings, Lucy J

REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0118 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-855-4155

TELEFAX: 415-845-4156

APPLICATION NUMBER: 08/712,709

NAME: Billings, Lucy J

REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0118 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-855-4155

TELEFAX: 415-845-4156

APPLICATION NUMBER: 08/712,709

NAME: Billings, Lucy J

REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0118 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-855-4155

TELEFAX: 415-845-4156

APPLICATION NUMBER: 08/712,709

NAME: Billings, Lucy J

REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0118 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-855-4155

TELEFAX: 415-845-4156

APPLICATION NUMBER: 08/712,709

NAME: Billings, Lucy J

REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0118 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-855-4155

TELEFAX: 415-845-4156

APPLICATION NUMBER: 08/712,709

NAME: Billings, Lucy J

REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0118 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-855-4155

TELEFAX: 415-845-4156

APPLICATION NUMBER: 08/712,709

NAME: Billings, Lucy J

REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0118 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-855-4155

TELEFAX: 415-845-4156

APPLICATION NUMBER: 08/712,709

NAME: Billings, Lucy J

REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0118 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-855-4155

TELEFAX: 415-845-4156

APPLICATION NUMBER: 08/712,709

NAME: Billings, Lucy J

REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0118 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-855-4155

TELEFAX: 415-845-4156

APPLICATION NUMBER: 08/712,709

NAME: Billings, Lucy J

REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0118 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-855-4155

TELEFAX: 415-845-4156

APPLICATION NUMBER: 08/712,709

NAME: Billings, Lucy J

REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0118 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-855-4155

TELEFAX: 415-845-4156

APPLICATION NUMBER: 08/712,709

NAME: Billings, Lucy J

REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0118 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-855-4155

TELEFAX: 415-845-4156

APPLICATION NUMBER: 08/712,709

NAME: Billings, Lucy J

REGISTRATION NUMBER: 36,749

TELEFAX: 415-845-4166
 INVENTOR: FOLEY & LARONER
 SEQUENCE CHARACTERISTICS:
 LENGTH: 431 amino acids
 TYPE: amino acid
 COMPOSITION: 19.5% acidic
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 IMMEDIATE SOURCE:
 CLONING: Consensus

US-09-541-228-5
 Query Match 100.0% Score 85; DP 3; Length 431;
 Basic Local Similarity 100.0%; Pred. No. 8.8e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENFLGFSYAPPTDSFL 16
 DB 416 ENFLGFSYAPPTDSFL 431

RESULT 5
 US-09-011-295-2
 Sequence 2, Application US/09031295
 GENERAL INFORMATION:
 APPLICANT: LANG, Florian
 APPLICANT: MALDOGGER, Tubingen
 TITLE OF INVENTION: CELL VOLUME-REGULATED HUMAN KINASE H-SOK
 FILING DATE: 28-FEB-1997
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: FOLEY & LARONER
 STREET: 3000 K Street, N.W.
 CITY: Washington
 STATE: D.C.
 COUNTRY: U.S.A.
 ZIP: 20007-5109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS DOS
 SOFTWARE: GENBANK RELEASE 11.0, Version #1.30
 CURRENT APPLICATION DATA: US/09/031,295
 FILING DATE: 28-FEB-1998
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: DE 197-08-173.8
 FILING DATE: 28-FEB-1997
 NAME: Lang, Florian
 APPLICANT: SANDERCOCK, Colin G.
 REGISTRATION NUMBER: 31,298
 REFERENCE/DOCKET NUMBER: 058315/0123
 TELEPHONE: (202) 672-5300

TELEFAX: (202) 672-5399
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 431
 TYPE: amino acid
 TOPOLOGY: linear
 IMMEDIATE SOURCE: protein
 CLONING: Consensus

US-09-011-295-2
 Query Match 100.0% Score 85; DP 4; Length 431;
 Basic Local Similarity 100.0%; Pred. No. 8.8e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENFLGFSYAPPTDSFL 16
 DB 416 ENFLGFSYAPPTDSFL 431

RESULT 6
 US-08-712-709-9
 Sequence 9, Application US/08712709
 Patent No. 5863780
 GENERAL INFORMATION:
 APPLICANT: Au Young, Janice
 APPLICANT: Guegler, Karl J.
 APPLICANT: HAWKINS, PHILLIP K.
 TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES
 NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Incyte Pharmaceuticals, Inc.
 STREET: 1774 Porter Drive
 CITY: Palo Alto
 STATE: CA
 COUNTRY: U.S.
 ZIP: 94304

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: PC-DOS/MS DOS
 SOFTWARE: GENBANK RELEASE 11.3
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/712,709
 FILING DATE: Filled Herewith
 NAME: Billings, Lucy J
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PF-0118 US
 TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES
 TELEPHONE: 415-845-0553
 TELEFAX: 415-845-4166
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 431
 TYPE: amino acid
 TOPOLOGY: linear
 STRANDEDNESS: single
 IMMEDIATE SOURCE: peptide
 LIBRARY: GenBank
 CLONE: 294637

US-08-712-709-9
 Query Match 92.98; Score 79; DP 2; Length 430;
 Basic Local Similarity 93.88; Pred. No. 7.6e-05;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ENFLGFSYAPPTDSFL 16
 DB 415 ENFLGFSYAPPTDSFL 430

RESULT 7
 US-09-111-444-9
 Sequence 9, Application US/0911444
 Patent No. 6045792
 GENERAL INFORMATION:
 APPLICANT: Au Young, Janice
 APPLICANT: Guegler, Karl J.
 APPLICANT: HAWKINS, PHILLIP K.
 TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES
 NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Incyte Pharmaceuticals, Inc.
 STREET: 3174 Porter Drive
 CITY: Palo Alto
 STATE: CA
 COUNTRY: U.S.
 ZIP: 94304

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette

```

1  COMPUTER: IBM Compatible
2  SOFTWARE: FASTSEQ version 1.5
3  CURRENT APPLICATION DATA:
4  APPLICATION NUMBER: US/09/111,444
5  PRIOR APPLICATION DATA:
6  APPLICATION NUMBER: 08/712,709
7  FILING DATE:
8  NAME: Billings, Lucy J
9  REGISTRATION NUMBER: 36,749
10 REFERENCE/DOCKET NUMBER: PF-0118 US
11 TELEPHONE: 415-845-4166
12 TELEFAX: 415-845-4166
13 INFORMATION FOR SEQ ID NO: 9:
14 SEQUENCE CHARACTERISTICS:
15 LENGTH: 430 amino acids
16 TYPE: amino acid
17 STRANDEDNESS: single
18 MOLECULE TYPE: peptide
19 IMMEDIATE SOURCE:
20 LIBRARY: GenBank
21 US-09-111-444-9
22
23 Query Match 92.9%; Score 79; DB 3; Length 430;
24 Best Local Similarity 92.8%; Pred. No. 7.6e-05;
25 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
26
27 Oy 1 EAFLGSTAPPTDSTL 16
28 Db 415 EAFLGSTAPPTDSTL 430
29
30 RESULT 8
31 US-09-541-228-9
32 Sequence 9, Application US/09/541,228
33 Patent No. 6232077
34 GENERAL INFORMATION:
35 APPLICANT: Au-Young, Janice
36 APPLICANT: Guebler, Karl J.
37 APPLICANT: Hewlett, Phillip R.
38 APPLICANT: Hwang, Daniel
39 NUMBER OF SEQUENCES: 9
40 CORRESPONDENCE ADDRESS:
41 ADDRESSEE: Incyte Pharmaceuticals, Inc.
42 STREET: 1100 Winter Drive
43 CITY: Palo Alto
44 STATE: CA
45 COUNTRY: U.S.
46
47 COMPUTER READABLE FORM:
48 MEDIUM TYPE: Diskette
49 COMPUTER: IBM Compatible
50 SOFTWARE: FASTSEQ version 1.5
51 CURRENT APPLICATION DATA:
52 APPLICATION NUMBER: US/09/541,228
53 FILING DATE:
54 APPLICATION NUMBER: 08/712,709
55
56 ATTORNEY/AGENT INFORMATION:
57 FIRM:
58 REGISTRATION NUMBER: 36,749
59 REFERENCE/DOCKET NUMBER: PF-0118 US
60 TELECOMMUNICATION INFORMATION:
61 TELEPHONE: 415-845-4166
62 TELEFAX: 415-845-4166
63 INFORMATION FOR SEQ ID NO: 9:

```

```

1  SEQUENCE CHARACTERISTICS:
2  LENGTH: 430 amino acids
3  TYPE: amino acid
4  STRANDEDNESS: single
5  TOPOLOGY: linear
6  MOLECULE TYPE: peptide
7  IMMEDIATE SOURCE:
8  LIBRARY: GenBank
9  US-09-541-228-9
10
11 Query Match 92.9%; Score 79; DB 3; Length 430;
12 Best Local Similarity 92.8%; Pred. No. 7.6e-05;
13 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
14
15 Oy 1 EAFLGSTAPPTDSTL 16
16 Db 415 EAFLGSTAPPTDSTL 430
17
18 RESULT 9
19 US-09-541-228-9
20 Sequence 7, Application US/09/541,228
21 Patent No. 6372467
22 GENERAL INFORMATION:
23 APPLICANT: John Blenis
24 APPLICANT: Joseph E. Friedman
25 APPLICANT: Calvin J. Kuo
26
27 TITLE OF INVENTION: P5456K AND P8556K GENES; PROTEINS,
28 TITLE OF INVENTION: PRIMERS, PROBES, AND DETECTION METHODS
29 CURRENT APPLICATION NUMBER: US/09/430,564
30 PRIOR APPLICATION NUMBER: 09/430,564
31 PRIOR FILING DATE: 1998-10-29
32 NUMBER OF SEQ ID NOS: 16
33 SOFTWARE: FASTSEQ for Windows Version 4.0
34 SEQ ID NO: 7
35 LENGTH: 66
36 TYPE: PRT
37 ORGANISM: Homo sapiens
38 US-09-430-564-7
39
40 Query Match 50.6%; Score 43; DB 4; Length 66;
41 Best Local Similarity 50.3%; Pred. No. 5.2;
42 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
43
44 Oy 1 EAFLGSTAPPT 12
45 Db 31 EAFLGSTAPPTVNS 62
46
47 RESULT 10
48 US-09-430-564-13
49 Sequence 7, Application US/09/430,564
50 Patent No. 6372467
51 GENERAL INFORMATION:
52 APPLICANT: John Blenis
53 APPLICANT: Joseph E. Friedman
54 APPLICANT: Calvin J. Kuo
55
56 TITLE OF INVENTION: P5456K AND P8556K GENES; PROTEINS,
57 TITLE OF INVENTION: PRIMERS, PROBES, AND DETECTION METHODS
58 CURRENT APPLICATION NUMBER: US/09/430,564
59 PRIOR APPLICATION NUMBER: 09/430,564
60 PRIOR FILING DATE: 1998-10-29
61 NUMBER OF SEQ ID NOS: 16
62 SOFTWARE: FASTSEQ for Windows Version 4.0
63 SEQ ID NO 13
64 LENGTH: 66
65 TYPE: PRT
66 ORGANISM: Homo sapiens

```


1 COUNTRY: USA
 2 COMPUTER READABLE FORM:
 3 MEDIUM TYPE: Floppy disk
 4 COMPUTER: IBM PC Compatible
 5 OPERATING SYSTEM: PC-DOS/MS-DOS
 6 CURRENT APPLICATION DATA: Release #1.0, Version #1.30
 7 APPLICATION NUMBER: US/08/624,125
 8 FILING DATE: 29-MAR-1996
 9 CLASSIFICATION:
 10 ATTORNEY/AGENT INFORMATION:
 11 NAME: KELBER, STEVEN B.
 12 REGISTRATION NUMBER: 30,073
 13 TELEPHONE: 703-413-3000
 14 TELECOMMUNICATION INFORMATION:
 15 TELEPHONE: 703-413-3000
 16 TELEFAX: 703-413-2220
 17 INVENTOR INFORMATION:
 18 NAME: KELBER, STEVEN B.
 19 REGISTRATION NUMBER: 30,073
 20 TELEPHONE: 703-413-3000
 21 TELEFAX: 703-413-2220
 22 SEQUENCE CHARACTERISTICS:
 23 LENGTH: 162 amino acids
 24 TYPE: amino acid
 25 STRANDEDNESS: single
 26 MOLECULE TYPE: protein
 27 US-08-624-125-5

Query Match 48.2%; Score 41; DB 1: Length 162;
 Best Local Similarity 77.8%; Pred. No. 26;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 5 GFSYAPPD 13
 DB 134 GFIAPPVD 142

RESULT 15
 US-08-624-125-8
 Sequence 8, Application US/08624125
 Patent No. 5744341
 GENE INFORMATION:
 APPLICANT: CUNNINGHAM JR., FRANCIS X.
 APPLICANT: SUN, ZAIREN
 TITLE OF INVENTION: GENES OF CAROTENOID BIOSYNTHESIS AND
 THEIR EXPRESSION IN METABOLISM AND A SYSTEM FOR SCREENING SUCH GENES
 NUMBER OF INVENTORS: 1
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
 ATTORNEYS AT LAW
 STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
 CITY: ARLINGTON
 STATE: VA
 COUNTRY: USA
 CL. NO.: 2202
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/624,125 -
 FILING DATE: 29-MAR-1996
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: KELBER, STEVEN B.
 REGISTRATION NUMBER: 30,073
 TELEPHONE: 703-413-3000
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 703-413-3000
 TELEFAX: 703-413-2220
 INVENTOR INFORMATION:
 NAME: KELBER, STEVEN B.
 REGISTRATION NUMBER: 30,073
 TELEPHONE: 703-413-3000
 TELEFAX: 703-413-2220
 SEQUENCE CHARACTERISTICS:
 LENGTH: 162 amino acids

Query Match 48.2%; Score 41; DB 1: Length 162;
 Best Local Similarity 77.8%; Pred. No. 26;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 5 GFSYAPPD 13
 DB 134 GFIAPPVD 142

Search completed: August 11, 2003, 08:24:45
 Job time : 3.26609 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compaq Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: August 11, 2003, 08:24:50 ; Search time 448 Seconds
(without alignments)
1461.056 Million cell updates/sec

Title: US-10-000-039a-4

Sequence: 85 1 FARGSTAPPDPSVL 16

Scoring table: BLOSUM62

Xgapop 10.0 ; Xgapext 0.5
Xgapop 10.0 ; Xgapext 0.5
Xgapop 6.0 ; Delcost 7.0
Xgapop 6.0 ; Delcost 7.0

Searched: 2688711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODE=frame_p2n.model
-DB=GenBank
-OM=FASTAP-SUFFIX-rge
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdd -LIST=45
-LOCALIZATION=200 -THR_SCORE=pct -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-USFR=US1000039.ACQU.1.1.5563 -runat.01082003.085418.27511 -NCPU=6 -ICPU=3
-NO_MAP -LARGOQUERY -NEG_SCORES=0 -WAT7 -DSPEL/COR=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -10AFZAN=0.3 -DELTOP=6 -DELEXT=7

Database :

1: gb.bas*
2: gb.in*
3: gb.in*
4: gb.om*
5: gb.ov*
6: gb.ov*
7: gb.ph*
8: gb.pl*
9: gb.pr*
10: gb.pr*
11: gb.scs*
12: gb.sv*
13: gb.un*
14: gb.un*
15: gb.un*
16: em.fun*
17: em.hun*
18: em.hun*
19: em.hun*
20: em.om*
21: em.or*
22: em.ov*
23: em.ov*
24: em.ph*
25: em.pl*
26: em.to*
27: em.to*
28: em.un*

29: em.vl*
30: em.vl*
31: em.hg*
32: em.hg*
33: em.hg*
34: em.hg*
35: em.hg*
36: em.hg*
37: em.hg*
38: em.hg*
39: em.hg*
40: em.hg*
41: em.hg*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being plotted, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	UP	ID	Description
1	85	100.0	684	6	AX201922	Sequence
2	85	100.0	1286	6	AX056374	Sequence
3	85	100.0	1286	6	AX056374	Sequence
4	85	100.0	2281	6	AX524988	Sequence
5	85	100.0	2281	6	BU134455	Human nuc
6	85	100.0	2311	6	AF151380	Sequence
7	85	100.0	2311	6	AF151380	Sequence
8	85	100.0	2311	6	BD021928	Sequence
9	85	100.0	2354	6	AX553549	Sequence
10	85	100.0	2364	9	AK098509	Homo sapi
11	85	100.0	2370	6	AF179441	Sequence
12	85	100.0	2370	6	AF179441	Sequence
13	85	100.0	2370	6	AX337834	Sequence
14	85	100.0	2370	6	AX411211	Sequence
15	85	100.0	2370	9	HSRNMSTPK	Sequence
16	85	100.0	2382	9	BC001263	Homo sapi
17	85	100.0	2382	9	BC001263	Homo sapi
18	85	100.0	3136	6	AX713538	Sequence
19	85	100.0	3196	9	AK055077	Homo sapi
20	85	100.0	3196	9	AK055077	Homo sapi
21	85	100.0	113673	9	AL135839	Human DNA
22	80	94.1	431	6	AX305574	Sequence
23	80	94.1	1659	9	BC002222	Mus muscu
24	80	94.1	2436	10	AF058655	Mus muscu
25	80	94.1	2436	10	AF058655	Mus muscu
26	80	94.1	2439	10	AF139638	Mus muscu
27	80	94.1	2432	6	AX063735	Sequence
28	80	94.1	200453	9	AF196939	Sequence
29	79	92.9	1920	4	AF196939	Sequence
30	79	92.9	2435	10	BAT5CRK	Sequence
31	79	92.9	142609	2	AC118095	Rattus no
32	79	92.9	142609	2	AC118095	Rattus no
33	79	92.9	200716	2	AC112380	Rattus no
34	79	92.9	200716	2	AC112380	Rattus no
35	76	89.4	3105	5	SAC232716	Sequence
36	76	89.4	2470	5	SAC232716	Sequence
37	72	84.7	447	5	BC057138	Sequence
38	68	80.0	2339	5	BC052134	Sequence
39	68	80.0	18682	2	BA323831	Sequence
40	65	79.4	22264	2	BAT70095	Sequence
41	65	79.4	187456	2	BA323831	Sequence
42	58.5	68.8	606	6	E3270	Sequence
43	58.5	68.8	1768	9	BC015346	Sequence
44	58.5	68.8	1803	10	AF112007	Sequence
45	58.5	68.8	2250	6	AX056377	Sequence

ALIGNMENTS

RESULT 1

```

AX051922      694 bp      DNA      linear      PAT 30-AUG-2001
DEFINITION    Sequence 54 from Patent WO0153524.
ACCESSION     AX051922
VERSION       AX051922.1 GI:15391773
ORGANISM      Homo sapiens (human)
SOURCE        Homo sapiens
ORGANISM      Homo sapiens
REFERENCE     1 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
AUTHORS       Pees R.C., Li G. and Wan, S.
TITLE         Cancer associated genes and their products
JOURNAL       The Nottingham Trent University (GB)
FEATURES     source
              1..694 aa=Homo sapiens"
              /db_xref="taxon:9606"
              /mol_type="genomic DNA"
BASE COUNT    148 a 153 c 172 g 203 t 18 others
ORIGIN
Alignment Scores:
  Pred. No.: 649a-06      Length: 694
  Score: 85.00           Matches: 16
  Percent Similarity: 100.0%      Conservative: 0
  Best Local Similarity: 100.0%   Mismatches: 0
  Query Match: 100.0%           Indels: 0
  DB: 6                    Gaps: 0

US-10-000-039a-4 (1-16) x AX051922 (1-694)
Qy 1 GluAlaPheLeuGlyPheSerTyrAlaProThrAspSerPheLeu 16
Db 112 GAGCGTTTCTAGGCTTTTCTATGCGCTCCACGAGACTTTCTCTC 159

RESULT 2
LOCUS         AX056374
DEFINITION    Sequence 18 from Patent WO0073469.
ACCESSION     AX056374
VERSION       AX056374.1 GI:12225081
ORGANISM      Homo sapiens (human)
SOURCE        Homo sapiens
ORGANISM      Homo sapiens
REFERENCE     1 Owen G.D., Martinez R., Whyte D. and Sudarsanam S.
TITLE         Protein kinases
JOURNAL       Sugen, Inc. (US)
FEATURES     source
              1..1296 aa=Homo sapiens"
              /db_xref="taxon:9606"
              /mol_type="genomic DNA"
BASE COUNT    345 a 333 c 293 g 325 t
ORIGIN
Alignment Scores:
  Pred. No.: 1236-05      Length: 1296
  Score: 85.00           Matches: 16
  Percent Similarity: 100.0%      Conservative: 0
  Best Local Similarity: 100.0%   Mismatches: 0
  Query Match: 100.0%           Indels: 0
  DB: 6                    Gaps: 0

US-10-000-039a-4 (1-16) x AX056374 (1-1296)
Qy 1 GluAlaPheLeuGlyPheSerTyrAlaProThrAspSerPheLeu 16
Db 112 GAGCGTTTCTAGGCTTTTCTATGCGCTCCACGAGACTTTCTCTC 159

```

```

Db 1246 GAGCGTTTCTAGGCTTTTCTATGCGCTCCACGAGACTTTCTCTC 1249

RESULT 3
LOCUS         AX017284
DEFINITION    Sequence 39 from Patent WO9947669.
ACCESSION     AX017284
VERSION       AX017284.1 GI:10042202
ORGANISM      Homo sapiens (human)
SOURCE        Homo sapiens
ORGANISM      Homo sapiens
REFERENCE     1 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
AUTHORS       Schmitt A., Specht T., Dahl E., Hinzmann B., Rosenthal A. and
              Piletsky C.
TITLE         cDNA acid sequences from tissue of breast tumors
JOURNAL       Patent WO 9947669 A 39 25-SEP-1999;
              SCHMITT ARMIN (DE); SPECHT THOMAS (DE); DAHL EDGAR (DE); HINZMANN
              BERND (DE); ROSENTHAL ANDRE (DE); METAGEN GES FUER GERMANYNSCHN
              (DE); PILETSKY C.
FEATURES     source
              1..2281 aa=Homo sapiens"
              /db_xref="taxon:9606"
              /mol_type="genomic DNA"
BASE COUNT    601 a 498 c 494 g 688 t
ORIGIN
Alignment Scores:
  Pred. No.: 218a-05      Length: 2281
  Score: 85.00           Matches: 16
  Percent Similarity: 100.0%      Conservative: 0
  Best Local Similarity: 100.0%   Mismatches: 0
  Query Match: 100.0%           Indels: 0
  DB: 6                    Gaps: 0

US-10-000-039a-4 (1-16) x AX017284 (1-2281)
Qy 1 GluAlaPheLeuGlyPheSerTyrAlaProThrAspSerPheLeu 16
Db 1188 GAGCGTTTCTAGGCTTTTCTATGCGCTCCACGAGACTTTCTCTC 1235

RESULT 4
LOCUS         AX524988
DEFINITION    Sequence 39 from Patent EP1236799.
ACCESSION     AX524988
VERSION       AX524988.1 GI:25170070
ORGANISM      Homo sapiens (human)
SOURCE        Homo sapiens
ORGANISM      Homo sapiens
REFERENCE     1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
AUTHORS       Specht T., Hinzmann B., Schmitt A., Piletsky C., Dahl E. and
              Rosenthal A.
TITLE         Human cDNA acid sequences derived from breast tumor tissue
JOURNAL       Patent EP 1236799 A 39 04-SEP-2002;
              metagen Pharmaceuticals GmbH (DE)
FEATURES     source
              1..2281 aa=Homo sapiens"
              /db_xref="taxon:9606"
              /mol_type="genomic DNA"
BASE COUNT    601 a 498 c 494 g 688 t
ORIGIN
Alignment Scores:
  Pred. No.: 218a-05      Length: 2281
  Score: 85.00           Matches: 16
  Percent Similarity: 100.0%      Conservative: 0
  Best Local Similarity: 100.0%   Mismatches: 0

```


Query Match: 100.0% Indels: 0
 DB: 6 Gaps: 0

US-10-000-039a-4 (1-16) x A524988 (1-2281)

Qy 1 GluAlaPheLeuGlyPheSerTyAlaProThrAspSerPheLeu 16
 Db 1188 GAGGCTTTCTTAGGCTTTTCCTATGCGCTCCACGGACTCTTCTC 1235

RESULT 5
 LOCUS BD134455 2281 bp DNA linear PAT 18-SEP-2002
 DEFINITION Human nucleic acid sequence originating in mammary tumor tissue.
 ACCESSION BD134455 1 GI:23229400
 KEYWORDS JP 2002506643-A/733
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1 (bases 1 to 2281)
 SPECT, T., HINTZMAN, B., ARMIN, S., PIRASKI, C., EDGAR, D. and
 HINTZMAN, B. Human nucleic acid sequence originating in mammary tumor tissue
 PATENT: JP 2002506643-A 33 05-MAR-2002;
 JOURNAL METAGEN GESELLSCHAFT FUER GENOME FORSCHUNG MBH
 COMMENT PR JP 2002506643-A/733
 PD 05-MAR-2002 JP 2000536452
 PF 19-MAR-1999 JP 10004832 3
 PI ANDRE ROSENTHAL
 PI THOMAS SPEFT, BERND HINTZMAN, SHOMIT ARMIN, CHRISTIAN PIRASKI,
 PI DUHL EDGAR.
 PC C07K16/18, A61K31/711, A61K38/00, A61K48/00, A61P35/00, C07K14/47,
 PC C12N1/19, C12N5/10, C12N5/00, A61K37/02, C12N5/00 CC Human
 nucleic acid sequence originating in mammary tumor. CC
 FEATURES FT source 1. 2281 Location/Qualifiers
 FT source 1. 2281 /organism="Homo sapiens (human)".
 FT source 1. 2281 /organism="Homo sapiens"
 FT source 1. 2281 /mol-type="genomic DNA"
 FT source 1. 2281 /dbxref="acc:BD134455"

BASE COUNT 601 a 498 c 494 g 688 t

Alignment Scores: 2,18e-05 Length: 2281
 Pred. No.: 85.00 Matches: 16
 Score: 100.00% Conservative: 0
 Percent Similarity: 100.00% Positive: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-10-000-039a-4 (1-16) x BD134455 (1-2281)

Qy 1 GluAlaPheLeuGlyPheSerTyAlaProThrAspSerPheLeu 16
 Db 1188 GAGGCTTTCTTAGGCTTTTCCTATGCGCTCCACGGACTCTTCTC 1235

RESULT 6
 LOCUS AR151390 2311 bp DNA linear PAT 08-AUG-2001
 DEFINITION Human protein kinase.
 ACCESSION AR151390 6 from patent US 623077.
 KEYWORDS AR151390.1 GI:1517440
 SOURCE Unknown.
 ORGANISM Unknown.

Unclassified (to 2311)
 AUTHORS Au-Young, J., Guegler, K.J. and Harkins, P.R.
 TITLE Human protein kinases
 JOURNAL Patent: US 623077-A 6 15-MAY-2001;
 FEATURES Location/Qualifiers
 SOURCE 1. 2311 /organism="unknown"

BASE COUNT 604 a 508 c 506 g 692 t 1 others

Alignment Scores: 2,21e-05 Length: 2311
 Pred. No.: 85.00 Matches: 16
 Score: 100.00% Conservative: 0
 Percent Similarity: 100.00% Positive: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-10-000-039a-4 (1-16) x AR151390 (1-2311)

Qy 1 GluAlaPheLeuGlyPheSerTyAlaProThrAspSerPheLeu 16
 Db 1255 GAGGCTTTCTTAGGCTTTTCCTATGCGCTCCACGGACTCTTCTC 1302

RESULT 7
 LOCUS AR270209 2311 bp DNA linear PAT 10-APR-2003
 DEFINITION Sequence 772 from patent US 6500938.
 ACCESSION AR270209 1 GI:29701443
 KEYWORDS AR270209.1 GI:29701443
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 2311)
 AUTHORS Au-Young, J. and Seillhammer, J.J.
 TITLE Composition and uses of a protein of signaling pathway gene expression
 JOURNAL Patent: US 6500938-A 1 10-APR-2003;
 FEATURES Location/Qualifiers
 SOURCE 1. 2311 /organism="unknown"

BASE COUNT 604 a 508 c 506 g 692 t 1 others

Alignment Scores: 2,21e-05 Length: 2311
 Pred. No.: 85.00 Matches: 16
 Score: 100.00% Conservative: 0
 Percent Similarity: 100.00% Positive: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-10-000-039a-4 (1-16) x AR270209 (1-2311)

Qy 1 GluAlaPheLeuGlyPheSerTyAlaProThrAspSerPheLeu 16
 Db 1255 GAGGCTTTCTTAGGCTTTTCCTATGCGCTCCACGGACTCTTCTC 1302

RESULT 8
 LOCUS BD021928 2311 bp DNA linear PAT 27-AUG-2002
 DEFINITION Human protein kinases.
 ACCESSION BD021928 6 from patent US 623077.
 KEYWORDS BD021928.1 GI:22563151
 SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE 1 (bases 1 to 2311)
 AUTHORS Young, J.O., Guegler, K.J. and Harkins, P.R.
 TITLE Human protein kinases
 JOURNAL Patent: JP 2001508443-A 3 23-MAY-2001;


```

PD XX 26-JUL-2001.
PF XX 18-JAN-2001; 2001MO-G000188..
XX XX
XX XX 18-JAN-2000; 2000GB-0000993.
XX XX
PA (UINO-) UNIV NOTTINGHAM TRENT.
XX XX
XX XX Rees RC, Li G, Mian S.
XX XX
XX XX WPI; 2001-476124/51.
DR XX
XX XX Use of cancer-associated genes and their products in detecting
XX XX cancer, treating or preventing cancer, specifically prostate
XX XX cancer, and in developing DNA-based vaccines that promote anti-tumor
XX XX responses.
XX XX
XX XX Claim 1; Page 29; 43pp; English.
XX XX
XX XX AAH42781-AAH42846 represent the nucleotide sequences of cancer
XX XX associated genes, specifically Expression Cloning. The genes are overexpressed
XX XX in prostate cancer, and some are overexpressed in other cancers such as
XX XX stomach cancer and oesophageal cancer. The nucleic acids are useful for
XX XX detecting and monitoring cancer, and for the treatment or prevention of cancer.
XX XX They are
XX XX producing DNA-based vaccines against prostate cancer or that promote
XX XX anti-tumor immune responses, and to raise antibodies. The expression of
XX XX genes and detection of their protein products may be used for
XX XX diagnosis, prognosis, and as a prognostic
XX XX indicator of initial disease status of the patient.
XX XX
XX XX Sequence 694 BP; 148 A; 153 G; 172 G; 203 T; 18 other;
XX XX
XX XX Alignment Scores:
XX XX Pred. No.: 8.88e-06 Length: 694
XX XX Score: 85.00 Matches: 16
XX XX Percent Similarity: 100.00% Mismatches: 0
XX XX Best Local Similarity: 100.00% Mismatches: 0
XX XX Query Match: 100.00% Indels: 0
XX XX DB: 22 Gaps: 0
XX XX
US-10-000-039a-4 (1-16) x AAH42835 (1-694)
Oy 1 GluAlaPheLeuGlyPheSerTyrAlaProThrAspSerPheLeu 16
Db 112 GAGGCTTCCTAGAGCTTTTCCTATGCGGCTCCACGAGACTCTTCTC 159
AAAF4639
RESULT 2
ID AAH4639 standard; cDNA; 1296 BP.
AC AAH4639;
XX XX
XX XX 27-MAR-2001 (first entry)
DT
XX XX
XX XX Novel protein kinase cDNA, SEQ ID NO: 18.
XX XX
XX XX Human; mouse; protein kinase; antiarthritis; antisclerotic; osteopathic;
XX XX demyelinating; immunomodulatory; immunoregulatory; immunosuppressive;
XX XX immunological; antidiabetic; antifertility; gene therapy; vaccine;
XX XX immune disorder; cardiovascular disease; neurodegenerative disease;
XX XX cancer; autoimmune disorder; stroke; inflammatory bowel disease;
XX XX inflammatory pelvic disease; multiple sclerosis; psoriasis; ss.
XX XX
XX XX Homo sapiens.
XX XX
XX XX W0200073469-A2.
XX XX
XX XX 07-DEC-2000.
XX XX
XX XX 26-MAY-2000; 2000NO-U014842.
XX XX

```

```

PR XX 28-MAY-1999; 99US-0136503.
XX XX (SUGE-) SUGEN INC.
XX XX
XX XX Plowman GD, Martinez R, Whyte D, Sudarsanam S.
XX XX
XX XX WPI; 2001-032161/04.
XX XX
XX XX DR P-PSDB; AAB65613.
XX XX
XX XX Nucleic acids encoding kinase polypeptides, useful for diagnosing and
XX XX treating immune-related diseases and disorders, cardiovascular disease,
XX XX neurodegenerative diseases and/or cancers.
XX XX
XX XX Disclosure: Fig 2; 310pp; English.
XX XX
XX XX The present sequence encodes a novel protein kinase. The nucleic acids
XX XX and the protein kinases they encode may be used in the treatment and
XX XX diagnosis of diseases associated with inappropriate kinase expression
XX XX such as immune-related diseases and disorders, cardiovascular disease,
XX XX neurodegenerative diseases and/or cancers. The nucleic acids and
XX XX complementary sequences may also be used as DNA probes in diagnostic
XX XX assays. The kinase polypeptides may be used as antigens in the production
XX XX of antibodies of kinase expression and activity. Anti-kinase antibodies
XX XX and kinase antagonists may be used in the treatment and diagnosis of
XX XX activity include rheumatoid arthritis, atherosclerosis, autoimmune
XX XX disorders, complications of organ transplantation, myocardial infarction,
XX XX immune disorders, cardiovascular diseases, chronic inflammatory bowel disease,
XX XX chronic inflammatory pelvic disease, multiple sclerosis, asthma,
XX XX osteoarthritis, psoriasis, rhinitis, autoimmune, diabetes, cancers and
XX XX reproductive disorders.
XX XX
XX XX Sequence 1296 BP; 345 A; 333 G; 293 G; 325 T; 0 other;
XX XX
XX XX Alignment Scores:
XX XX Pred. No.: 1.97e-05 Length: 1296
XX XX Score: 85.00 Matches: 16
XX XX Percent Similarity: 100.00% Mismatches: 0
XX XX Best Local Similarity: 100.00% Mismatches: 0
XX XX Query Match: 100.00% Indels: 0
XX XX DB: 22 Gaps: 0
XX XX
US-10-000-039a-4 (1-16) x AAF44639 (1-1296)
Oy 1 GluAlaPheLeuGlyPheSerTyrAlaProThrAspSerPheLeu 16
Db 1246 GAGGCTTTCTAGAGCTTTTCTGATGCGGCTCCACGAGACTCTTCTC 1293
AAAF4639
RESULT 3
ID AAH4639 standard; cDNA; 1296 BP.
AC AAH4639;
XX XX
XX XX 08-DEC-1999 (first entry)
DT
XX XX
XX XX Human breast tumour-associated EST 37.
XX XX
XX XX Expressed sequence tag; EST; human; breast; cancer; gene therapy;
XX XX treatment; tumour; cytostatic; medicament; ss.
XX XX
XX XX Homo sapiens.
XX XX
XX XX DE19813833-A1.
XX XX
XX XX 23-SEP-1999.
XX XX
XX XX W0200073469-A2.
XX XX
XX XX 20-MAR-1998; 98DE-1013839.
XX XX
XX XX 20-MAR-1998; 98DE-1013839.
XX XX
XX XX (META-) METAGEN GES GENOMFORSCHUNG MHH.
XX XX

```


The Aug 12 10:56:07 2003

CC diagnosis and treatment of cancer and immunopathology and neuropathology.
 CC The microarray is useful in diagnostics and treatment regimens. drug
 CC discovery and development, toxicological and carcinogenicity studies,
 CC forensics and pharmacokinetics, and in the diagnosis and treatment of
 CC various diseases and for developing sophisticated
 CC profiles for the effects of currently available therapeutic drugs. The
 CC combination is also useful for purifying a subpopulation of mRNAs, cDNAs
 CC and genomic fragments and in releasing and identifying genes coding
 CC for different signaling pathway populations in a large number of genes coding
 CC for various diseases including cancer e.g. adenocarcinoma and leukemia
 CC and Parkinson's disease. The present sequence represents a polynucleotide
 CC immunopathies e.g. AIDS and asthma, neuropathies e.g. Alzheimer's
 CC disease and Parkinson's disease. The present sequence represents a polynucleotide
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification but was obtained in electronic form directly from USPTO
 CC at seqdata.uspto.gov/sequence.html?docid=963009388.

SO Sequence 2311 BP; 604 A; 508 C; 506 G; 692 T; 1 other;

Alignment Scores: 3.71e-05 Length: 2311
 Score: 85.00 Matches: 16
 Percent Similarity: 100.00 Conservative: 0
 Best Local Similarity: 100.00 Mismatches: 0
 Query Match: 100.00 Indels: 0
 Gaps: 25

US-10-000-039A-4 (1-16) x ACN56174 (1-2311)

Qy 1 GUAUaPhLeuGlyPhSeSerTyAlaProProThrAspSerPheLeu 16

Db 1255 GAGGCTTCCTAGCGCTTTCCTATGCGCTCCAGCGCTCTTCCTC 1302

RESULT 5
 ABX74395
 ID ABX74395 standard; cDNA; 2343 BP.

XX ABX74395;

XX 21-MAR-2003 (first entry)

XX Human cDNA sequence #6 up-regulated in non-aggressive CC-RCC.

XX Human; microarray; solid surface; immobilised probe; CC-RCC;
 XX differential expression profile; aggressive type; clear cell renal carcinoma;
 XX gene expression profiling; tumour tissue; gene; ss.

XX OS Homo sapiens.

XX NC W0200279411-A2.

XX PD 10-OCT-2002.

XX 25-MAR-2002; 2002NO-US09576.

XX 25-MAR-2002; 2001US-279411P.

XX (VAND-) VAN ANDEL INST.

XX Haab B, Rhodes D, Teh BT, Takashi M;

XX WPI; 2003-040679/03.

XX New microarray, comprising a matrix of cDNA probe from a set of probes
 XX immobilised to a solid surface in predetermined order, useful in the
 XX prognosis of patients with clear cell renal carcinoma

XX Claim 1; Page 79-80; 17pp; English.

XX The present invention relates to a microarray comprising a matrix of

XX at least one cDNA probe from a set of probes immobilised to a solid

CC

CC surface in a predetermined order, where a row of pixels corresponds
 CC to replicates of nucleic acid sequences that are expressed
 CC differentially in aggressive as compared to non-aggressive types of
 CC clear cell renal carcinoma (CC-RCC) and that hybridise with probes
 CC under high stringency with CC-RCC, wherein aggressive and
 CC non-aggressive CC-RCC tumour types are characterised by differential
 CC expression profiles of genes that hybridise with one or more probes
 CC immobilised on the microarray, and normal tissues. The present
 CC sequence represents a human cDNA sequence up-regulated in
 CC non-aggressive CC-RCC phenotypes.

SO Sequence 2343 BP; 612 A; 517 C; 511 G; 703 T; 0 other;

Alignment Scores:

Score: 3.78e-05 Length: 2343
 Percent Similarity: 100.00 Conservative: 16
 Best Local Similarity: 100.00 Mismatches: 0
 Query Match: 100.00 Indels: 0
 Gaps: 25

US-10-000-039A-4 (1-16) x ABX74395 (1-2343)

Qy 1 GUAUaPhLeuGlyPhSeSerTyAlaProProThrAspSerPheLeu 16

Db 1281 GAGGCTTCCTAGCGCTTTCCTATGCGCTCCAGCGCTCTTCCTC 1328

RESULT 7

AAV74190

XX AAV74190 standard; DNA; 2346 BP.

XX AC AAV74190;

XX 15-MAR-1999 (first entry)

XX Human sgk DNA.

XX Serum glucocorticoid regulated kinase; sgk; human; treatment; inhibitor;
 XX acine/threonine protein kinase family; antagonists; diabetic nephropathy;
 XX chronic renal failure; inflammation; Alzheimers disease; wound; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 45..1340

XX /product="sgk"

XX /transl_except= (pos:1185..1187, aa:Asp)

XX EF887081-A2.

XX PD 30-DEC-1998.

XX 27-MAY-1998; 98EP-0304189.

XX 27-JUN-1997; 97US-0051124.

XX (SMK) SMITHKLINE BEECHAM CORP.

XX Kumar JM;

XX NFI; 1999-047627/05.

XX P-PSDB; AM901039.

XX Treating chronic renal failure, diabetic nephropathy and Alzheimer's
 XX disease - by administration of nucleic acids and antagonists which
 XX inhibit activity or expression of human serum glucocorticoid
 XX regulated kinase (sgk), a serine/threonine protein kinase

XX Disclosure; Page 14-15; 17pp; English.

PS

PR 25-SEP-2000; 2000US-235082P.
 PR 25-SEP-2000; 2000US-235134P.
 PR 25-SEP-2000; 2000US-235280P.
 PR 26-SEP-2000; 2000US-235637P.
 PR 26-SEP-2000; 2000US-235711P.
 PR 26-SEP-2000; 2000US-235711P.
 PR 27-SEP-2000; 2000US-235720P.
 PR 27-SEP-2000; 2000US-235840P.
 PR 27-SEP-2000; 2000US-235840P.
 PR 28-SEP-2000; 2000US-236028P.
 PR 28-SEP-2000; 2000US-236032P.
 PR 28-SEP-2000; 2000US-236033P.
 PR 28-SEP-2000; 2000US-236109P.
 PR 28-SEP-2000; 2000US-236109P.
 PR 28-SEP-2000; 2000US-236111P.
 PR 29-SEP-2000; 2000US-236842P.
 PR 29-SEP-2000; 2000US-236911P.
 PR 02-OCT-2000; 2000US-237173P.
 PR 02-OCT-2000; 2000US-237278P.
 PR 02-OCT-2000; 2000US-237278P.
 PR 02-OCT-2000; 2000US-237294P.
 PR 02-OCT-2000; 2000US-237316P.
 PR 03-OCT-2000; 2000US-237425P.
 PR 03-OCT-2000; 2000US-237598P.
 PR 03-OCT-2000; 2000US-237598P.
 PR 03-OCT-2000; 2000US-237606P.
 PR 03-OCT-2000; 2000US-237606P.
 PR 01-NOV-2000; 2000US-244867P.
 PR 01-NOV-2000; 2000US-245084P.
 PR (AVAL-1) AVALON PHARM.
 XX
 XX Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
 YI Soppet DR, Weaver Z;
 YI WPI; 2002-188264/24.
 DR
 XX
 XX Screening for anti-neoplastic agent involves exposing cells to a
 PT determining a change in expression of a gene of a signature gene set -
 PT
 XX Claim 1: SEQ ID 8343; 44pp; English.
 XX
 XX The present invention describes a method (M1) for screening for an
 CC anti-neoplastic agent. The method involves exposing cells to a chemical
 CC agent to be tested for anti-neoplastic activity, determining the
 CC expression of a gene of a signature gene set, and where (1) in
 CC a particular sequence (S) selected from 8447 sequences (given in ABL6164
 CC to ABL70110), or is at least 95% identical to (S), where a change in
 CC expression is indicative of anti-neoplastic activity. (1) has cytostatic
 CC activity, and can be used as an agent, and can be used for producing a product which
 CC is the data collected with respect to the anti-neoplastic agent as a
 CC result of M1, and the data is sufficient to convey the chemical
 CC structure and/or properties of the agent. The agent is selected from the group
 CC consisting of: ovarian, kidney, prostate or pancreatic cancer;
 CC adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,
 CC infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine
 CC carcinoma, papillary carcinoma and Wilms' tumor.
 XX
 XX Sequence 2370 BP; 636 A; 517 G; 513 C; 704 T; 0 other;
 S0
 Alignment Scores: 3,83e-05 Length: 2370
 No.: 85.00 Matches: 16
 Score: 100.00% Conservative: 0
 Percent Similarity: 100.00% Mismatches: 0
 Best Local Similarity: 100.00% Gaps: 0
 Query Match: 24
 DB:

OY 1 GUALAphedGlyPheSerTyrAlaProProThrAspSerPheLeu 16
 DB 1288 GAGCGCTTCTAGGCTTTCTATGCGCTCCAGACACTCTTCTC 1335
 RESULT 12
 XX AB199409 standard; cDNA; 431 BP.
 XX
 XX AC AB199409;
 XX
 XX 07-MAR-2002 (first entry)
 XX
 XX DE House ischaemic condition related cDNA sequence SEQ ID NO:325.
 XX House: ischaemia; compressive ischaemia; occlusive ischaemia;
 XX vaspasptic ischaemia; ischaemic condition; ischaemic disease; ns.
 XX
 XX OS Mus musculus.
 XX
 XX PR W0200188188-A2.
 XX
 XX PD 22-NOV-2001.
 XX
 XX PR 18-MAY-2000; 2000JP-0145977.
 XX
 XX PR (UNY-) UNIV NIKON SCHOOL JURIDICAL PEKSON.
 XX
 XX Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;
 PI WPI; 2002-034733/04.
 XX
 XX Examining the ischaemic condition (e.g. occlusive ischaemia) by measuring
 PT expression levels of particular genes defined in the specification or
 PT by determining the expression profile of a gene group comprising these
 XX genes -
 XX
 XX Claim 2: Page 893; 2690pp; English.
 XX
 XX The present invention describes a method for examining ischaemic
 CC genes (1) in a test sample or determining the expression levels of particular
 CC gene group in the sample comprising genes selected from (1). The method
 CC is useful for examining ischaemic condition (e.g. occlusive ischaemia;
 CC vaspasptic ischaemia; ischaemic condition; ischaemic disease; ns.)
 CC expression levels of particular genes (AB199202 to AB199912, enclosing
 CC the protein sequences in ABB57020 to ABB57774) or by determining the
 CC expression profile of a gene group comprising these genes (1) or by
 CC using the expression profile of a gene group as an indicator when screening for
 CC drugs or therapeutics for ischaemic diseases. AB199913 and AB199914
 CC represent PCR primers for a mouse ischaemic condition related sequence,
 CC which are used in the exemplification of the present invention.
 XX
 XX Sequence 431 BP; 75 A; 128 G; 115 C; 111 T; 2 other;
 S0
 Alignment Scores: 3,9e-05 Length: 431
 No.: 80.00 Matches: 15
 Score: 93.75% Conservative: 0
 Percent Similarity: 93.75% Mismatches: 0
 Best Local Similarity: 93.75% Gaps: 0
 Query Match: 24
 DB:

US-10-000-039A-4 (1-16) x AB199409 (1-431)
 OY 1 GUALAphedGlyPheSerTyrAlaProProThrAspSerPheLeu 16
 DB 105 GAAGCGCTTCTAGGCTTTCTATGCGCTCCAGACACTCTTCTC 152
 RESULT 13

us-10-000-039a-4.rng

Percent Similarity: 93.75%
Best Local Similarity: 93.75%
Query Match: 92.94%
DB: 25

US-10-000-039a-4 (1-16) x ABK42261 (1-404)
Oy 1 GluAlaPheLeuGlyPheSerTyrAlaProGlnThrAspSerPheLeu 16
DB 274 GAGCGCTTCCTGGGCTTTTCCTATGCACTCCCATGGACTCTTCTCTC 321

RESUL7 15
AAA46592 standard: DNA; 2365 BP.
XX 10-AAA46592 standard: DNA; 2365 BP.
AC AAA46592;
XX 25-SEP-2000 (first entry)
XX DE DNA encoding a rat serum and glucocorticoid induced protein kinase.
XX PROTEIN KINASE; Pkl1, Pkl2; Ypk1, Ypk2; protein kinase A-alpha;
XX serum and glucocorticoid induced protein kinase; SGK; PKBalpha;
XX 3-phosphoinositide-dependent protein kinase-1; PDK1; fungal infection;
XX thrush; cancer; diabetes; obesity; antifungal; Candida infection; ss.
XX Rattus sp.

CC Infections, e.g. thrush.
XX Sequence 2365 BP; 591 A; 580 C; 518 G; 676 T; 0 other;
SO Alignment Scores:
Pred. No.: 0,00045 Length: 2345
Score: 93.75% Cons: 93.75%
Best Local Similarity: 93.75% Mismatches: 0
Query Match: 92.94% Indels: 1
DB: 21 Gaps: 0

US-10-000-039a-4 (1-16) x AAA46592 (1-2365)
Oy 1 GluAlaPheLeuGlyPheSerTyrAlaProGlnThrAspSerPheLeu 16
DB 1238 GAGCGCTTCCTGGGCTTTTCCTATGCACTCCCATGGACTCTTCTCTC 1285

Search completed: August 11, 2003, 09:53:02
Job time : 01.0304 secs

XX Key Location/Qualifiers
XX CHS 1-168 a
XX /feature a
XX /product "serum and glucocorticoid induced protein
XX kinase (SGK)"
XX /transl_except Pos. 1-168, Thr1
XX /note "Encoded according Met at position 1 and
XX pro at position 318 are not given"

XX W0200036135-A2.
XX 22-JUN-2000.
XX 14-DIC-1999; 99NO-QR04228.
XX 14-DIC-1998. 98US-0112114.
XX (MEDI-) MEDICAL RES COUNCIL.
XX (REDC-) UNIV CALIFORNIA.
XX Thorner JW, Alessi DR, Torrance PD, Casamayor A;
XX WPI: 2000-442591/38.
XX P-PSDB: AMY93550.
XX Screening method identifying compounds which modulate protein kinase
XX activity for use in treating fungal infections and cancer -
XX Disclosure: Fig 12; 155pp: English.
XX The present sequence encodes a rat serum and glucocorticoid induced
XX protein kinase (SGK). The specification describes a screening method
XX for identifying compounds which modulate the activity of SGK from
XX different sources, using host yeast cells. The method is used to
XX identify a compound which modulates (inhibits) the activity of a
XX protein kinase. Pkl1 or Pkl2 phosphorylate and activate Ypk1, Ypk2,
XX SGK or protein kinase B-alpha (PKBalpha). Phosphorylation of Ypk1 or
XX Ypk2 or SGK but not PKBalpha or p70S6 kinase. Compounds identified by
XX the methods are used to treat fungal infections e.g. thrush, and to
XX treat cancer. To treat cancer, the compounds inhibit PKB, PDK1 or the
XX activation of PKB by growth factors. Compounds which inhibit SGK can be
XX used to treat obesity or diabetes or obesity and compounds which
XX inhibit a fungal functional homologue of Pkl1 (Pkl1 or Pkl2) or SGK
XX (Ypk1 or Yrk2) can be used as an antifungal agent to treat Candida

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: August 11, 2003, 08:36:34 ; Search time 15:27:27 Seconds
462,401 Million cell updates/sec

Title: US-10-000-039A-4

Perfect score: 85

Sequence: 1 EAFGLGFSVAPPTDSSL 16

Scoring table: BLOSUM62 0, Gapext 0.5

Xgapop 10.0, Gapext 0.5

Fgapop 6.0, Fgapext 7.0

delop 6.0, delext 7.0

Searched: 509978 seqs, 20691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 4 summaries

Command line parameters:

-MODEL=frame_p2n_model -DEV=1p
-DB=Issued Patents NA -OFPM=fastap -SUFFIX=crni -MINMATCH=0.1 -LOGPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=BLOSUM62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR_SCORE=PCT -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-DB=US10000039 -WGN=1.145 -RUNTIME=01082003.085119.27535 -ICPU=6 -ICPU=3
-NO_WMAP -LARGEDUQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-NO_TIMEOUT=120 -WARM_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents.NA:

1: /cgn2.6/pdata1/1/na/5A.COMB.seq.*
2: /cgn2.6/pdata1/1/na/5B.COMB.seq.*
3: /cgn2.6/pdata1/1/na/5C.COMB.seq.*
4: /cgn2.6/pdata1/1/na/6B.COMB.seq.*
5: /cgn2.6/pdata1/1/na/PCTUS.COMB.seq.*
6: /cgn2.6/pdata1/1/na/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	85	100.0	2311	2	US-08-712-709-6
2	85	100.0	2311	3	US-09-111-444-6
3	85	100.0	2311	3	US-09-511-228-6
4	85	100.0	2311	4	US-09-511-228-6
5	85	100.0	2311	4	US-09-031-295-12
6	46	54.1	1440	4	US-09-620-312D-614
c 7	45	52.9	993	4	US-09-252-991A-7223
8	45	52.9	3888	4	US-09-439-702B-50
c 9	45	52.9	1285	4	US-09-439-702B-50
c 10	43	50.6	1607	2	US-08-749-902-4
11	43	50.6	1607	4	US-09-016-434-126
12	43	50.6	1732	4	US-09-430-564-1

C 13 42 49.4 2281 4 US-06-392-772-9
14 42 49.4 5197 1 US-08-131-3658-53
15 42 49.4 5197 2 US-08-668-121-53
16 42 49.4 5197 2 US-08-668-121-53
c 17 41 48.2 489 1 US-08-663-910-3
18 41 48.2 489 1 US-08-663-910-3
19 41 48.2 489 1 US-08-663-910-3
20 41 48.2 489 2 US-09-006-491-3
21 41 48.2 489 2 US-09-006-491-3
22 41 48.2 489 3 US-09-335-919-10
23 41 48.2 1261 3 US-08-990-832-30
24 41 48.2 1261 3 US-08-990-832-30
25 41 48.2 1631 2 US-09-008-491-12
26 41 48.2 1631 2 US-09-008-491-12
c 27 41 48.2 1631 3 US-09-335-919-12
28 41 48.2 1741 3 US-08-795-430-12
29 41 48.2 1741 3 US-08-795-430-12
30 41 48.2 1741 3 US-08-795-430-12
31 41 48.2 2886 1 US-08-663-310-7
32 41 48.2 2886 2 US-09-006-491-7
33 41 48.2 2886 2 US-09-006-491-7
34 41 48.2 14255 1 US-08-320-559-1
35 41 48.2 14255 1 US-08-320-559-1
36 41 48.2 14255 1 US-08-306-691B-55
37 41 48.2 14255 1 US-08-306-691B-55
38 41 48.2 14255 1 US-08-306-691B-55
39 41 48.2 62804 1 PCT-US94-04406-1
c 40 41 48.2 62804 1 US-09-800-460-3
c 41 40.5 47.6 1176 4 US-09-009-913-1
c 42 40.5 47.6 1176 4 US-09-134-001C-853
c 43 40 47.1 278 3 US-09-128-111-190
c 44 40 47.1 369 4 US-09-252-991A-12545
45 40 47.1 606 3 US-09-385-982-255

ALIGNMENTS

RESULT 1, 12-709-6
US-08-712-709-6

Sequence 6, Application US/08712709

Patent No. 5863780

GENERAL INFORMATION:

APPLICANT: An-Tsung, Jenice

INVENTOR: Hawkins, Phillip K.

TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES

NUMBER OF SEQUENCES: 1

COMMENTS: NO COMMENTS

ADDRESS: Incyte Pharmaceuticals, Inc.

STREET: 3174 Potter Drive

CITY: Palo Alto

COUNTRY: U.S.

ZIP: 94304

COMPUTER READABLE FORM:

SEARCHED: YES

COMPUTER ISN CORRELABLE

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ Version 1.5

CURRENT APPLICATION DATA: /08/712,709

FILING DATE: Filed Herewith

ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.

REFERENCE: US 6,749

REFERENCE: US 6,749

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-855-0555

TELEFAX: 415-845-4166

INFORMATION: 415-845-4166

SEQUENCE CHARACTERISTICS: 6

LENGTH: 2311 base pairs

TYPE: nucleic acid

STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 LIBRARY: Consensus
 CLONE: 712-709-6

Alignment Scores:
 Pred. No.: 4,12e-06 Length: 2311
 Score: 85.00 Matches: 16
 Percent Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 2 Gaps: 0

US-10-000-039a-4 (1-16) x US-08-712-709-6 (1-2311)

Oy 1 GluAlaPheLeuGlyPheSerTyraLapProThrAspSerPheLeu 16
 Db 1255 GAGCGTTTCCTAGGCTTTCTCTATGCGCTCCGAGGACTCTTCTTC 1302

RESULT 2

US-09-111-444-6 (1-16) x Application US/09111444
 Sequence 6, 6045792
 Patent No. 6232077
 GENERAL INFORMATION:
 APPLICANT: Au-Young, Janice
 APPLICANT: Higgins, Phillip R.
 APPLICANT: Hawkins, Phillip K.
 TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES
 NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Incyte Pharmaceuticals, Inc.
 STREET: 3174 Porter Drive
 CITY: Palo Alto
 STATE: CA
 COUNTRY: U.S.
 ZIP: 94304

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSQ Version 1.5
 CURRENT APPLICATION DATA:
 FILING DATE: US/09/11,444
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/712,709
 FILING DATE:
 ATTORNEY INFORMATION:
 NAME: Billings, Lucy J
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PP-0118 US
 TELEPHONE: 415-855-0555
 TELEFAX: 415-845-4166
 INFORMATION FOR SEQ ID NO: 6:
 SUBSEQUENCE LENGTH: 2311 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 MOLECULE TYPE: cDNA
 IMMEDIATE SOURCE:
 LIBRARY: Consensus
 US-09-111-444-6

Alignment Scores:
 Pred. No.: 4,12e-06 Length: 2311
 Score: 85.00 Matches: 16
 Percent Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 2 Gaps: 0

Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 3 Gaps: 0

US-10-000-039a-4 (1-16) x US-09-111-444-6 (1-2311)

Oy 1 GluAlaPheLeuGlyPheSerTyraLapProThrAspSerPheLeu 16
 Db 1255 GAGCGTTTCCTAGGCTTTCTCTATGCGCTCCGAGGACTCTTCTTC 1302

RESULT 3

US-09-541-228-6 (1-16) x Application US/09541228
 Sequence 6, 6045792
 Patent No. 6232077
 GENERAL INFORMATION:
 APPLICANT: Au-Young, Janice
 APPLICANT: Higgins, Phillip R.
 APPLICANT: Hawkins, Phillip K.
 TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES
 NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Incyte Pharmaceuticals, Inc.
 STREET: 3174 Porter Drive
 CITY: Palo Alto
 STATE: CA
 COUNTRY: U.S.
 ZIP: 94304

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSQ Version 1.5
 CURRENT APPLICATION DATA:
 FILING DATE: US/09/541,228
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/712,709
 FILING DATE:
 ATTORNEY INFORMATION:
 NAME: Billings, Lucy J
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PP-0118 US
 TELEPHONE: 415-855-0555
 TELEFAX: 415-845-4166
 INFORMATION FOR SEQ ID NO: 6:
 SUBSEQUENCE LENGTH: 2311 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 MOLECULE TYPE: cDNA
 IMMEDIATE SOURCE:
 LIBRARY: Consensus
 US-09-541-228-6

Alignment Scores:
 Pred. No.: 4,12e-06 Length: 2311
 Score: 85.00 Matches: 16
 Percent Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 3 Gaps: 0

US-10-000-039a-4 (1-16) x US-09-541-228-6 (1-2311)

Oy 1 GluAlaPheLeuGlyPheSerTyraLapProThrAspSerPheLeu 16
 Db 1255 GAGCGTTTCCTAGGCTTTCTCTATGCGCTCCGAGGACTCTTCTTC 1302

RESULT 4

US-09-016-434-772

```

: Sequence 772, Application US/09016434
: Patent No. 6500938
: GENERAL INFORMATION: Au-Yang
: APPLICANT: Jeffrey J. Soullamer
: TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
: TITLE OF INVENTION: PATHWAY GENE EXPRESSION
: NUMBER OF SEQUENCES: 490
: ADDRESS: INCYTE PHARMACEUTICALS, INC.
: STREET: 3174 PORTER DRIVE
: CITY: PALO ALTO
: STATE: CALIFORNIA
: COUNTRY: USA
: ZIP: 94304
: COMPUTER READABLE FORM: disk
: OPERATING SYSTEM: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
: CURRENT APPLICATION DATA: US/09/016,434
: FILING DATE: HEREWITH
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: William J. 37, 071
: REGISTRATION NUMBER: PA-0002 US
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (650) 951-0555
: FAX: (650) 951-0555
: INFORMATION FOR SEQ ID NO: 772:
: LENGTH: 2311 base pairs
: STRANDEDNESS: single
: TOPOLOGY: linear
: IMMEDIATE SOURCE:
: CIBRARY: 47262D701
: US-09-016-434-772

Alignment Scores:
Pred. No.: Length: 2311
Score: 85.00 Matches: 16
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Mismatch: 0
DB: 4 Gaps: 0

US-10-000-039A-4 (1-16) x US-09-016-434-772 (1-2311)
Oy 1 GualapahelenglyPheSerTyraProforthAspSerPheleu 16
Db 1255 GAGGCTTCCTAGGCTTTCTATGCCCTCCAGGACTCTTTCCTC 1302

RESULT 5
: Sequence 1, Application US/09031295
: Patent No. 6326181
: GENERAL INFORMATION: Florian
: APPLICANT: LANG
: TITLE OF INVENTION: CELL VOLUME-REGULATED HUMAN KINASE H-SOK
: NUMBER OF SEQUENCES: 4
: ADDRESS: FOLEY & LARDNER
: STREET: 3000 K Street, N.W.
: CITY: Washington

```

```

: STATE: D.C.
: COUNTRY: U.S.A.
: ZIP: 20007-5109
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
: CURRENT APPLICATION DATA: US/09/031,295
: APPLICATION NUMBER: US/09/031,295
: FILING DATE: 26-FEB-1998
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: UK 197-08-173.8
: FILING DATE: 28-FEB-1997
: ATTORNEY/AGENT INFORMATION:
: NAME: William J. 37, 071
: REGISTRATION NUMBER: 31 298
: REFERENCE/DOCKET NUMBER: 058315/0123
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202) 721-5300
: FAX: (202) 721-5300
: INFORMATION FOR SEQ ID NO: 1:
: LENGTH: 2370 base pairs
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE KEY: CDS
: LOCATION: 43..1335
: US-09-031-295-1

Alignment Scores:
Pred. No.: Length: 2370
Score: 85.00 Matches: 16
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Mismatch: 0
DB: 4 Gaps: 0

US-10-000-039A-4 (1-16) x US-09-031-295-1 (1-2370)
Oy 1 GualapahelenglyPheSerTyraProforthAspSerPheleu 16
Db 1288 GAGGCTTCCTAGGCTTTCTATGCCCTCCAGGACTCTTTCCTC 1415

RESULT 6
: Sequence 614, Application US/09620312D
: Patent No. 6326181
: GENERAL INFORMATION:
: APPLICANT: Tang, Y. Tom
: APPLICANT: Liu, Chenghua
: APPLICANT: Asundi, Vinod
: APPLICANT: Ren, Feiyan
: APPLICANT: Chen, Rui-hong
: APPLICANT: Zhao, Qing A.
: APPLICANT: Behrmann, Tom
: APPLICANT: Xu, Jidong J.
: APPLICANT: Yang, Yonghong
: APPLICANT: Wang, Jian-Rui
: APPLICANT: Zhou, Ping
: APPLICANT: Wang, Jun
: APPLICANT: Wang, Dairui
: APPLICANT: Wang, Zhiwei
: APPLICANT: John Tilligloast
: ADDRESS: 6000 Woodloch Forest, Redwood City, CA 94061
: TITLE OF INVENTION: Redwood Forest
: STREET: 6000 Woodloch Forest, Redwood City, CA 94061
: CITY: Redwood City, CA 94061
: TITLE OF INVENTION: Polypeptides
: FILE REFERENCE: 784CIP2B

```



```

; CURRENT APPLICATION NUMBER: US/09/620,312D
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PUBLICATION NUMBER: 6,635,723
; PRIOR FILING DATE: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; COMPUTER PROGRAM: PLF_genes version 1.0
; SEQ ID NO: 614
; LENGTH: 1440
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: CDS
; LOCATION: (387)..(1187)
US-09-620-312D-614

```

```

Alignment Scores:
Pred. No.: 32.2 Length: 1440
Score: 46.00 Matches: 8
Percent Similarity: 32.6 Mismatches: 3
Best Local Similarity: 66.67% Indels: 0
Query Match: 54.12% Gaps: 0
DB:

```

```
US-10-000-039a-4 (1-16) x US-09-620-312D-614 (1-1440)
```

```
Oy 3 PheLendylPheSerTyralaProthrAspSer 14
```

```
Db 59 TGCCTGGCTTCCTGCTACTCTCTGCTCCCAAGC 94
```

```

RESULT 7
US-09-252-991A-7223/C
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US/09/252,991A
; NUMBER OF SEQ ID NOS: 3312
; SEQ ID NO: 7223
; LENGTH: 993
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7223

```

```

Alignment Scores:
Pred. No.: 31 Length: 993
Score: 45.00 Matches: 7
Percent Similarity: 81.82% Mismatches: 2
Best Local Similarity: 63.64% Indels: 0
Query Match: 52.94% Gaps: 0
DB:

```

```
US-10-000-039a-4 (1-16) x US-09-252-991A-7223 (1-993)
```

```
Oy 1 GualapheLendylPheSerTyralaProthr 11
```

```
Db 917 GAGCGCTTCACGGATCGACGACCGCCGCC 885
```

```

RESULT 8
US-09-453-702B-50
; CURRENT APPLICATION NUMBER: US/09/453,702B
; PRIOR FILING DATE: 1998-11-24
; PRIOR APPLICATION NUMBER: US/09/453,702B
; NUMBER OF SEQ ID NOS: 6845
; SEQ ID NO: 702B
; LENGTH: 1230025
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae

```

```

; Burland, Valerie
; Penna, Nicole T.
; Plunkett, Guy
; TITLE OF INVENTION: NO. 6365723a1 Sequences of E. coli 0157
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS: 6 Newby
; ADDRESS: 6 Newby
; STREET: 1 South Planchney Street
; CITY: Madison
; STATE: WI
; COUNTRY: US
; COUNT: 137,012,2113
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44MB storage
; COMPUTER: IBM PC compatible
; SOFTWARE: Word Perfect 8.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/453,702B
; PRIOR APPLICATION NUMBER: 60/110,955
; CLASSIFICATION: UNKNOWN
; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J.
; REGISTRATION NUMBER: 27386
; TELEPHONE: (608) 251-5000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 251-9166
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE LENGTH: 3584
; TYPE: nucleic acid
; STRANDEDNESS: double
; MOLECULE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 50:
US-09-453-702B-50

```

```

Alignment Scores:
Pred. No.: 2.88e+03 Length: 31584
Score: 45.00 Matches: 8
Percent Similarity: 73.33% Mismatches: 3
Best Local Similarity: 52.94% Indels: 0
Query Match: 4 Gaps: 0
DB:

```

```
US-10-000-039a-4 (1-16) x US-09-453-702B-50 (1-38584)
```

```
Oy 1 GualapheLendylPheSerTyralaProthrAspSerPhe 15
```

```
Db 35023 GAGCCTTCATCGTTTATGTCGCCAGATACGACTCTAT 35067
```

```
RESULT 9
```

```
US-09-198-452A-1/C
```

```
Sequence 1, Application US/09198452A
```

```
GENERAL INFORMATION:
```

```
APPLICANT: Griffiths, R.
```

```
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, frame
```

```
FILE OF INVENTION: 9710-003-999
```

```
FILE REFERENCE: 9710-003-999
```

```
CURRENT APPLICATION NUMBER: US/09/198,452A
```

```
CURRENT FILING DATE: 1998-11-24
```

```
SEQ ID NO: 1 SEQ ID NOS: 6845
```

```
LENGTH: 1230025
```

```
TYPE: DNA
```

```
ORGANISM: Chlamydia pneumoniae
```


LOCATION: (720001)..(735000)
 NAME/KEY: misc_feature
 LOCATION: (743500)..(750000)
 NAME/KEY: misc_feature or c or g or t
 LOCATION: (750001)..(765000)
 NAME/KEY: misc_feature or c or g or t
 LOCATION: (765001)..(780000)
 NAME/KEY: misc_feature or c or g or t
 LOCATION: (780001)..(810000)
 NAME/KEY: misc_feature or c or g or t
 LOCATION: (810001)..(825000)
 NAME/KEY: misc_feature or c or g or t
 LOCATION: (825001)..(840000)
 NAME/KEY: misc_feature or c or g or t
 LOCATION: (840001)..(855000)
 NAME/KEY: misc_feature or c or g or t
 LOCATION: (855001)..(870000)
 NAME/KEY: misc_feature or c or g or t
 LOCATION: (870001)..(885000)
 NAME/KEY: misc_feature or c or g or t
 LOCATION: (885001)..(900000)
 NAME/KEY: misc_feature or c or g or t
 LOCATION: (900001)..(915000)
 NAME/KEY: misc_feature or c or g or t
 NAME/KEY: misc_feature

Alignment Scores:
 Pred. No.: 15
 Percent Similarity: 73.3%
 Best Local Similarity: 46.67%
 Query Match: 0
 DB: 4

US-10-000-039a-4 (1-16) x US-09-198-452a-1 (1-1230025)

Oy 1 GluAlaPheSerGlyPheSerValAlaProThrAspSerPhe 15

Db 168821 GAAGCCTTCTGCGCTTGTCTCTCTGATGACTAT 168777

RESULT 10
 US-08-745-902-4
 Sequence 4, Application US/08749902
 Patent No. 5985635
 GENERAL INFORMATION:
 APPLICANT: Goli, Surya K.
 APPLICANT: Hillman, Jennifer L.
 TITLE OF INVENTION: NOVEL HUMAN SERINE/THREONINE
 KINASES
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
 STREET: 3174 Porter Drive
 CITY: FOLSOM
 STATE: CA
 COUNTRY: US
 ZIP: 94304
 COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: Windows 4.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/749-902
 FILING DATE: Filed Herewith.
 PRIORITY DATE: Filed Herewith.
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Zeller, Karen J.
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PF-0150 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-345-1555
 TELEFAX: 415-345-1665
 INFORMATION FOR SEQ ID NO: 4:
 LENGTH: 1607 base pairs
 TYPE: Coding acid
 STRANDEDNESS: Single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 US-08-745-902-4
 Alignment Scores:
 Pred. No.: 131
 Percent Similarity: 83.3%
 Best Local Similarity: 58.33%
 Query Match: 2
 DB: 0

US-10-000-039a-4 (1-16) x US-08-749-902-4 (1-1607)
 Oy 1 GluAlaPheSerGlyPheSerValAlaProThr 12
 Db 1253 GAGCCTTCTGCGCTTACATGTCGCGCTCT 1288

RESULT 11
 US-09-016-434-126
 Sequence 126, Application US/09016434
 Patent No. 6500938
 GENERAL INFORMATION:
 APPLICANT: Jeffrey J. Seilhammer
 APPLICANT: Au-Young
 TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
 TITLE OF INVENTION: PATHWAY GENE EXPRESSION
 NUMBER OF SEQUENCES: 450
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
 STREET: 3174 PORTER DRIVE
 CITY: FOLSOM
 STATE: CALIFORNIA
 COUNTRY: USA
 ZIP: 94304
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC Compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
 APPLICATION NUMBER: US/09/016,434
 FILING DATE: HEREWITH
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 PRIORITY NUMBER:
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Zeller, Karen J.

```

; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TITLE OF INVENTION: 1281
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 126:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1607 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; INFORMATION SOURCE:
; LIBRARY: COLNFET02
; CLONE: 1309705
; ORIGIN: 1261
US-09-016-434-126

Alignment Scores:
Prod. No.: 131 Length: 1607
Score: 43.00 Matches: 7
Percent Similarity: 83.33% Conservative: 3
Best Local Similarity: 83.33% Mismatches: 3
Query Match: 30.58% Indels: 0
DB: 4 Gaps: 0

US-10-000-039a-4 (1-16) x US-09-016-434-126 (1-1607)
Qy 1 GluAlaPheLeuGlyPheSerTyAlaProGthr 12
Db 1253 CAGGCGCTTCGGGCTTCACATACGCGCCGGCTC 1248
RESULT 12
US-09-430-564-1
; Sequence 1, Application US/09430564
; Patent No. 6372467
; GENERAL INFORMATION:
; APPLICANT: John Blenis
; APPLICANT: Gary A. Lee-Fruman
; APPLICANT: Ciba
; TITLE OF INVENTION: P5456K AND P8556K GENES; PROTEINS.
; FILE REFERENCE: 00246/506002/09/430_564
; CURRENT FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: 60/106,141
; PRIOR FILING DATE: 1998-10-29
; INFORMATION FOR SEQ ID NO 1:
; SOFTWARE: PASTSEQ for Windows Version 4.0
; SEQ ID NO 1: PASTSEQ
; LENGTH: 1732
; ORIGIN: Homo sapiens
; ORIGIN: 1732
US-09-430-564-1

Alignment Scores:
Prod. No.: 143 Length: 1732
Score: 43.00 Matches: 7
Percent Similarity: 83.33% Conservative: 3
Best Local Similarity: 58.33% Mismatches: 2
Query Match: 50.58% Indels: 0
DB: 4 Gaps: 0

US-10-000-039a-4 (1-16) x US-09-430-564-1 (1-1732)
Qy 1 GluAlaPheLeuGlyPheSerTyAlaProGthr 12
Db 1179 CAGGCGCTTCGGGCTTCACATACGCGCCGGCTC 1214
RESULT 13
US-09-392-772-9/C
; Sequence 9, Application US/09392772
; Patent No. 6346403
; GENERAL INFORMATION:
; APPLICANT: Ramdoo, Layo O.
; APPLICANT: Antoni Rafalski
; TITLE OF INVENTION: Metabolic Enzymes
; REFERENCE/DOCKET NUMBER: US/09392772
; CURRENT FILING DATE: 1999-09-07
; EARLIER APPLICATION NUMBER: 60/099,519
; EARLIER FILING DATE: 1998-09-08
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2281 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; INFORMATION SOURCE:
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 9:
; ORIGIN: 2281
; ORIGIN: 2281
US-09-392-772-9

Alignment Scores:
Prod. No.: 307 Length: 2281
Score: 42.00 Matches: 5
Percent Similarity: 66.75% Conservative: 5
Best Local Similarity: 49.51% Mismatches: 5
Query Match: 37.40% Indels: 0
DB: 4 Gaps: 0

US-10-000-039a-4 (1-16) x US-09-392-772-9 (1-2281)
Qy 1 GluAlaPheLeuGlyPheSerTyAlaProGthrAspSerPheLeu 16
Db 1452 GATTGTTTCGGTGCTCTTTTGTTCATCATGATTAATTGTTG 1405
RESULT 14
US-08-131-365B-53
; Sequence 53, Application US/08131365B
; Patent No. 5527590
; GENERAL INFORMATION:
; APPLICANT: Michael S. Briggs
; APPLICANT: Briggs, Xiaodong
; APPLICANT: Wang, Xiaodong
; APPLICANT: Goldstein, Joseph L.
; TITLE OF INVENTION: TO STEROID REGULATORY ELEMENT BINDING
; NUMBER OF SEQUENCES: 64
; COMPARISON ADDRESS:
; ADDRESSER: 10000 Little & Burkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; CHARACTER SET: ASCII
; OPERATING SYSTEM: CICS/US-1005
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/131.365B
; FILING DATE: May 1995
; CLASSIFICATION: C12 353
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, David L.
; FIRM: PARKER, DAVID L.
; REFERENCE/DOCKET NUMBER: US/08-372/PAR
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5197 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "fna"

```

US-08-131-365B-53

Alignment Scores: 852 Length: 5197
 Score: 42.00 Matches: 10
 Percent Similarity: 66.67% Conservative: 0
 Best Local Similarity: 66.67% Mismatches: 5
 Query Match: 49.41% Indels: 0
 Gaps: 1

US-10-000-039a-4 (1-16) x US-08-131-365B-53 (1-5197)

QY 2 AlaPheLeuGlyPheSerTyrAlaProProGlnHisSerPheLeu 16
 DB 3838 GCCTTCCTGAGTTCTCTCTCTGACCTACTCTCTCTCTTTTG 3882

RESULT 15

US-08-668-123-53

; Sequence 53, Application US/08668123

; Patent No. 5891331 ON;

; GENERAL INFORMATION:

; APPLICANT: Brown, Michael S.

; APPLICANT: Briggs, Michael R.

; APPLICANT: Wang, Xiaodong

; APPLICANT: Gao, Joseph L.

; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING

; TITLE OF INVENTION: TO STEROL REGULATORY ELEMENT BINDING

; NUMBER OF SEQUENCES: 64

; NUMBER OF SEQUENCES: 64

; CONTACT PERSON: Arnold, White & Durkee

; ADDRESS: P.O. Box 4433

; CITY: Houston

; STATE: Texas

; COUNTRY: U.S.A.

; ZIP: 77210

; COMPUTER READABLE FORM:

; MEDIUM TYPE: floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT IN CHARGE: Arnold, White & Durkee

; APPLICATION NUMBER: US/08/668.123

; FILING DATE: 14-JUN-1996

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA: 08/131,365

; FILING DATE: 01-OCT-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Parker, David L.

; REFERENCE/DOCKET NUMBER: 2,165

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (512) 418-3000

; TELEFAX: (512) 418-3777

; INFORMATION FOR SEQ ID NO: 53:

; LENGTH: 5197 base pairs

; TYPE: nucleic acid

; TOPOLOGY: linear

; MOLECULE TYPE: other nucleic acid

; DESCRIPTION: /desc = "DNA"

US-08-668-123-53

Alignment Scores:

Pred. No.: 852 Length: 5197
 Score: 42.00 Matches: 10
 Percent Similarity: 66.67% Conservative: 0
 Best Local Similarity: 66.67% Mismatches: 5
 Query Match: 49.41% Indels: 0
 Gaps: 2

US-10-000-039a-4 (1-16) x US-08-668-123-53 (1-5197)

QY 2 AlaPheLeuGlyPheSerTyrAlaProProGlnHisSerPheLeu 16
 DB 3838 GCCTTCCTGAGTTCTCTCTCTGACCTACTCTCTCTTTTG 3882

Search completed: August 11, 2003, 12:08:51

Job time : 116.273 secs

[illegible][illegible]

DR PRODOM: PD000001; Prot_kinase; 1.
 DR SHANT; SH0023; PH; A; 1.
 DR SHANT; SH0033; S; TK; X; 1.
 DR PROSITE; PS00033; PL_DOMAIN; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 KW SEQUENCE 481 AA: 5604 MW: 856694.6454303 CRC64;
 SO

Query Valtch 39.08; Score 863.5; DB 13; Length 481;
 Best Local Similarity 45.53; Pred. No. 1.3e-63;
 Matches 177; Conservative 63; Mismatches 124; Indels 25; Gaps 7;
 28 MQORBNGLNDFQK-----TANNYACHHFE-----VQSLIKISOPQPELNNAP 73
 QY 63 MKTERPKPMTFIICLQMTVIERTFIVDSFEEREHQIOWADNLKQOEEEMERVS 122
 DB 74 SPSPSSQOINGSSPNHAKP-----SDPHLEKVIQKSGKSVLLARKVAEVTAK 127
 QY 123 Q--DPSNSGAECHMSHSKPKHYVMTEFYLKLLGKGTGVLLVMEKATGYTAK 180
 DB 128 VQKALIKKEKHENKNNVLLANKKPPVLFHFSFQVADKLVVDYDNGEELFN 187
 QY 181 ILKAEVIVADVAHTLLE-NRYLONSRRPFLTALYSFQTHDLCFWETANGELFN 239
 DB 180 LQSRGFLPAPYARVATASAGLYUS-LANIVFDKLVKPNLLSDSGHIVDFGLCE 246
 QY 240 LSRERFSEDRARTGAETVSAALDYLHSEKNVYVROLLENLMDKQGHIKITDAG 299
 QY 247 NIEHNTSTSTGCTGPKAPLVHQPORYVQACGLAVIEMVLGLPFFYSMTAEY 306
 DB 300 GIKQATKTCFGTPELPAPELVNDYDGRAVDNGLVGVYVEMWCKSLPYNQHEKLF 359
 QY 307 DNLKPELQKPNITNSRHILLSELLOKQRTKL-GAKDQFMKSHVFFSLNMDOLN 365
 DB 360 RLTKAEIRFPRLPEKSLLSGLLQKQYDQEGSDPDAKEIQKHKTFACIVQDTE 419
 QY 366 KLTTPFPNPNVSGNELRHDPDETPPV 394
 DB 420 KLVLPFPKQVTSITDITFDSEPHNMI 448

Search completed: August 11, 2003, 08:22:10
 SDB time : 110.612 secs

RESUME 15
 082526
 ID 082526 PRELIMINARY: PRT: 452 AA.
 AC 082526;
 DT 01-MAR-2003 (TRENDEL. 23, Created)
 DT 01-MAR-2003 (TRENDEL. 23, Last annotation update)
 DE Thymoma viral proto-oncogene 1.
 OS Mus musculus (Mouse).
 CC Mammalia; Eutheria; Rodentia; Chordata; Gracilata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID:10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE:22354683; PubMed:12466851;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT 60,776 bp; full-length cDNA; transcription based on functional annotation of
 RL Nature 420:563-573(2002).
 DR ENBL; AK040758; BAC30695.1; --
 SQ SEQUENCE 432 AA: 52619 MW: 82030846A18EE5E CRC64;
 Query Watch 37.58; Score 851; DB 11; Length 452;
 Best Local Similarity 45.48; Pred. No. 1.3e-62;
 Matches 176; Conservative 67; Mismatches 111; Indels 34; Gaps 8;
 28 MQORBNGLNDFQK-----TANNYACHHFE-----VQSLIKISOPQPELNNAP 73
 QY

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

ON protein - protein search, using sw model

Run on: August 11, 2003, 08:14:59 ; Search time 61.0429 Seconds
298,740 Million cell updates/sec

Title: US-10-000-039a-2

Sequences: 1 MTVTWKAAGTLTYSRHWBKENAEALGFSVAPPTDSFL 431

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

1: Issued Patents AA*

2: /cgn2.6/ptodata/1/aa/5A.COMB.pep*

3: /cgn2.6/ptodata/1/aa/6A.COMB.pep*

4: /cgn2.6/ptodata/1/aa/7A.COMB.pep*

5: /cgn2.6/ptodata/1/aa/8A.COMB.pep*

6: /cgn2.6/ptodata/1/aa/backfiles.pep*

Pred. No. is the number of results predicted by chance to have a
match as high as the one being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	2204.5	99.1	431	1	Sequence 2, Appl
2	2204.5	99.3	431	2	Sequence 1, Appl
3	2254	99.3	431	3	Sequence 5, Appl
4	2254	99.3	431	4	Sequence 5, Appl
5	2204.5	97.1	430	5	Sequence 9, Appl
6	2204.5	97.1	430	6	Sequence 9, Appl
7	2204.5	97.1	430	7	Sequence 9, Appl
8	850.5	37.5	726	8	Sequence 71, Appl
9	850	37.4	480	9	Sequence 2, Appl
10	806.5	35.5	482	10	Sequence 139, App
11	806.5	35.5	482	11	Sequence 139, App
12	806.5	35.5	482	12	Sequence 139, App
13	803	35.4	525	13	Sequence 3, Appl
14	803	35.4	525	14	Sequence 3, Appl
15	803	35.4	525	15	Sequence 3, Appl
16	780.5	34.4	916	16	Sequence 7, Appl
17	780	34.4	637	17	Sequence 2, Appl
18	774.5	34.1	737	18	Sequence 2, Appl
19	774.5	34.1	737	19	Sequence 2, Appl
20	771	34.0	671	20	Sequence 2, Appl
21	752.5	33.1	584	21	Sequence 2, Appl
22	697.5	30.7	343	22	Sequence 38, Appl
23	697.5	30.7	355	23	Sequence 69, Appl
24	697.5	30.7	355	24	Sequence 69, Appl
25	692.5	30.5	355	25	Sequence 6, Appl
26	691	30.4	1151	26	Sequence 11, Appl
27	690.5	30.4	676	27	Sequence 2, Appl

28 688.5 30.3 351 4 US-09-394-455-4
Sequence 4, Appl
29 687.5 30.3 336 4 US-09-394-455-2
Sequence 2, Appl
30 687.5 30.3 343 4 US-09-394-455-34
Sequence 34, Appl
31 687.5 30.3 343 4 US-09-394-455-34
Sequence 34, Appl
32 669.5 29.5 264 2 US-07-857-2248-15
Sequence 15, Appl
33 666.5 29.4 264 2 US-07-857-2248-10
Sequence 10, Appl
34 666 29.3 268 4 US-09-430-564-12
Sequence 12, Appl
35 665.5 29.3 264 2 US-07-857-2248-12
Sequence 12, Appl
36 665.5 29.1 264 2 US-07-857-2248-12
Sequence 12, Appl
37 661.5 29.1 264 2 US-07-857-2248-12
Sequence 12, Appl
38 658 29.0 269 2 US-07-857-2248-14
Sequence 14, Appl
39 657.5 29.0 264 2 US-07-857-2248-16
Sequence 16, Appl
40 657.5 29.0 264 2 US-07-857-2248-16
Sequence 16, Appl
41 649.5 28.6 258 2 US-09-430-564-5
Sequence 5, Appl
42 636.5 28.0 260 2 US-07-857-2248-3
Sequence 3, Appl
43 632.5 27.9 260 2 US-07-857-2248-2
Sequence 2, Appl
44 624.5 27.5 260 2 US-07-857-2248-2
Sequence 2, Appl
45 620.5 27.3 260 2 US-07-857-2248-6
Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-09-031-295-2
Sequence 2, Appl
Sequence 2, Appl
GENERAL INFORMATION:
APPLICANT: LANG, Florian
APPLICANT: WADDOGER, Tutingun
INVENTOR: WADDOGER, Tutingun
NUMBER OF SEQUENCES: 4
TITLE: SMALL VOLUME-REGULATED HUMAN KINASE H-SK
CORRESPONDENCE ADDRESSES:
ADDRESSEE: FOLEY & LARIMER
ADDRESSEE: 1000 K Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
PUBLICATION NO.: 7000-5109
COMPUTER: IBM PC compatible
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA: US-09-031-295
CURRENT APPLICATION NUMBER: US-09-031-295
FILING DATE: 26-FEB-1998
PRIORITY DATE: 26-FEB-1998
APPLICATION NUMBER: 197-08-173.8
PRIOR APPLICATION DATA:
FILING DATE: 28-FEB-1997
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 058315/0123
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5390
FAX: (202) 672-5390
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 431 amino acids
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-031-295-2

Query Match 100.0% Score 2270; DB 4; Length 431;
Best Local Similarity 100.0% Pred. No. 4, 26-209; Gaps 0;
Matches 41; Conservative 0; Mismatches 0; Indels 0;
0? 1 MTVTWKAAGTLTYSRHWB...KENAEALGFSVAPPTDSFLK 60
|||||
1 MTVTWKAAGTLTYSRHWB...KENAEALGFSVAPPTDSFLK 60
DB 1 MTVTWKAAGTLTYSRHWB...KENAEALGFSVAPPTDSFLK 60
|||||

? INFORMATION FOR SEQ ID NO: 5:
 ? SEQUENCE CHARACTERISTICS:
 ? LENGTH: 431 amino acids
 ? TYPE: amino acid
 ? STRANDEDNESS: single
 ? TOPOLOGY: linear
 ? MOLECULE TYPE: peptide
 ? IMMEDIATE SOURCE:
 ? LIBRARY:
 ? CLONE: Consensus
 ? US-09-111-444-5

Query Match 99.3%; Score 2254; DB 3; Length 431;

Best Local Similarity 99.3%; Pred. No. 1.4e-207;

Matches 428; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MYWTEAKAGTGLTYSMKGQVALLTAPMKORRGNDIFOKTANNYSACKHPVEVSTLKI 60
 DB 1 MAVTEAKAGTGLTYSMKGQVALLTAPMKORRGNDIFOKTANNYSACKHPVEVSTLKI 60
 QY 61 SQDQEPFLMANPSPSPSOQINLGPSSNPKHAKSDPEFLVKGSGFKVLLARMAE 120
 DB 61 SQDQEPFLMANPSPSPSOQINLGPSSNPKHAKSDPEFLVKGSGFKVLLARMAE 120
 QY 121 EPTAYKVKLOKATLKKKEKHINSESNVLLKWKHPFLVGLHSFQADKLYFVDIYN 180
 DB 121 EPTAYKVKLOKATLKKKEKHINSESNVLLKWKHPFLVGLHSFQADKLYFVDIYN 180
 QY 181 GGLPYHLQRECFLEPPARFYAAEIASALQYJHSLNIVYROLAPENILLDSQGHVLT 240
 DB 181 GGLPYHLQRECFLEPPARFYAAEIASALQYJHSLNIVYROLAPENILLDSQGHVLT 240
 QY 241 PLCKENIEHNSTSTFCGTPETLAPVLRHQPTDRTVDMWCLGAVLYENLYGLPPFYSR 300
 DB 241 PLCKENIEHNSTSTFCGTPETLAPVLRHQPTDRTVDMWCLGAVLYENLYGLPPFYSR 300
 QY 301 NTAKENDINLWFLQKKNITNSARHLLEGLQKRTKLGADDPMEIKSNVYSLINW 360
 DB 301 NTAKENDINLWFLQKKNITNSARHLLEGLQKRTKLGADDPMEIKSNVYSLINW 360
 QY 361 DDLINKITPPFNVSQPNELRHDPDETEEPVNSIGKSPDSVIVTASVKNAEAFLG 420
 DB 361 DDLINKITPPFNVSQPNELRHDPDETEEPVNSIGKSPDSVIVTASVKNAEAFLG 420
 QY 421 FSVAPPTDSTL 431
 DB 421 FSVAPPTDSTL 431

RESULT 4

US-09-541-228-5

; Sequence 5, Application US/09541228

; Patent No. 6232077

; GENERAL INFORMATION:

; INVENTOR: Incyte, Inc., Incyte, Janice

; APPLICANT: Incyte, Inc., Incyte, Janice

; TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES

; CURRENT APPLICATION DATA:

; ADDRESS: Incyte Pharmaceuticals, Inc.

; CITY: Palo Alto

; COUNTRY: U.S.

; ZIP: 94304

; COMPUTER READABLE FORM:

; OPERATING SYSTEM: DOS

; SOFTWARE: FASTSEQ Version 1.5

; APPLICATION NUMBER: US/09-541-228

? FILING DATE:
 ? PRIOR APPLICATION DATA:
 ? APPLICATION NUMBER: 08/712-709
 ? ATTORNEY/AGENT INFORMATION:
 ? NAME: Billings, Lucy J.
 ? REGISTRATION NUMBER: 36,749
 ? ADDRESS/POSTAL NUMBER: PF-0118 US
 ? TELEPHONE: 415-855-0555
 ? TELEFAX: 415-845-4166
 ? INFORMATION FOR SEQ ID NO: 5:
 ? SEQUENCE CHARACTERISTICS:
 ? LENGTH: 431 amino acids
 ? TYPE: amino acid
 ? STRANDEDNESS: single
 ? TOPOLOGY: linear
 ? MOLECULE TYPE: peptide
 ? IMMEDIATE SOURCE:
 ? LIBRARY:
 ? CLONE: Consensus
 ? US-09-341-228-5

Query Match 99.3%; Score 2254; DB 3; Length 431;

Best Local Similarity 99.3%; Pred. No. 1.4e-207;

Matches 428; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MYWTEAKAGTGLTYSMKGQVALLTAPMKORRGNDIFOKTANNYSACKHPVEVSTLKI 60
 DB 1 MAVTEAKAGTGLTYSMKGQVALLTAPMKORRGNDIFOKTANNYSACKHPVEVSTLKI 60
 QY 61 SQDQEPFLMANPSPSPSOQINLGPSSNPKHAKSDPEFLVKGSGFKVLLARMAE 120
 DB 61 SQDQEPFLMANPSPSPSOQINLGPSSNPKHAKSDPEFLVKGSGFKVLLARMAE 120
 QY 121 EPTAYKVKLOKATLKKKEKHINSESNVLLKWKHPFLVGLHSFQADKLYFVDIYN 180
 DB 121 EPTAYKVKLOKATLKKKEKHINSESNVLLKWKHPFLVGLHSFQADKLYFVDIYN 180
 QY 181 GGLPYHLQRECFLEPPARFYAAEIASALQYJHSLNIVYROLAPENILLDSQGHVLT 240
 DB 181 GGLPYHLQRECFLEPPARFYAAEIASALQYJHSLNIVYROLAPENILLDSQGHVLT 240
 QY 241 PLCKENIEHNSTSTFCGTPETLAPVLRHQPTDRTVDMWCLGAVLYENLYGLPPFYSR 300
 DB 241 PLCKENIEHNSTSTFCGTPETLAPVLRHQPTDRTVDMWCLGAVLYENLYGLPPFYSR 300
 QY 301 NTAKENDINLWFLQKKNITNSARHLLEGLQKRTKLGADDPMEIKSNVYSLINW 360
 DB 301 NTAKENDINLWFLQKKNITNSARHLLEGLQKRTKLGADDPMEIKSNVYSLINW 360
 QY 361 DDLINKITPPFNVSQPNELRHDPDETEEPVNSIGKSPDSVIVTASVKNAEAFLG 420
 DB 361 DDLINKITPPFNVSQPNELRHDPDETEEPVNSIGKSPDSVIVTASVKNAEAFLG 420
 QY 421 FSVAPPTDSTL 431
 DB 421 FSVAPPTDSTL 431

RESULT 5

US-08-712-700-9

; Sequence 9, Application US/08712709

; Patent No. 5863780

; GENERAL INFORMATION:

; INVENTOR: Incyte, Inc., Incyte, Janice

; APPLICANT: Incyte, Inc., Incyte, Janice

; TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES

; CURRENT APPLICATION DATA:

; ADDRESS: Incyte Pharmaceuticals, Inc.

; CITY: Palo Alto

; COUNTRY: U.S.

; ZIP: 94304

; COMPUTER READABLE FORM:

; OPERATING SYSTEM: DOS

; SOFTWARE: FASTSEQ Version 1.5

; APPLICATION NUMBER: US/08-712-700-9

CITY: Palo Alto
 STATE: CA
 COUNTRY: U.S.
 ZIP: 94304
 COMPUTER READABLE FORM:
 TITLE OF INVENTION: FASTSD
 INVENTOR: GUEGLIER, KARL J.
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSD Version 1.5
 CUMULATIVE INDEXED: YES
 APPLICATION NUMBER: US/08/712,709
 FILING DATE: Filed herewith
 ATTORNEY/AGENT INFORMATION:
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PF-0118 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-845-4165
 TELEFAX: 415-845-4166
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 430 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE: GenBank
 LIBRARY: GenBank
 CLONE: 294637

US-08-712-709-3
 Query Match 97.13; Score 2204.5; DB 2; Length 430;
 Best Local Similarity 96.8%; Pred. No. 8e-203;
 Matches 417; Conservative 6; Mismatches 5; Indels 1; Gaps 1;

QY 1 MYVTEAAAGTLTSSRMGVAIIAFMKQRNGLNDFOKTANNSTACKHPVQSLKI 60
 DB 1 MYVTEAAAGTLTSSRMGVAIIAFMKQRNGLNDFOKTANNSTACKHPVQSLKI 60
 QY 61 SQQPEFLMANNSPPSPSQOINLQPSNHPKSDSFHFKVYKGSFGKVLLAHKAE 120
 DB 61 SQQPEFLMANNSPPSPSQOINLQPSNHPKSDSFHFKVYKGSFGKVLLAHKAE 120
 QY 121 EYFVAVVYVQKALAKKEKHIMSERVLLKNWKEHFFVAGLFESFOTADKIYVLOYIN 180
 DB 121 EYFVAVVYVQKALAKKEKHIMSERVLLKNWKEHFFVAGLFESFOTADKIYVLOYIN 180
 QY 181 GUEFLYVLOREKTEPLEPFAFYAEASALGYLHSLNIVYROLKPNILDSQGHVLT 240
 DB 181 GUEFLYVLOREKTEPLEPFAFYAEASALGYLHSLNIVYROLKPNILDSQGHVLT 240
 QY 241 FOLCENIEHNSTSTFCQTPETLAPVLRQPIORTDVMCLGAVLYEMVLGPPYSR 300
 DB 241 FOLCENIEHNSTSTFCQTPETLAPVLRQPIORTDVMCLGAVLYEMVLGPPYSR 300
 QY 301 NTAENDYTLNKLQKLNITSARHLLLEGLOKORTKRGAKDDPMETKSHVPSLIN 360
 DB 301 NTAENDYTLNKLQKLNITSARHLLLEGLOKORTKRGAKDDPMETKSHVPSLIN 360
 QY 361 DDLINKITPPPNPNVSGPSDUNHFDPEFTPEVPNVSIGKSPSVLTASVKEAFAFLG 420
 DB 361 DDLINKITPPPNPNVSGPSDUNHFDPEFTPEVPNVSIGKSPSVLTASVKEAFAFLG 420
 QY 421 FSYAPPMDSFL 430
 DB 421 FSYAPPMDSFL 430

RESULT 6
 US-09-111-444-9
 ; Sequence 9, Application US/09111444
 ; Patent No. 6013792
 ; GENERAL INFORMATION:

APPLICANT: Au-Young, Janice
 APPLICANT: Guegler, Karl J.
 TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES
 INVENTOR: GUEGLIER, KARL J.
 CORRESPONDENCE ADDRESS:
 STREET: Incyte Pharmaceuticals, Inc.
 CITY: Palo Alto
 STATE: CA
 COUNTRY: U.S.
 ZIP: 94304
 COMPUTER READABLE FORM:
 TITLE OF INVENTION: FASTSD
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSD Version 1.5
 CUMULATIVE INDEXED: YES
 APPLICATION NUMBER: US/09/111,444
 FILING DATE:
 PRIOR APPLICATION DATA: 08/712,709
 REGISTRATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PF-0118 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-855-0555
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 430 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE: GenBank
 CLONE: 294637

US-09-111-444-9

Query Match 97.13; Score 2204.5; DB 3; Length 430;
 Best Local Similarity 96.8%; Pred. No. 8e-203;
 Matches 417; Conservative 6; Mismatches 5; Indels 1; Gaps 1;

QY 1 MYVTEAAAGTLTSSRMGVAIIAFMKQRNGLNDFOKTANNSTACKHPVQSLKI 60
 DB 1 MYVTEAAAGTLTSSRMGVAIIAFMKQRNGLNDFOKTANNSTACKHPVQSLKI 60
 QY 61 SQQPEFLMANNSPPSPSQOINLQPSNHPKSDSFHFKVYKGSFGKVLLAHKAE 120
 DB 61 SQQPEFLMANNSPPSPSQOINLQPSNHPKSDSFHFKVYKGSFGKVLLAHKAE 120
 QY 121 EYFVAVVYVQKALAKKEKHIMSERVLLKNWKEHFFVAGLFESFOTADKIYVLOYIN 180
 DB 121 EYFVAVVYVQKALAKKEKHIMSERVLLKNWKEHFFVAGLFESFOTADKIYVLOYIN 180
 QY 181 GUEFLYVLOREKTEPLEPFAFYAEASALGYLHSLNIVYROLKPNILDSQGHVLT 240
 DB 181 GUEFLYVLOREKTEPLEPFAFYAEASALGYLHSLNIVYROLKPNILDSQGHVLT 240
 QY 241 FOLCENIEHNSTSTFCQTPETLAPVLRQPIORTDVMCLGAVLYEMVLGPPYSR 300
 DB 241 FOLCENIEHNSTSTFCQTPETLAPVLRQPIORTDVMCLGAVLYEMVLGPPYSR 300
 QY 301 NTAENDYTLNKLQKLNITSARHLLLEGLOKORTKRGAKDDPMETKSHVPSLIN 360
 DB 301 NTAENDYTLNKLQKLNITSARHLLLEGLOKORTKRGAKDDPMETKSHVPSLIN 360
 QY 361 DDLINKITPPPNPNVSGPSDUNHFDPEFTPEVPNVSIGKSPSVLTASVKEAFAFLG 420
 DB 361 DDLINKITPPPNPNVSGPSDUNHFDPEFTPEVPNVSIGKSPSVLTASVKEAFAFLG 420


```

OY 65 BPELANPSP-----PPSPSQ-----INLGPSS-NPHAKSPDFELKVGK 106
DB 20 BPELSPADACFLAEAAAGELVGVHVEVETTSVNGVERIGPIC-----FELLVVGK 75
OY 107 GSKGYLLARHAEV-----FYAVKYLKALK-KEKHHSERNVLANKHVPLVG 161
DB 76 GGVGVFOVR-KVQGTINLQKLYAMKVLKRAKIVMANQTAHRAENI-LESYKHPPVE 133
OY 162 LHSFQDPAKLYVLOYITNGELFYHLORECELEPARFYAASALGYLHSLNIVR 221
DB 134 LAVATGSKLYLLCGLSGELFTHLEREGIELEDTACFLAEITLALGHLSQGITR 193
OY 222 DLKPEMLLSQGHVITDFGLCKENHSTFSTCTGPEYLAPELVKOPDYTDVDM 281
DB 194 DLKPEMLLSQGHVITDFGLCKENHSTFSTCTGPEYLAPELVKOPDYTDVDM 281
OY 282 CLAVYKLVGLPPGYGNTFVWONLWKNFOLKENTNSANHLLEGLQNDREL- 340
DB 254 SLCAVAKMLTGLSPFTFAENDKITKGLAPPTTPDARLVKFLAKRPSORG 313
OY 341 QAKDQFVLSKVFELNDDKLNKTPFPKFNWSPGNELEHPPDFTPE-PPVNSIG 359
DB 314 GQGDAAVQVRFPHMMDDLLANKVDPFPRCLOSEDSQDFTFRTQTV-----368
OY 400 KSPDSVLVAVKAEAFGLSPVAPPT 427
DB 369 DSDPD---TALSSENAOFLGTTYVAPS 393

```

```

RESULT 12
: Sequence 3, Application US/09430564
: Patent No. 6372467
: GENERAL INFORMATION:
: APPLICANT: Kev K. Lee-Fruman
: TITLE OF INVENTION: P5458K AND P8656K GENE, PROTEINS,
: AND METHODS FOR THEIR PRODUCTION, PROSES, AND DETECTION METHODS
: FILE REFERENCE: 00245/206002
: CURRENT APPLICATION NUMBER: US/09/430,564
: PRIOR FILING DATE: 1995-10-29
: PRIOR FILING DATE: 1995-10-29
: NUMBER OF SEQ ID NOS: 16
: SOFTWARE: FastSeq for Windows version 4.0
: SEQ ID NO 3
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-09-430-564-3

```

```

Query Match 35.54; Score 806.5; DB 4; Length 495;
Best Local Similarity 44.3%; Pred. No. 8.5e-69;
Matches 172; Conservative 66; Mismatches 111; Indels 39; Gaps 12;

```

```

OY 65 BPELANPSP-----PPSPSQ-----INLGPSS-NPHAKSPDFELKVGK 106
DB 33 BPELSPADACFLAEAAAGELVGVHVEVETTSVNGVERIGPIC-----FELLVVGK 88
OY 107 GSKGYLLARHAEV-----FYAVKYLKALK-KEKHHSERNVLANKHVPLVG 161
DB 89 GGVGVFOVR-KVQGTINLQKLYAMKVLKRAKIVMANQTAHRAENI-LESYKHPPVE 146
OY 162 LHSFQDPAKLYVLOYITNGELFYHLORECELEPARFYAASALGYLHSLNIVR 221
DB 147 LAVATGSKLYLLCGLSGELFTHLEREGIELEDTACFLAEITLALGHLSQGITR 206
OY 222 DLKPEMLLSQGHVITDFGLCKENHSTFSTCTGPEYLAPELVKOPDYTDVDM 281
DB 207 DLKPEMLLSQGHVITDFGLCKENHSTFSTCTGPEYLAPELVKOPDYTDVDM 266

```

```

OY 282 CLAVYKLVGLPPGYGNTFVWONLWKNFOLKENTNSANHLLEGLQNDREL- 340
DB 267 SLCAVAKMLTGLSPFTFAENDKITKGLAPPTTPDARLVKFLAKRPSORG 326
OY 341 QAKDQFVLSKVFELNDDKLNKTPFPKFNWSPGNELEHPPDFTPE-PPVNSIG 399
DB 327 GQGDAAVQVRFPHMMDDLLANKVDPFPRCLOSEDSQDFTFRTQTV-----381
OY 400 KSPDSVLVAVKAEAFGLSPVAPPT 427
DB 382 DSDPD---TALSSENAOFLGTTYVAPS 406

```

RESULT 13

```

: US-08-749-902-7
: Sequence 7, Application US/08749902
: Patent No. 6372467
: GENERAL INFORMATION:
: APPLICANT: Bandman, Olga
: TITLE OF INVENTION: NOVEL HUMAN SERINE/THREONINE
: KINASES
: NUMBER OF SEQUENCES: 8
: SOFTWARE: FASTA
: ADDRESS: 3174 Porter Drive
: STREET: 3174 Porter Drive
: CITY: Palo Alto
: STATE: CA
: COUNTRY: US
: ZIP: 94304
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: CHARACTER SET: ASCII
: OPERATING SYSTEM: DOS
: SOFTWARE: FastSeq Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: 08/08749,902
: PRIORITY DATE: 1995-10-29
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE: INFORMATION:
: ATTORNEY/AGENT:
: NAME: Billings, Lucy J.
: REGISTRATION NUMBER: 36,749
: REFERENCE/DOCKET NUMBER: PP-0150 US
: TELECOMMUNICATIONS INFORMATION:
: TELEPHONE: 415-845-0555
: TELEFAX: 415-845-4166
: INFORMATION FOR SEQ ID NO: 7:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 305 amino acids
: TYPE: amino acid
: STRANDNESS: -single
: TOPOLOGY: linear
: IMMEDIATE SOURCE:
: LIBRARY: GenBank
: CLONE: 189508
: US-08-749-902-7

```

```

Query Match 35.4%; Score 803; DB 2; Length 525;
Best Local Similarity 46.3%; Pred. No. 2e-68;
Matches 163; Conservative 64; Mismatches 105; Indels 20; Gaps 9;

```

```

OY 83 INLGPSSNPHAKSPDFELKVGKSGFVKYLLARH---KAEYFYAVKYLKALK- 137
DB 79 VNRPEK---IRPECFELLVVGKGGYGVKVFYKTAQTKIP-AKVYKRAKIVMAN 134
OY 138 KEKHHSERNVLANKHVPLVGITNGELFYHLORECELEPARFYAASALGYLHSLNIVR 197
DB 135 KATYKRAKIVMANHSTFSTCTGPEYLAPELVKOPDYTDVDM 193
OY 198 RARYTAMETASNLGTHLSINIVTHDKLVPEMLLSQGHVITDFGLCKENHSTFST 257

```

```

194 TACFYLAELSMALHGIHQKGI:::VROLKPNILNIQHQVKLDFGLCKES:::HOGVYTHFF 253
Oy 198 RARFYAAETASALATYLSHNLTVYROLKPNILNDSQSHVILDFGLCKENIHNSTSTF 257
Db 194 TACFYLAELSMALHGIHQKGI:::HOLAPENILNIQHQVKLDFGLCKES:::HOGVYTHFF 253
Oy 258 CGTPEYLAPEVLIHQPTDYDVMWGLGAVLYKLYGLPPTYSNTAEYDNI LNKPLQK 317
Db 254 CGTETMAPELLSHNRADVMSGLAIDKLTGAPPTGNNRKTIDKILCKNLPL 313
Oy 310 PNTNSAMHLLGLQKORTKUGA-KODPHEISKVSFSLINMODLNKKTTPPPNHW 376
Db 314 PYLTQEAROLLKLLKNAASRGAGDAGVQAPFFRHLNWEELARKVPEFPKLL 373
Oy 377 SGPNLRFHPDETTEE-PVYNSIGKSPDSVLYATSKENAEAFGVSAPPT 427
Db 374 QSEEDVSQFDSKFTQTPV-----DSPDDSTLSES-----ANQVFLGTYTVA 417

RESULT 14
US-08-749-902-8
; Sequence 8, Application US/08749902
; Patent No. 6186355
; Owner: INVIVOGEN, INC.
; APPLICANT: Bandman, Olga
; APPLICANT: Goll, Surya K.
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: SERINE/THREONINE
; TITLE OF INVENTION: PROTEIN KINASES
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESSES:
; ADDRESS: 3177 Webster Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP CODE: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM compatible
; SOFTWARE: FASTA
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08749,902
; FILING DATE: 08/07/90
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; INFORMATION:
; ANNOTATION:
; NAME: INVIVOGEN
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0150 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-945-4166
; TELEFAX: 415-945-4166
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; INFORMATION SOURCE:
; LIBRARY: Genbank
; CLONE: 1562
;
US-08-749-902-8
Query Match 35.4%; Score 803; Db 2; Length 525;
Best Local Similarity 46.3%; Prod No. 2e-68;
Matches 163; Conservative 64; Mismatches 105; Indels 20; Gaps 9;

Oy 83 INGPSNPHNPSDFHFYKNGKSGCKVLARH---KAEVYFAVVLQKAILKK- 137
Db 79 VNRGPEK---IRPECFELLYLKGNGVQVRYKGTANTGKIF-ANVLLKAMIVRNA 134
Oy 138 KEKHINSENNVLLKNKHPVLGVHFSQTAOKLYFDVINGGELFYHLOHEKCYKLEP 197
Db 135 KDTATKAEANN-LSEYKHIPPVLDLYATQGGALVILITELSGELFPHQLREHIFMD 193
Oy 198 RARFYAAETASALATYLSHNLTVYROLKPNILNDSQSHVILDFGLCKENIHNSTSTF 257
Db 194 TACFYLAELSMALHGIHQKGI:::VROLKPNILNIQHQVKLDFGLCKES:::HOGVYTHFF 253
Oy 258 CGTPEYLAPEVLIHQPTDYDVMWGLGAVLYKLYGLPPTYSNTAEYDNI LNKPLQK 317
Db 254 CGTETMAPELLSHNRADVMSGLAIDKLTGAPPTGNNRKTIDKILCKNLPL 313
Oy 310 PNTNSAMHLLGLQKORTKUGA-KODPHEISKVSFSLINMODLNKKTTPPPNHW 376
Db 314 PYLTQEAROLLKLLKNAASRGAGDAGVQAPFFRHLNWEELARKVPEFPKLL 373
Oy 377 SGPNLRFHPDETTEE-PVYNSIGKSPDSVLYATSKENAEAFGVSAPPT 427
Db 374 QSEEDVSQFDSKFTQTPV-----DSPDDSTLSES-----ANQVFLGTYTVA 417

Search completed: August 11, 2003, 08:24:43
Job time : 63.0425 secs

```

```

Db 135 KDTATKAEANN-LSEYKHIPPVLDLYATQGGALVILITELSGELFPHQLREHIFMD 193
Oy 198 RARFYAAETASALATYLSHNLTVYROLKPNILNDSQSHVILDFGLCKENIHNSTSTF 257
Db 194 TACFYLAELSMALHGIHQKGI:::HOLAPENILNIQHQVKLDFGLCKES:::HOGVYTHFF 253
Oy 258 CGTPEYLAPEVLIHQPTDYDVMWGLGAVLYKLYGLPPTYSNTAEYDNI LNKPLQK 317
Db 254 CGTETMAPELLSHNRADVMSGLAIDKLTGAPPTGNNRKTIDKILCKNLPL 313
Oy 310 PNTNSAMHLLGLQKORTKUGA-KODPHEISKVSFSLINMODLNKKTTPPPNHW 376
Db 314 PYLTQEAROLLKLLKNAASRGAGDAGVQAPFFRHLNWEELARKVPEFPKLL 373
Oy 377 SGPNLRFHPDETTEE-PVYNSIGKSPDSVLYATSKENAEAFGVSAPPT 427
Db 374 QSEEDVSQFDSKFTQTPV-----DSPDDSTLSES-----ANQVFLGTYTVA 417

RESULT 15
US-09-430-564-16
; Sequence 16, Application US/09430564
; Patent No. 6372465
; GENERAL INFORMATION:
; APPLICANT: John Blenis
; APPLICANT: John Blenis
; APPLICANT: Ray K. Lee-Frumkin
; TITLE OF INVENTION: PHASEK AND PR556A GENES, PROTEINS,
; FILE REFERENCE: 00246/506002
; CURRENT PRIORITY APPLICATION NUMBER: US/09430,564
; CURRENT FILING DATE: 1998-10-24
; PRIOR APPLICATION NUMBER: 50/106,141
; PRIOR FILING DATE: 1998-10-29
; ADDRESS: 16 Winthrop Drive, Room 16
; CITY: Cambridge, MA 02142
; STATE: MA
; COUNTRY: US
; SOFTWARE: FASTA
; SEQ ID NO 16
; LENGTH: 525
; ORIGIN:
; ORGANISM: Homo sapiens
;
US-09-430-564-16
Query Match 35.4%; Score 803; Db 4; Length 525;
Best Local Similarity 46.3%; Prod No. 2e-68;
Matches 163; Conservative 64; Mismatches 105; Indels 20; Gaps 9;

Oy 83 INGPSNPHNPSDFHFYKNGKSGCKVLARH---KAEVYFAVVLQKAILKK- 137
Db 79 VNRGPEK---IRPECFELLYLKGNGVQVRYKGTANTGKIF-ANVLLKAMIVRNA 134
Oy 138 KEKHINSENNVLLKNKHPVLGVHFSQTAOKLYFDVINGGELFYHLOHEKCYKLEP 197
Db 135 KDTATKAEANN-LSEYKHIPPVLDLYATQGGALVILITELSGELFPHQLREHIFMD 193
Oy 198 RARFYAAETASALATYLSHNLTVYROLKPNILNDSQSHVILDFGLCKENIHNSTSTF 257
Db 194 TACFYLAELSMALHGIHQKGI:::VROLKPNILNIQHQVKLDFGLCKES:::HOGVYTHFF 253
Oy 258 CGTPEYLAPEVLIHQPTDYDVMWGLGAVLYKLYGLPPTYSNTAEYDNI LNKPLQK 317
Db 254 CGTETMAPELLSHNRADVMSGLAIDKLTGAPPTGNNRKTIDKILCKNLPL 313
Oy 310 PNTNSAMHLLGLQKORTKUGA-KODPHEISKVSFSLINMODLNKKTTPPPNHW 376
Db 314 PYLTQEAROLLKLLKNAASRGAGDAGVQAPFFRHLNWEELARKVPEFPKLL 373
Oy 377 SGPNLRFHPDETTEE-PVYNSIGKSPDSVLYATSKENAEAFGVSAPPT 427
Db 374 QSEEDVSQFDSKFTQTPV-----DSPDDSTLSES-----ANQVFLGTYTVA 417

```


IT Involving changes in cell volume, e.g. renal insufficiency,
 PT inflammation, infections etc.

PS Discloure, Fig 1; 15pp; German.

CC The human cell-volume regulating kinase h-sgk is inhibited by the
 swelling of cells (or presence of urea), whereas cell shrinkage
 stimulates its expression. The nucleic acid sequence, specifically for
 CC diagnosis of conditions that involve such changes, e.g. hyper- and hypo-
 natremia, diabetes mellitus, renal insufficiency, hypercatabolism,
 CC hepatic encephalopathy, inflammation, macrobials/viral infection, fructose
 CC the nucleic acid, protein and products including receptors that bind
 CC h-sgk, can be used to treat these disorders.

XX Sequence 431 AA;

Query Match 100.0%; Score 2270; DB 19; Length 431;
 Best Local Similarity 100.0%; Pred. No. 2,8e-204; Indels 0; Gaps 0;
 Matches 431; Conservative 0; Mismatches 0;

0Y 1 MYVTEAAAGTLTYSNRGHWALLAFKQRRKGLNDPFIQKIANNACKIPVQSILKI 60
 DB 1 MYVTEAAAGTLTYSNRGHWALLAFKQRRKGLNDPFIQKIANNACKIPVQSILKI 60
 61 SQPEPELMANFPSPSPSQIINGPSSNPHAFPSDFHFKVIGKSPGVLLARHAE 120
 DB 61 SQPEPELMANFPSPSPSQIINGPSSNPHAFPSDFHFKVIGKSPGVLLARHAE 120
 121 EVFYAVKLOKKAALKKEEKHINSEKRNVLKANKHPTLVGLHFSQTADKLVPYDIN 180
 DB 121 EVFYAVKLOKKAALKKEEKHINSEKRNVLKANKHPTLVGLHFSQTADKLVPYDIN 180
 181 GSEFLYHQERCTLEPRARYAATASAGLYLSNLTVDLKPENILDSQGHVLT 240
 DB 181 GSEFLYHQERCTLEPRARYAATASAGLYLSNLTVDLKPENILDSQGHVLT 240
 241 FGLCKENINNSTSTFCGTPEYLAPEVLIHQKPTDYTMWGLGAVLYEMLYGLPYTSR 300
 DB 241 FGLCKENINNSTSTFCGTPEYLAPEVLIHQKPTDYTMWGLGAVLYEMLYGLPYTSR 300
 301 NTAEDYONILNPKLPQLKPNINSAHLLGGLKDKTRGAKMDPMEIKSNVFSILNW 360
 DB 301 NTAEDYONILNPKLPQLKPNINSAHLLGGLKDKTRGAKMDPMEIKSNVFSILNW 360
 361 DDLNKKITPPENPNVSGNELRHDFDETEEPVPSIGKSPSVLTASVKAENAFUG 420
 DB 361 DDLNKKITPPENPNVSGNELRHDFDETEEPVPSIGKSPSVLTASVKAENAFUG 420
 421 FSVAPPTDSFL 431
 DB 421 FSVAPPTDSFL 431

RESULT 2
 ID AAB24115
 AB24115 standard; Protein: 431 AA.

XX AAB24115;

DT 29-JAN-2001 (first entry)

XX Human serum and glucocorticoid regulated kinase protein (HSK).

XX Human; STK3; serine threonine kinase; HSKG; RSKG;

XX serum and glucocorticoid regulated kinase.

XX Homo sapiens.

XX CH125957-A.

PN 12-JUL-2000.

PD

XX 29-OCT-1998; 98CN-0124822.
 XX 29-OCT-1998; 98CN-0124822.

PA (UFWU-) UNIV FUDAN.

XX Yu L, Fu Q, Zhao Y;

XX HP1; 2000-587991/56.

DR New human serine threonine protein kinase, its code sequence,
 preparation, and use.

PT Example 3; Fig 3; 29pp; Chinese.

CC The present invention describes human serine threonine kinase STK3,
 CC which is a new member of the serine/threonine protein kinase family.
 CC Human STK3 shares homology with human serum and glucocorticoid
 CC regulated kinase (HSKG) and rat SKR (HSK). The present sequence
 CC represents the human HSKR protein sequence from the present invention.

XX Sequence 431 AA;

Query Match 100.0%; Score 2270; DB 21; Length 431;
 Best Local Similarity 100.0%; Pred. No. 2,8e-204;
 Matches 431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

0Y 1 MYVTEAAAGTLTYSNRGHWALLAFKQRRKGLNDPFIQKIANNACKIPVQSILKI 60
 DB 1 MYVTEAAAGTLTYSNRGHWALLAFKQRRKGLNDPFIQKIANNACKIPVQSILKI 60
 61 SQPEPELMANFPSPSPSQIINGPSSNPHAFPSDFHFKVIGKSPGVLLARHAE 120
 DB 61 SQPEPELMANFPSPSPSQIINGPSSNPHAFPSDFHFKVIGKSPGVLLARHAE 120
 121 EVFYAVKLOKKAALKKEEKHINSEKRNVLKANKHPTLVGLHFSQTADKLVPYDIN 180
 DB 121 EVFYAVKLOKKAALKKEEKHINSEKRNVLKANKHPTLVGLHFSQTADKLVPYDIN 180
 181 GSEFLYHQERCTLEPRARYAATASAGLYLSNLTVDLKPENILDSQGHVLT 240
 DB 181 GSEFLYHQERCTLEPRARYAATASAGLYLSNLTVDLKPENILDSQGHVLT 240
 241 FGLCKENINNSTSTFCGTPEYLAPEVLIHQKPTDYTMWGLGAVLYEMLYGLPYTSR 300
 DB 241 FGLCKENINNSTSTFCGTPEYLAPEVLIHQKPTDYTMWGLGAVLYEMLYGLPYTSR 300
 301 NTAEDYONILNPKLPQLKPNINSAHLLGGLKDKTRGAKMDPMEIKSNVFSILNW 360
 DB 301 NTAEDYONILNPKLPQLKPNINSAHLLGGLKDKTRGAKMDPMEIKSNVFSILNW 360
 361 DDLNKKITPPENPNVSGNELRHDFDETEEPVPSIGKSPSVLTASVKAENAFUG 420
 DB 361 DDLNKKITPPENPNVSGNELRHDFDETEEPVPSIGKSPSVLTASVKAENAFUG 420
 421 FSVAPPTDSFL 431
 DB 421 FSVAPPTDSFL 431

RESULT 3

ID AAB65613

XX AAB65613 standard; Protein: 431 AA.

AC AAB65613;

XX 27-MAR-2001 (first entry)

XX Novel protein kinase, SEQ ID NO: 139.

XX Human; mouse; protein kinase; antiarthritis; antisclerotic; osteopathic;

XX immunosuppressive; cardiotonic; renal; antiinflammatory; antisclerotic;

dermatological; antidiabetic; antinfertility; gene therapy; vaccine;
 immune disorder; cardiovascular disease; neurodegenerative disease;
 cancer; autoimmune disorder; stroke; inflammatory bowel disease;
 inflammatory pelvic disease; multiple sclerosis; psoriasis;
 OS Homo sapiens.

XX W0200073469-A2.

XX PA

XX PD

XX PO

XX PP

XX PR

XX RA

XX RB

XX RC

XX RD

XX RE

XX RF

XX RG

XX RH

XX RI

XX RJ

XX RK

XX RL

XX RM

XX RN

XX RO

XX RP

XX RS

XX RT

XX RU

XX RV

XX RW

XX RX

XX RY

XX RZ

XX SA

XX SB

XX SC

XX SD

XX SE

XX SF

XX SG

XX SH

XX SI

XX SJ

XX SK

XX SL

XX SM

XX SN

XX SO

XX SP

XX SQ

XX SR

XX SS

XX ST

XX SU

XX SV

XX SW

XX SX

XX SY

XX SZ

XX Nucleic acids encoding kinase polypeptides, useful for diagnosing and
 treating immune-related diseases and disorders, cardiovascular disease,
 neurodegenerative diseases and/or cancers -
 Claim 10; Fig 1: 310pp; English.
 The present sequence is a novel protein kinase. The novel protein kinases
 and the nucleic acids that encode them may be used in the treatment and
 diagnosis of immune-related diseases and disorders, cardiovascular disease,
 neurodegenerative diseases and/or cancers. The nucleic acids and
 complementary sequences may also be used as DNA probes in diagnostic
 assays. The nucleic acids and complementary sequences may also be used
 of antibodies of kinase expression and activity. Anti-kinase antibodies
 and kinase antagonists may also be used to down regulate kinase
 expression and activity. Diseases related to kinase expression and
 activity, such as immune-related diseases and disorders, cardiovascular
 diseases, complications of organ transplantation, myocardial infarction,
 immune disorders, cardiomyopathies, strokes, renal failure,
 oxidative-stress related disorders, chronic inflammatory bowel disease,
 chronic autoimmune diseases, multiple sclerosis, asthma,
 osteoporosis, psoriasis, rheumatoid arthritis, diabetes, cancers and
 reproductive diseases.

XX Sequence 431 AA;

Query Watch 100.0%; Score 2270; DB 22; Length 431;
 Best Local Similarity 100.0%; Pred. No. 2.8e+204;
 Matches 431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 MYVTEAKGTITYSMRQVALLIAPKMRGRLNDIOTKANNACKHPPEVOSLKI 60
 Db 1 MYVTEAKGTITYSMRQVALLIAPKMRGRLNDIOTKANNACKHPPEVOSLKI 60
 Oy 61 SOPEELMANNPPSPSQOINGSPSNHAKPSDFPELVYKSGSKVLLARHAE 120
 Db 61 SOPEELMANNPPSPSQOINGSPSNHAKPSDFPELVYKSGSKVLLARHAE 120
 Oy 121 EYFVAVKYLQKALKKEEKHEENLVNKKVHPGLRSPADKLYFVLDYN 180
 Db 121 EYFVAVKYLQKALKKEEKHEENLVNKKVHPGLRSPADKLYFVLDYN 180
 Oy 181 GRLFKPLQROEPTTBRPARYAFATSGVLSLTVKRAKRNILLOSCHVID 240
 Db 181 GRLFKPLQROEPTTBRPARYAFATSGVLSLTVKRAKRNILLOSCHVID 240
 Oy 241 FGLCKENIENSTSTFGPTPEYLAPEVJHQPOTDYDMVLCGLVYGLPPTSR 300
 Db 241 FGLCKENIENSTSTFGPTPEYLAPEVJHQPOTDYDMVLCGLVYGLPPTSR 300
 Oy 301 NTAKMDVNLKPLQKPNINSARHLLSGLOKRTKRLGAKDDMEIKSNVFFSLNW 360

Db 301 NTAKMDVNLKPLQKPNINSARHLLSGLOKRTKRLGAKDDMEIKSNVFFSLNW 360
 Oy 361 DDLINKITPPNNSQVPLIHHYHVPKSPVNSIGKSPSVLTVSKAKFAELG 420
 Db 361 DDLINKITPPNNSQVPLIHHYHVPKSPVNSIGKSPSVLTVSKAKFAELG 420
 Oy 421 FSYAPPTDSPL 431

Db 421 FSYAPPTDSPL 431

XX RESULT 4

XX AAK90139

XX ID AAK90139 standard; Protein; 431 AA.

XX AC AAK90139;

XX UC AAK90139; (first entry)

XX DT 15-MAR-1999;

XX DE Human sgk protein.

XX KM Serum glucocorticoid regulated kinase; sgk; human; treatment; inhibitor;

XX KM serine/threonine protein kinase family; antagonist; diabetic nephropathy;

XX KM chronic renal failure; inflammation; Alzheimers disease; wound.

XX KM Homo sapiens.

XX FH Key

XX FT Misc-difference 381

XX FT /note- *encoded by GAG*

XX PN EP887081-A2.

XX XX 30-DEC-1998.

XX PF 27-MAY-1998; 98EP-0304189.

XX XX 27-JUN-1997; 97US-0051124.

XX PA (SMK) SMITHKLINE BEECHAM CORP.

XX PI Kumar JM;

XX DR WPI, 1999-047637/05.

XX DR N-PSDB; AAV74190.

XX XX Treating chronic renal failure, diabetic nephropathy and Alzheimers'

XX XX inhibit activity or expression of human serum glucocorticoid

XX XX regulated kinase (sgk), a serine/threonine protein kinase

XX XX Disclosure; Page 16-17; 17pp; English.

XX CC This sequence represents a novel human serum glucocorticoid regulated

XX CC kinase (sgk) protein which is a member of the serine/threonine protein

XX CC kinase family. This protein is used for the treatment of a subject having

XX CC need to inhibit/ down regulate the activity of the kinase. The polypeptide e.g. for the treatment of chronic renal failure, diabetic

XX CC nephropathy, inflammation, Alzheimers disease and wounds.

XX CC Sequence 431 AA;

XX Query Watch 99.9%; Score 2267; DB 20; Length 431;

XX Best Local Similarity 99.8%; Pred. No. 5.3e+204;

XX Matches 430; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MYVTEAKGTITYSMRQVALLIAPKMRGRLNDIOTKANNACKHPPEVOSLKI 60

Db 1 MYVTEAKGTITYSMRQVALLIAPKMRGRLNDIOTKANNACKHPPEVOSLKI 60

Oy 61 SOPEELMANNPPSPSQOINGSPSNHAKPSDFPELVYKSGSKVLLARHAE 120

Db 61 SOPEELMANNPPSPSQOINGSPSNHAKPSDFPELVYKSGSKVLLARHAE 120

Oy 121 EYFVAVKYLQKALKKEEKHEENLVNKKVHPGLRSPADKLYFVLDYN 180

Db 121 EYFVAVKYLQKALKKEEKHEENLVNKKVHPGLRSPADKLYFVLDYN 180

Oy 181 GRLFKPLQROEPTTBRPARYAFATSGVLSLTVKRAKRNILLOSCHVID 240

Db 181 GRLFKPLQROEPTTBRPARYAFATSGVLSLTVKRAKRNILLOSCHVID 240

Oy 241 FGLCKENIENSTSTFGPTPEYLAPEVJHQPOTDYDMVLCGLVYGLPPTSR 300

Db 241 FGLCKENIENSTSTFGPTPEYLAPEVJHQPOTDYDMVLCGLVYGLPPTSR 300

Oy 301 NTAKMDVNLKPLQKPNINSARHLLSGLOKRTKRLGAKDDMEIKSNVFFSLNW 360

61 SPOPELNNANPPSPSSQO NLGSSPNHAKPSDFHFKLVGKSGKGLVHAKAE 120
 121 EYFVAVKYLQKALKKEKKEKHINSERNVLLANNKHHPFLVGLHESFOTAKLVPLVDYIN 180
 122 EYFVAVKYLQKALKKEKKEKHINSERNVLLANNKHHPFLVGLHESFOTAKLVPLVDYIN 180
 123 EYFVAVKYLQKALKKEKKEKHINSERNVLLANNKHHPFLVGLHESFOTAKLVPLVDYIN 180
 181 GGEFLYHLQKRCFLFEPAPRTAAETASALGTHLSINIVYRDLKPHENILDSQGHVLTLD 240
 182 GGEFLYHLQKRCFLFEPAPRTAAETASALGTHLSINIVYRDLKPHENILDSQGHVLTLD 240
 183 GGEFLYHLQKRCFLFEPAPRTAAETASALGTHLSINIVYRDLKPHENILDSQGHVLTLD 240
 241 FGLCKENHNSTSTFCOTFEYLAPEVLRKQPDYDTVMRCGLGAVYEMLYGLPFFTSR 300
 242 FGLCKENHNSTSTFCOTFEYLAPEVLRKQPDYDTVMRCGLGAVYEMLYGLPFFTSR 300
 301 NTABNDYDNLNKPQLQKPHITNSARHLLGLQKDFKRLGAKDQFMEKSHVFFSLNW 360
 302 NTABNDYDNLNKPQLQKPHITNSARHLLGLQKDFKRLGAKDQFMEKSHVFFSLNW 360
 303 NTABNDYDNLNKPQLQKPHITNSARHLLGLQKDFKRLGAKDQFMEKSHVFFSLNW 360
 361 DDLNKKITPTFPNPNVSGNENLRHDFEETPEEPVNSIGKSPDVLVATYASKEAAEAFUG 420
 362 DDLNKKITPTFPNPNVSGNENLRHDFEETPEEPVNSIGKSPDVLVATYASKEAAEAFUG 420
 363 DDLNKKITPTFPNPNVSGNENLRHDFEETPEEPVNSIGKSPDVLVATYASKEAAEAFUG 420
 421 FSVAPPTDSFL 431
 422 FSVAPPTDSFL 431

RESULT 5

AAAY95279 standard; Protein: 431 AA.

AAAY95279

AC AAAY95279;

XX 12-SEP-2000 (first entry)

XX Human serum and glucocorticoid-induced protein kinase.

XX Serum and glucocorticoid-induced protein kinase SGK.

XX Human; phosphorylation; cancer; diabetes; ischaemia; therapy.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Modified-site 255 /note= "o-phosphorylated"

XX Modified-site 422 /note= "o-phosphorylated"

XX M0200035946-A1.

XX 27-JUN-2000.

XX 14-DEC-1999; 99MO-G804232.

XX 14-DEC-1998; 9805-0112247.

XX 13-AUG-1999; 9905-0019676.

XX (YDNU-) UNIV DUNDIE.

XX Cohen P, Kobayashi T, Deak M;

XX WPI; 2000-442364/38.

XX Modulation of serum and glucocorticoid-induced protein kinase (SGK) by

XX phosphorylation with 3-phosphoinositide-dependent protein kinase-1

XX (PKD1) or dephosphorylation, useful for treatment of cancer, diabetes

XX and ischaemic diseases -

XX Disclosure; Fig 13; 127pp; English.

XX The present sequence is that of human serum and

XX glucocorticoid-induced protein kinase (SGK). SGK was initially

XX identified as a glucocorticoid and osmotic stress-responsive gene.

CC It is activated by phosphorylation of its Thr-308 and Ser-472
 CC residues. Novel isoforms of SGK, i.e. SGK2 and SGK3 (see
 CC AA95275-78), have been identified. The invention provides methods
 CC for identifying and isolating compounds that modulate the activity of
 CC 3-phosphoinositide-dependent protein kinase-1 (PKD1), and of
 CC reducing the activity of SGK by dephosphorylation. The invention
 CC also provides a method of identifying a compound that modulates the
 CC activity of SGK. Such compounds are useful for the treatment of
 CC cancer, diabetes or ischaemic disease.

Query Match

Best Local Similarity 99.6%; Score 2261; DB 21; Length 431;

Matches 430; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 MYTVEAAAGTGLTSEHSHVVALIAFKHKKHGLNDPQIKANNSTACKIPKVEVSLIK 60
 1 MYTVEAAAGTGLTSEHSHVVALIAFKHKKHGLNDPQIKANNSTACKIPKVEVSLIK 60
 61 SPOPELNNANPPSPSSQO NLGSSPNHAKPSDFHFKLVGKSGKGLVHAKAE 120
 61 SPOPELNNANPPSPSSQO NLGSSPNHAKPSDFHFKLVGKSGKGLVHAKAE 120
 121 EYFVAVKYLQKALKKEKKEKHINSERNVLLANNKHHPFLVGLHESFOTAKLVPLVDYIN 180
 122 EYFVAVKYLQKALKKEKKEKHINSERNVLLANNKHHPFLVGLHESFOTAKLVPLVDYIN 180
 181 GGEFLYHLQKRCFLFEPAPRTAAETASALGTHLSINIVYRDLKPHENILDSQGHVLTLD 240
 182 GGEFLYHLQKRCFLFEPAPRTAAETASALGTHLSINIVYRDLKPHENILDSQGHVLTLD 240
 241 FGLCKENHNSTSTFCOTFEYLAPEVLRKQPDYDTVMRCGLGAVYEMLYGLPFFTSR 300
 242 FGLCKENHNSTSTFCOTFEYLAPEVLRKQPDYDTVMRCGLGAVYEMLYGLPFFTSR 300
 301 NTABNDYDNLNKPQLQKPHITNSARHLLGLQKDFKRLGAKDQFMEKSHVFFSLNW 360
 302 NTABNDYDNLNKPQLQKPHITNSARHLLGLQKDFKRLGAKDQFMEKSHVFFSLNW 360
 303 NTABNDYDNLNKPQLQKPHITNSARHLLGLQKDFKRLGAKDQFMEKSHVFFSLNW 360
 361 DDLNKKITPTFPNPNVSGNENLRHDFEETPEEPVNSIGKSPDVLVATYASKEAAEAFUG 420
 362 DDLNKKITPTFPNPNVSGNENLRHDFEETPEEPVNSIGKSPDVLVATYASKEAAEAFUG 420
 421 FSVAPPTDSFL 431
 422 FSVAPPTDSFL 431

RESULT 6

AAAM54025 standard; Protein: 431 AA.

AAAM54025

XX AAAM54025;

XX 31-JUL-1998 (first entry)

XX Human protein kinase HPK-3.

XX Protein kinase; human; HPK; signalling cascade; kinase expression;

XX Alzheimer's disease; cancer; anti-inflammatory agent; immunosuppressor;

XX lymphoma; therapy.

XX Homo sapiens.

XX M09811234-A2.

XX 19-MAR-1998.

XX 10-SEP-1997; 97MO-US15923.

AY933530 standard; Protein: 431 AA.	
AY933530;	
25-SEP-2000 (first entry)	
A rat serum and glucocorticoid induced protein kinase.	
Protein kinase, Pkh1, Phk1, Yrk1, Yrk2; protein kinase B-alpha;	
protein kinase C-beta; phosphatidylinositol-dependent protein kinase-1;	
3-phosphoinositide dependent protein kinase-1; PKM1; fungal infection;	
thrush; cancer; diabetes; obesity; antifungal; Candida infection.	
Ratus sp.	
WO2000036135-A2.	
22-JUN-2000.	
14-DEC-1998; 99NO-GBO4228.	
14-DEC-1998; 98US-O112114.	
(MED-) MEDICAL RES COUNCIL.	
(REGC) UNIV CALIFORNIA.	
Thorner JW, Alessi DR, Torrance PD, Casamayor A;	
NP1: 2000-442391/38.	
N-PDSB; AAA46592.	
Screening method identifying compounds which modulate protein kinase activity for use in treating fungal infections and cancer -	
Disclosure; Fig 13: 155pp; English.	
The present sequence represents a rat serum and glucocorticoid induced protein kinase (SKK). The specification describes a screening method to identify a compound which modulates the activity of protein kinases from different sources, using host yeast cells. The method is used to screen a library composed of cDNA clones encoding various forms of Yrk2 protein kinase Pkh1 or Phk2 phosphorylate and activate Yrk1. Yrk2 SKK or protein kinase B-alpha (PKBApha). 3-phosphoinositide-dependent protein kinase B-alpha (PKBDalpha) is used to phosphorylate and activate Ypk1 and Yrk2 or SKK but not Ralalpha or p70S6 kinase. Compounds identified by Yrk2 SKK or PKBApha are screened for their ability to inhibit Yrk2 SKK treat cancer. To treat cancer, the compounds inhibit PKB, PKD1 or activation of PRB by PKD1. Compounds which activate PKB or PKD1 can be used in the treatment of diabetes or obesity, and compounds which inhibit the treatment of diabetes or obesity. Yrk2 SKK, PKD1 or PKH2 or SKK (Ypk1 or Yrk2) can be used as an antifungal agent to treat candida infections, e.g. thrush.	
Sequence 431 AA:	
Query Match 97.9%; Score 2222; DB 21: Length 431;	
Best Local Similarity 97.0%; Pred. No. 9e+200;	
Matches 418; Conservative 8; Mismatches 5; Indels 0; Gaps 0;	
1 MYVTKTAAGTCTTSYRKGNVALLPKKPCKRGMLNDFTOKLANNACKKHVSSTIKI 60	
1 MYVTEARASTSYRRMRGVALLPAPKQRGLMDFTOKLANNACKKHVPQSITKI 60	
61 SQPGPEELNNANPPSPSSOOLNGSPNSPNAPGHFRTLVKGSGTCGVLLAHRAE 120	
61 SQPGPEELNNANPPSPSSOOLNGSPNSPNAPGHFRTLVKGSGTCGVLLAHRAE 120	
121 EYTAVKVYVKALKKKKEKHISERNVLKNRVKLNFVLGVHSFOTADKLFVLYDTIN 180	
121 EATVANVYLKALNKLNLSERENLKARNVFVGSHSFOTADKLFVLYDTIN 180	
181 GGELPHLOREKFCEFPARPFAVMTASAGLTSLNLNVIRDLKENILMSDGHTVID 240	
181 GGELPHLOREKFCEFPARPFAVMTASAGLTSLNLNVIRDLKENILMSDGHTVID 240	

Db	181	GGEZTLHQRBECFLPWPMYYAEIASALSTJNLNTVTYRDPLPNNLIJSUQHVIWD 241
Oy	241	FGLCFENHNHSTSTFCGPETLAPEVLRHPQDYORTVMKCLGVLRYLGYLPFFSR 300
Oy	241	FGLCFENHNHGTISTFGCPETLAPEVLRHPQDYORTVMKCLGVLRYLGYLPFFSR 300
Oy	241	VUCHEMNHGQTPQQKTPTNARILLQLQDKORTKRGLAKGDPMFKSHVFSLINM 360
Oy	301	NWTAMDINTLNKPQLKFNNTSNRLLEGLQDKORTKRGLAKGDPMFKSHVFSLINM 360
Db	301	NWTAMDINTLNKPQLKFNNTSNRLLEGLQDKORTKRGLAKGDPMFKSHVFSLINM 360
Oy	361	DOLLINKTTIPPNVSCGMPELRFDPTFEYPNSIGKSPOSVDYTVASKVAEAFLG 420
Oy	361	DOLLINKTTIPPFPNVPNSCDLARDFDFTFEYPVPSIGRSPTSILVTVASKVAEAFLG 420
Oy	421	TSVAPPDSEFL 431
Oy	421	TSVAPPDSEFL 431
Db		
RESULT 9		
AA865614		
ID	AA865614 standard; Protein: 430 AA.	
XX	AA865614	
XX	AA865614	
XX	27-MAR-2001 (first entry)	
XX	Human protein kinase, SEQ ID NO: 140.	
XX	Mouse; mouse; protein kinase; antiarthritic; antisclerotic; osteopathic;	
XX	Immunosuppressive; cardiac; renal; antiinflammatory; antislimic;	
XX	dematological; antididiabetic; antiinfertility; gene therapy; vaccine;	
XX	cancer; autoimmune disorder; stroke; inflammatory bowel disease;	
XX	Inflammatory pelvic disease; multiple sclerosis; psoriasis.	
XX	Mus musculus.	
XX	MO2000073469-A2.	
PN	07-DEC-2000.	
XX	26-MAY-2000; 2000MO-US14842.	
PF	28-MAY-1999; 99US-O136503.	
PR	(SUOE-) SUGEN INC.	
PX	Plowman GD, Martinez K, Whyte D, Suderisnam S;	
P1	WP1: 2001-032151/04.	
XX	N-FSDB; ANP44640.	
DR	Nucleic acids encoding kinase polypeptides, useful for diagnosing and treating immune-related diseases and disorders, cardiovascular disease, neurodegenerative diseases and/or cancers -	
XX	Claim 10; Fig 1: 310pp; English.	
XX	The Present sequence is a novel protein kinase. The novel protein kinases have been isolated from mice and used in the treatment and diagnosis of diseases associated with inappropriate kinase activities, such as immune-related diseases and disorders, cardiovascular disease, neurodegenerative diseases and/or cancers. The nucleic acids and complementary sequences may also be used as DNA probes in diagnostic assays and may be used as reagents in immunoassays. Antisense oligonucleotides of kinase expression and active site regions of antibodies and kinases antagonists may also be used to down regulate kinase expression and activity. Diseases related to kinase expression and activity include Rheumatoid arthritis, atherosclerosis, autoimmune disease, tumor promotion, myocardial infarction, immunologic disorders, cardiomyopathies, chronic inflammatory bowel disease, oxidative-stress related disorders, stroke; inflammatory bowel disease,	

PR 02-DEC-1999; 99US-0168559.
 PA (UYDU-) UNIV DUNDEE.
 XX Alessi D, Blondi R;
 PI 2001-390252/41.
 XX Identifying modulators of protein kinase (PK) activity, useful in
 PT developing drugs for treating cancer or diabetes, by measuring the
 PR ability of the compound to modulate or mimic the interaction of PK with
 PT interacting polypeptides -
 XX Disclosure; Fig 15; 180pp; English.
 XX The present invention describes a method for identifying a compound that
 CC modulates protein kinase activity. The method comprises measuring the
 CC ability of the compound to inhibit, promote or mimic the interaction of
 CC a polypeptide with a protein kinase. The interacting polypeptide interacts with the hydrophobic
 CC pocket of the protein kinase and/or comprises the amino acid sequence
 CC Phe/Tyr-Xaa-Xaa-Phe/Tyr (1). The method is useful in screening assays
 CC for polynucleotides from the present invention are useful in medicine
 CC or polynucleotides from the present invention are useful in medicine
 CC particularly in the manufacture of a medicament for treating a patient
 CC in need of modulation of signalling, e.g. a patient suffering from cancer
 CC or in need of inhibition of apoptosis, e.g. a patient suffering from tissue
 CC injury or ischaemic injury, including stroke. The compound or
 CC composition is also useful for inhibiting the interaction of a
 CC polypeptide with a protein kinase. The interacting polypeptide or
 CC compound is useful in methods of stabilising a hydrophobic pocket-
 CC containing protein kinase, where the protein kinase is exposed to the
 CC compound or polypeptide. A899786 to A899847 represent amino acid
 CC sequences and A899786 to A899847 represent oligonucleotide sequences,
 CC used in the exemplification of the present invention.

Sequence 373 AA:

Query Match 87.2%; Score 1979; DB 22: Length 373;
 Best Local Similarity 100.04; Pred. No. 4.8e-177;
 Matches 373; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 59 KTSQPEFLVWNPSPSPSSQNLGSPSNHAKPSDFHFLVTKGSGFGLVLAHKK 118
 DB 1 KTSQPEFLVWNPSPSPSSQNLGSPSNHAKPSDFHFLVTKGSGFGLVLAHKK 60
 QY 119 AEVYPAVYVQKALKLKEEKHNSFNVLVYKHPFLVGLVPSQTAQKLVFLDY 178
 DB 61 AEVYPAVYVQKALKLKEEKHNSFNVLVYKHPFLVGLVPSQTAQKLVFLDY 120
 QY 179 NGSEFLYHORECHLEPAPRYAAATASAGLYLSLNTVYRKLKPNLLDSQCHVL 238
 DB 121 NGSEFLYHORECHLEPAPRYAAATASAGLYLSLNTVYRKLKPNLLDSQCHVL 180
 QY 239 PDGLCKVENSUNSTSTFCSTQGVLAPELVHKQPDVQACVGLVYKMLGDEPPY 290
 DB 181 PDGLCKVENSUNSTSTFCSTQGVLAPELVHKQPDVQACVGLVYKMLGDEPPY 240
 QY 299 SNTAENYDNLKLPVLAQVFNKNSHLLLELQNDVQVGLKQNDKPKETKSHVPSLI 358
 DB 241 SNTAENYDNLKLPVLAQVFNKNSHLLLELQNDVQVGLKQNDKPKETKSHVPSLI 300
 QY 359 WMDLNLKLTTPFPNPNVSNPNEHAKHDFDEPTTEFPNPNIGKSPDSVLYVYAKAEAF 418
 DB 301 WMDLNLKLTTPFPNPNVSNPNEHAKHDFDEPTTEFPNPNIGKSPDSVLYVYAKAEAF 360
 QY 419 LGFSVAPPTDSEFL 431
 DB 361 LGFSVAPPTDSEFL 373

RESULT 12

A899836
 ID A899836 standard; Protein: J21 AA.
 XX A899836;
 XX 20-SEP-2001 (first entry)
 XX AGC protein kinase family member SKI protein sequence.
 DE Protein kinase: identification; hydrophobic pocket; interacting;
 KW cancer; diabetes; inhibition; apoptosis; tissue injury;
 KW ischaemic injury; stroke.
 XX homo sapiens.
 OS Synthetic.
 XX WO200144497-A2.
 PR 21-JUN-2001.
 XX 04-DEC-2000; 2000MO-GB04598.
 PF 02-DEC-1999; 99US-0168559.
 XX (UYDU-) UNIV DUNDEE.
 PA Alessi D, Blondi R;
 PI 2001-390252/41.
 XX Identifying modulators of protein kinase (PK) activity, useful in
 PT developing drugs for treating cancer or diabetes, by measuring the
 PR ability of the compound to modulate or mimic the interaction of PK with
 PT interacting polypeptides -
 XX Disclosure; Fig 16; 180pp; English.
 XX The present invention describes a method for identifying a compound that
 CC modulates protein kinase activity. The method comprises measuring the
 CC ability of the compound to inhibit, promote or mimic the interaction of
 CC a hydrophobic pocket-containing protein kinase with an interacting
 CC polypeptide. The interacting polypeptide interacts with the hydrophobic
 CC pocket of the protein kinase and/or comprises the amino acid sequence
 CC Phe/Tyr-Xaa-Xaa-Phe/Tyr (1). The method is useful in screening assays
 CC for developing pharmaceutical compounds or drugs. Compounds, polypeptides
 CC or polynucleotides from the present invention are useful in medicine
 CC or polynucleotides from the present invention are useful in medicine
 CC particularly in the manufacture of a medicament for treating a patient
 CC in need of modulation of signalling, e.g. a patient suffering from cancer
 CC or in need of inhibition of apoptosis, e.g. a patient suffering from tissue
 CC injury or ischaemic injury, including stroke. The compound or rate of
 CC phosphorylation by the protein kinase. The interacting polypeptide or
 CC composition is useful in methods of stabilising a hydrophobic pocket-
 CC containing protein kinase, where the protein kinase is exposed to the
 CC compound or polypeptide. A899786 to A899847 represent amino acid
 CC sequences and A899786 to A899847 represent oligonucleotide sequences,
 CC used in the exemplification of the present invention.

Sequence 321 AA:

Query Match 74.7%; Score 1695; DB 22: Length 321;
 Best Local Similarity 99.7%; Pred. No. 1.8e-150;
 Matches 320; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 111 KVLARHNKAEFVAVYVQKALKLKEEKHNSFNVLVYKHPFLVGLVPSQTAQK 170
 DB 1 KVLARHNKAEFVAVYVQKALKLKEEKHNSFNVLVYKHPFLVGLVPSQTAQK 60
 QY 171 KLYFLVDYINGSEFLYHORECHLEPAPRYAAATASAGLYLSLNTVYRKLKPNLL 230
 DB 61 KLYFLVDYINGSEFLYHORECHLEPAPRYAAATASAGLYLSLNTVYRKLKPNLL 120

XX Modulation of serum and glucocorticoid-induced protein kinase (SGK) by
 PT phosphorylation with 3-phosphoinositide-dependent protein kinase-1
 CC [PDK1] or dephosphorylation, useful for treatment of cancer, diabetes
 PT and ischemic diseases.
 XX
 XX Disclosure: Page 7; 127pp; English.
 XX
 XX The present sequence is that of human serum and
 CC glucocorticoid-induced protein kinase (SGK) isoform 3. SGK
 CC (see AY95279) was initially identified as a glucocorticoid and
 CC osmotic stress-responsive gene. SGK3 is activated by activation provides
 CC methods of activating SGK activity by phosphorylation using
 CC 3-phosphoinositide-dependent protein kinase-1 (PDK1), and of
 CC reducing the activity of SGK by dephosphorylation. The invention
 CC provides a method of modulating SGK activity in cells. The
 CC activity of SGK. Such compounds are useful for treating patients
 CC requiring modulation of SGK, such as patients with cancer, diabetes
 CC or ischemic disease.
 XX
 XX Sequence 429 AA:

Query Match 64-88; Score 1472; DB 21; Length 429;
 Matched similarity 12.24; Percent identity 49;
 Locs: 277; Conservative: 53; Mismatches 14; Gaps 3;
 OY 27 FKKRNLGNDFTQKIANNSACKHPVOSILKISQPEPELNNKNSPP----- 77
 DB 19 FIKRLNGLNEFONLVPEYLPNDFWRAFLQNSPEK---QSDSEEDERSOKLH 74
 OY 76 SFHQQLNGPSNHPANSPDHLKYGKSGFKGLAHNAEEFYAVKVKOKKALK 137
 DB 75 SFHQQLNGPSNHPANSPDHLKYGKSGFKGLAHNAEEFYAVKVKOKKALK 134
 OY 138 KEERKHSENNVLLKNWKPVLGVLHGFQFADKLFFVLYDINGSELYFVHQERCFLEP 197
 DB 135 KEQKHMAENNVLLKNWKPVLGVLHGFQFADKLFFVLYDINGSELYFVHQERCFLEP 194
 OY 198 RARFYAAIASALGYLNSLVTVYRDLKPNILLDSQGHVLTDFGLCKENHNSSTFP 257
 DB 195 RARFYAAIASALGYLNSLVTVYRDLKPNILLDSQGHVLTDFGLCKEGALSDITTF 254
 OY 258 CQTEFLAPLYHKQPDFTQYDMWCGAVLYENLYGLPFYSRBAETMDNLKPLQK 317
 DB 255 CQTEFLAPLYHKQPDFTQYDMWCGAVLYENLYGLPFYSRBAETMDNLKPLSLR 314
 OY 318 PNTNSAHHLEGLQKDRDYNWCGAVLYENLYGLPFYSRBAETMDNLKPLTPFPNVS 377
 DB 315 PNTNSAHHLEGLQKDRDYNWCGAVLYENLYGLPFYSRBAETMDNLKPLTPFPNVS 374
 OY 378 GNEMLHEDPFTPEPWPVNSKGSNVLVTSYAKAAFLGFSVAPPT-DSFL 431
 DB 375 GPDIDINFTAFTEETVPYVCSVSYVNSVLAQDAVFGESVAPPSDLFL 429

RESULT 15

AAU87228
 ID: AAU87228 standard; Protein: 436 AA.

XX
 AC AAU87228;

XX 05-JUN-2002 (first entry)

XX Novel central nervous system protein #138.

XX Central nervous system; CNS; autoimmune disease; rheumatoid arthritis;
 XX hyperproliferative disorder; neoplasia; cardiovascular disorder;
 XX nervous system disorder; Alzheimer's disease; AIDS; ocular disorder;
 XX acquired immunodeficiency virus; dysphagia; gastrointestinal disorder;
 XX adenocarcinoma; reproductive system disorder; testicular feminisation;
 XX endocrine disorder; diabetes; cancer; leukemia; neovascularization;

KW respiratory disorder; renal disorder; kidney failure; blood disorder;
 KW myocardial infarction; wound healing; cell proliferation; skin adhe;
 KW food additive; food preservative; gene therapy.

OS Homo sapiens.
 XX W0200155118-A2.

XX 02-AUG-2001.

XX 17-JAN-2001; 2001MO-US01332.

XX 31-JAN-2000; 2000US-0179055.

XX 04-FEB-2000; 2000US-0180658.

XX 24-FEB-2000; 2000US-0184654.

XX 02-MAR-2000; 2000US-0186950.

XX 17-MAR-2000; 2000US-0190076.

XX 18-APR-2000; 2000US-0198123.

XX 07-JUN-2000; 2000US-0205247.

XX 28-JUN-2000; 2000US-0214886.

XX 30-JUN-2000; 2000US-0215135.

XX 07-JUL-2000; 2000US-0216647.

XX 11-JUL-2000; 2000US-0217487.

XX 11-JUL-2000; 2000US-0217496.

XX 14-JUL-2000; 2000US-0218290.

XX 26-JUL-2000; 2000US-0220994.

XX 14-AUG-2000; 2000US-0224518.

XX 14-AUG-2000; 2000US-0224519.

XX 14-AUG-2000; 2000US-0225213.

XX 14-AUG-2000; 2000US-0225266.

XX 14-AUG-2000; 2000US-0225267.

XX 14-AUG-2000; 2000US-0225288.

XX 14-AUG-2000; 2000US-0226447.

XX 14-AUG-2000; 2000US-0226477.

XX 14-AUG-2000; 2000US-0226577.

XX 14-AUG-2000; 2000US-0226578.

XX 18-AUG-2000; 2000US-0226729.

XX 22-AUG-2000; 2000US-0226681.

XX 22-AUG-2000; 2000US-0226688.

XX 22-AUG-2000; 2000US-0227052.

XX 30-AUG-2000; 2000US-0228924.

XX 01-SEP-2000; 2000US-0229287.

XX 01-SEP-2000; 2000US-0229343.

XX 01-SEP-2000; 2000US-0229345.

XX 05-SEP-2000; 2000US-0229509.

XX 05-SEP-2000; 2000US-0229513.

XX 06-SEP-2000; 2000US-0230438.

XX 08-SEP-2000; 2000US-0231242.

XX 08-SEP-2000; 2000US-0231243.

XX 08-SEP-2000; 2000US-0231244.

XX 08-SEP-2000; 2000US-0231414.

XX 08-SEP-2000; 2000US-0232080.

XX 08-SEP-2000; 2000US-0232081.

XX 14-SEP-2000; 2000US-0232397.

XX 14-SEP-2000; 2000US-0232398.

XX 14-SEP-2000; 2000US-0232399.

XX 14-SEP-2000; 2000US-0232400.

XX 14-SEP-2000; 2000US-0233063.

XX 14-SEP-2000; 2000US-0233064.

XX 14-SEP-2000; 2000US-0233065.

XX 21-SEP-2000; 2000US-0234223.

PR 21-SEP-2000; 2000US-02314971.
 PR 21-SEP-2000; 2000US-02314972.
 PR 25-SEP-2000; 2000US-02314998.
 PR 26-SEP-2000; 2000US-02314984.
 PR 27-SEP-2000; 2000US-02315834.
 PR 28-SEP-2000; 2000US-02315835.
 PR 29-SEP-2000; 2000US-02316327.
 PR 29-SEP-2000; 2000US-02316357.
 PR 29-SEP-2000; 2000US-02316358.
 PR 29-SEP-2000; 2000US-02316359.
 PR 02-OCT-2000; 2000US-02316370.
 PR 02-OCT-2000; 2000US-02316802.
 PR 02-OCT-2000; 2000US-02317034.
 PR 02-OCT-2000; 2000US-02317035.
 PR 02-OCT-2000; 2000US-02317040.
 PR 13-OCT-2000; 2000US-02319597.
 PR 20-OCT-2000; 2000US-02409560.
 PR 20-OCT-2000; 2000US-02412121.
 PR 20-OCT-2000; 2000US-02412122.
 PR 20-OCT-2000; 2000US-02417867.
 PR 20-OCT-2000; 2000US-02417887.
 PR 20-OCT-2000; 2000US-02418008.
 PR 20-OCT-2000; 2000US-02418009.
 PR 01-NOV-2000; 2000US-02418036.
 PR 01-NOV-2000; 2000US-02418037.
 PR 08-NOV-2000; 2000US-02418474.
 PR 08-NOV-2000; 2000US-02418475.
 PR 08-NOV-2000; 2000US-02418476.
 PR 08-NOV-2000; 2000US-02418477.
 PR 08-NOV-2000; 2000US-02418478.
 PR 08-NOV-2000; 2000US-02418526.
 PR 08-NOV-2000; 2000US-02418527.
 PR 08-NOV-2000; 2000US-02418528.
 PR 08-NOV-2000; 2000US-02418532.
 PR 08-NOV-2000; 2000US-02418533.
 PR 08-NOV-2000; 2000US-02418534.
 PR 08-NOV-2000; 2000US-02418535.
 PR 08-NOV-2000; 2000US-02418536.
 PR 08-NOV-2000; 2000US-02418537.
 PR 08-NOV-2000; 2000US-02418538.
 PR 08-NOV-2000; 2000US-02418539.
 PR 08-NOV-2000; 2000US-02418540.
 PR 08-NOV-2000; 2000US-02418541.
 PR 08-NOV-2000; 2000US-02418542.
 PR 08-NOV-2000; 2000US-02418543.
 PR 08-NOV-2000; 2000US-02418544.
 PR 08-NOV-2000; 2000US-02418545.
 PR 08-NOV-2000; 2000US-02418546.
 PR 08-NOV-2000; 2000US-02418547.
 PR 08-NOV-2000; 2000US-02418548.
 PR 08-NOV-2000; 2000US-02418549.
 PR 08-NOV-2000; 2000US-02418550.
 PR 08-NOV-2000; 2000US-02418551.
 PR 08-NOV-2000; 2000US-02418552.
 PR 08-NOV-2000; 2000US-02418553.
 PR 08-NOV-2000; 2000US-02418554.
 PR 08-NOV-2000; 2000US-02418555.
 PR 08-NOV-2000; 2000US-02418556.
 PR 08-NOV-2000; 2000US-02418557.
 PR 08-NOV-2000; 2000US-02418558.
 PR 08-NOV-2000; 2000US-02418559.
 PR 08-NOV-2000; 2000US-02418560.
 PR 08-NOV-2000; 2000US-02418561.
 PR 08-NOV-2000; 2000US-02418562.
 PR 08-NOV-2000; 2000US-02418563.
 PR 08-NOV-2000; 2000US-02418564.
 PR 08-NOV-2000; 2000US-02418565.
 PR 08-NOV-2000; 2000US-02418566.
 PR 08-NOV-2000; 2000US-02418567.
 PR 08-NOV-2000; 2000US-02418568.
 PR 08-NOV-2000; 2000US-02418569.
 PR 08-NOV-2000; 2000US-02418570.
 PR 08-NOV-2000; 2000US-02418571.
 PR 08-NOV-2000; 2000US-02418572.
 PR 08-NOV-2000; 2000US-02418573.
 PR 08-NOV-2000; 2000US-02418574.
 PR 08-NOV-2000; 2000US-02418575.
 PR 08-NOV-2000; 2000US-02418576.
 PR 08-NOV-2000; 2000US-02418577.
 PR 08-NOV-2000; 2000US-02418578.
 PR 08-NOV-2000; 2000US-02418579.
 PR 08-NOV-2000; 2000US-02418580.
 PR 08-NOV-2000; 2000US-02418581.
 PR 08-NOV-2000; 2000US-02418582.
 PR 08-NOV-2000; 2000US-02418583.
 PR 08-NOV-2000; 2000US-02418584.
 PR 08-NOV-2000; 2000US-02418585.
 PR 08-NOV-2000; 2000US-02418586.
 PR 08-NOV-2000; 2000US-02418587.
 PR 08-NOV-2000; 2000US-02418588.
 PR 08-NOV-2000; 2000US-02418589.
 PR 08-NOV-2000; 2000US-02418590.

PR 11-DEC-2000; 2000US-02164007.
 PR 05-JAN-2001; 2001US-0259078.
 (HUMA-) HUMAN GENOME SC1 INC.
 PA ROSEN CA, BARASH SC, KUBEN SM;
 XX N-ESDB; ABK13558.
 DR WPI; 2001-501633/65.
 XX N-ESDB; ABK13558.

New isolated nucleic acid encoding a protein for diagnosing,
 preventing, treating or ameliorating medical conditions and used as
 food additives or preservatives.

Claim 9; SEQ ID No 746; 837pp; English.

The invention describes an isolated nucleic acid molecule (1) encoding a
 protein (2) which is useful for diagnosing, preventing, treating or
 ameliorating medical conditions and in diagnosis of a
 pathological condition. Disorders which are diagnosed or treated include
 autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders
 e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia,
 angiogenesis, nervous system disorders e.g. Alzheimer's disease and
 amyotrophic lateral sclerosis, infections caused by bacteria, viruses
 e.g. corneal infection, gastrointestinal disorders e.g. dysplasia,
 adenocarcinomas and irritable bowel syndrome, reproductive system
 disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes
 e.g. leukimia, disorders involving neovascularisation e.g. malignancies,
 respiratory disorders e.g. nonallergic rhinitis, renal disorders e.g.
 acute kidney failure and food related disorders e.g. anaphylaxis and
 epithelial cell proliferation, to prevent skin aging due to sunburn, to
 maintain organs before transplantation, for supporting cell culture of
 primary tissues, to regenerate tissues and to chemotactically
 increase or decrease storage capabilities: fat content, lipid, protein,
 increase or decrease storage capabilities: fat content, lipid, protein,

Query Match 64 81; Score 1172; 68 22; Length 496;

Best Local Similarity 64 24; Prod No 9e-129; Indels 14; Gaps 3;
 Matches 279; Conservative 53; Mismatches 69;

Oy 27 PMSKNGVGLMFKKQFAMSKYACKMKNVUSLLISQDPEELMANNSPPV----- 77
 Db 86 FIKORAGLANLEQINLYFERYKVLGKSGSVALLAKHAEVYKAWKALIK 137
 Oy 78 SPQSGVGLQSGWAKGKSGKSPKRYKVLGKSGSVALLAKHAEVYKAWKALIK 137
 Db 142 STSONIHLQPSGNPIARFTDFDLVILGKSGSVALLAKHAEVYKAWKALIK 137
 Oy 136 KSKKTHGKSNVLLKQWYKVFVGLHSPQKFKVFLVYVNGCLFNLQESRSP 197
 Db 202 KEOKHIAEKNVLLKQWYKVFVGLHSPQKFKVFLVYVNGCLFNLQESRSP 197
 Oy 198 KAPSTAFNEMALQYKJHEVYKVFVGLHSPQKFKVFLVYVNGCLFNLQESRSP 257
 Db 262 FARFYAAEIASLQISIKIYVYDLKFNILLDSGVHVLDTGLCKGKIALSDITTF 321
 Oy 258 CQKPYKAPVYKQWYKVFVGLHSPQKFKVFLVYVNGCLFNLQESRSP 317
 Db 322 CQKPYKAPVYKQWYKVFVGLHSPQKFKVFLVYVNGCLFNLQESRSP 317
 Oy 318 PNTYSARHLLLELLKQWYKVFVGLHSPQKFKVFLVYVNGCLFNLQESRSP 377
 Db 382 TQVYSARHLLLELLKQWYKVFVGLHSPQKFKVFLVYVNGCLFNLQESRSP 377
 Oy 378 QNELKRFDPFTEFPVNSIGKSPDSVAVTNSKDAEAFGFSVAPPT-DSFV 431
 Db 442 GPQDINRFDTFTFTVPSVNSVSDSVLNSVLEADAVTGSVAPPSDFV 496

Tue Aug 12 10:55:50 2003

us-10-000-039a-2.rag

Page 12

Search completed: August 11, 2003, 08:18:51
Job time : 139.884 secs


```

AX056374
LOCUS AX056374
SEQUENCE 18 from Patent W00073469.
ACCESSION AX056374.1 GI:12229081
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens (human)
REFERENCE 1 Ploemien,G.D., Martinez,R., Whyte,D. and Sudersanam,S.
AUTHORS
TITLES Cell volume-regulated human kinase h-sgk
JOURNAL
FEATURES
Location/Qualifiers
organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 345 a 333 c 293 g 325 t
Alignment Scores:
Pred. No.: 1,98e-65 Length: 1296
Score: 624.00 Matches: 0
Score Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-10-000-039A-2_COPY_313_431 (1-119) x AX056374 (1-1296)
QY 1 Proctengitlenulysprotsenlthetrhaseraltahgthistlenulgluglylenuleu 20
DB 937 CTTCTCCAGCTGACCAACAAATATTACAAATTCGACAGACACTCTCTGGAGGCGCTCTG 996
QY 21 Glulalagialualpheleuglyalulysleasphesgltulysserilis 40
DB 997 CAGAGAGACAGACAAAGCGCTCGGGCCAGAGATGATCTCATGAGATTAGAGATCAT 1056
QY 41 ValPhePheSerIleLysSerProtsenValLeuAlaSerVallys 60
DB 1057 GTCCTCTCTCTTAATACCTGGATGATGATCTTATTAAGAAGATTACTCCCTCTTT 1116
QY 61 AnProAnValSerCylProAnGluLeuAlaSerVallys 80
DB 1117 ACCCAATATGAGCGGCCACAGAGTAGCGACTTGTAGCCGAGTTTACCGAAG 1176
QY 81 ProvalProtsenSerIleLysSerProtsenValLeuAlaSerVallys 100
DB 1177 CTGTGTCACCACTCAATGGACAGTCCCTCGACAGCGTCTCTGTCACAGCCAGCTCAAG 1236
QY 101 Glulalagialualpheleuglyalulysleasphesgltulysserilis 119
DB 1237 GAGCTCGGAGCGCTTCTTAGCGCTTTCTTAGCGCTTCTTAGCGAGCTTCTCTGCTC 1293
RESULT 2
ARI79441
DEFINITION Sequence 1 from patent US 6326181.
ACCESSION ARI79441
VERSION ARI79441.1 GI:20220996
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1. (bases 1 to 2370)
AUTHORS Long P.P. and Waldeger, S.D.
TITLES Cell volume-regulated human kinase h-sgk
JOURNAL Patent: US 6326181-A 1 04-DEC-2001;
FEATURES
Location/Qualifiers
1..2370
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="HSNANSTPK"
BASE COUNT 636 a 517 c 513 g 704 t
Alignment Scores:
Pred. No.: 3.9e-65 Length: 2370
Score: 624.00 Matches: 0
Score Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-10-000-039A-2_COPY_313_431 (1-119) x AX002570 (1-2370)

```

```

BASE COUNT 636 a 517 c 513 g 704 t
ORGANISM
Alignment Scores:
Pred. No.: 3.9e-65 Length: 2370
Score: 624.00 Matches: 0
Score Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-10-000-039A-2_COPY_313_431 (1-119) x ARI79441 (1-2370)
QY 1 Proctengitlenulysprotsenlthetrhaseraltahgthistlenulgluglylenuleu 20
DB 979 CTTCTCCAGCTGACCAACAAATATTACAAATTCGACAGACACTCTCTGGAGGCGCTCTG 1038
QY 21 Glulalagialualpheleuglyalulysleasphesgltulysserilis 40
DB 1039 CAGAGAGACAGACAAAGCGCTCGGGCCAGAGATGATCTCATGAGATTAGAGATCAT 1098
QY 41 ValPhePheSerIleLysSerProtsenValLeuAlaSerVallys 60
DB 1099 GTCCTCTCTCTTAATACCTGGATGATGATCTTATTAAGAAGATTACTCCCTCTTT 1158
QY 61 AnProAnValSerCylProAnGluLeuAlaSerVallys 80
DB 1159 ACCCAATATGAGCGGCCACAGAGTAGCGACTTGTAGCCGAGTTTACCGAAG 1218
QY 81 ProvalProtsenSerIleLysSerProtsenValLeuAlaSerVallys 100
DB 1219 CTGTGTCACCACTCAATGGACAGTCCCTCGACAGCGTCTCTTAGCGCTTCTCTGCTC 1278
QY 101 Glulalagialualpheleuglyalulysleasphesgltulysserilis 119
DB 1279 GAGCTCGGAGCGCTTCTTAGCGCTTTCTTAGCGCTTCTTAGCGAGCTTCTCTGCTC 1335
RESULT 3
AX002570
LOCUS AX002570
ACCESSION AX002570
VERSION AX002570.1 GI:742111
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens (human)
REFERENCE 1. (bases 1 to 2370)
AUTHORS Mammila, Eutheria; Primates; Catarhinal; Hominidae; Homo.
TITLES Cell volume-regulated human kinase h-sgk
JOURNAL Patent: EP 0861896-A 1 02-SEP-1998;
FEATURES
Location/Qualifiers
1..2370
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="HSNANSTPK"
BASE COUNT 636 a 517 c 513 g 704 t
Alignment Scores:
Pred. No.: 3.9e-65 Length: 2370
Score: 624.00 Matches: 0
Score Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-10-000-039A-2_COPY_313_431 (1-119) x AX002570 (1-2370)

```

QY 1 ProLeuGlnLeuValSerGlyProAsnIleThrAsnSerAlaAargHisLeuGluGlyLeu 20
 Db 979 CTTCTCCAGCTGAACCAATATTCATATATTCCTCCAGACACTCTCTGGAGGCGCTCTG 1038
 QY 21 GlnValPheAsnValLeuValAspValLeuValAspPheMetGluIleYssSerHis 40
 Db 1039 CAGAGACAGACAGAACGGCTCGGGCCAGATGACTTCATGGAGATTAGAGTACT 1098
 QY 41 ValPhePheSerLeuIleAsnTrpAspAspLeuIleAsnLysLysIleThrProPhe 60
 Db 1099 GTCTCTCTCTCTTAATTAATCTGGGATCATCTCATTAAGAAGATTACTCCCTCTT 1158
 QY 61 AsnProAsnValSerGlyProAsnGlnLeuValGlnHisPheAspProGluPheThrGlu 80
 Db 1159 AACCCAAATGTAGTGGGCGGACGAGCTACGGACTTCTACCCGCGAGTTTACGGAAG 1218
 QY 81 ProValProAsnSerIleGlyYssSerProAspSerValLeuValThrAlaSerVal 100
 Db 1219 CTGTCTCCCACTCCATCTGGCAAGTCCCTTACNACGGTCTCTCCACACGACGATG 1278
 QY 101 GluAlaAlaGlnAlaPheLeuGlyPheSerTrpAlaProProThrAspSerPheLeu 119
 Db 1279 GAACTCCGAGGCTTTCTTAGGCTTTCTTATGCGCTCTCCACGAGACTCTTTCTTC 1335
 RESULT 4
 LOCUS AX337834 2370 bp DNA linear PAT 09-JAN-2002
 DEFINITION Sequence 8343 from Patent WO0194629.
 DESCRIPTION ACCSSION
 VERSION AX337834.1 GI:1812855
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM
 REFERENCES
 1 Young P.E., Augustus M., Carter K.C., Ehmer R., Endress G.,
 Cancer gene determination and therapeutic screening using signature
 gene sets
 JOURNAL Patent: WO 0194629-A 8343 (3-DEC-2001);
 TITLE Avalon Pharmaceuticals
 FEATURES
 1..2370
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="genbank:8343" accession No. Y10032*
 BASE COUNT 636 a 517 c 513 g 704 t
 ORIGIN
 Alignment Scores: Length: 2370
 Pred. No.: 624.00 Matches: 119
 Score: 624.00
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Gaps: 0
 Query Match: 100.00% Indels: 0
 DBs: 6
 US-10-000-039a-2_COPY_313_431 (1-119) x AX337834 (1-2370)
 QY 1 ProLeuGlnLeuValSerGlyProAsnIleThrAsnSerAlaAargHisLeuGluGlyLeu 20
 Db 979 CTTCTCCAGCTGAACCAATATTCATATATTCCTCCAGACACTCTCTGGAGGCGCTCTG 1038
 QY 21 GlnValPheAsnValLeuValAspValLeuValAspPheMetGluIleYssSerHis 40
 Db 1039 CAGAGACAGACAGAACGGCTCGGGCCAGATGACTTCATGGAGATTAGAGTACT 1098
 QY 41 ValPhePheSerLeuIleAsnTrpAspAspLeuIleAsnLysLysIleThrProPhe 60
 Db 1099 GTCTCTCTCTCTTAATTAATCTGGGATCATCTCATTAAGAAGATTACTCCCTCTT 1158
 QY 61 AsnProAsnValSerGlyProAsnGlnLeuValGlnHisPheAspProGluPheThrGlu 80
 Db 1159 AACCCAAATGTAGTGGGCGGACGAGCTACGGACTTCTACCCGCGAGTTTACGGAAG 1218
 QY 81 ProValProAsnSerIleGlyYssSerProAspSerValLeuValThrAlaSerVal 100
 Db 1219 CTGTCTCCCACTCCATCTGGCAAGTCCCTTACNACGGTCTCTCCACACGACGATG 1278
 QY 101 GluAlaAlaGlnAlaPheLeuGlyPheSerTrpAlaProProThrAspSerPheLeu 119
 Db 1279 GAACTCCGAGGCTTTCTTAGGCTTTCTTATGCGCTCTCCACGAGACTCTTTCTTC 1335
 RESULT 6
 LOCUS AX337834 2370 bp DNA linear PAT 09-JAN-2002
 DEFINITION Sequence 8343 from Patent WO0194629.
 DESCRIPTION ACCSSION
 VERSION AX337834.1 GI:1812855
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM
 REFERENCES
 1 Young P.E., Augustus M., Carter K.C., Ehmer R., Endress G.,
 Cancer gene determination and therapeutic screening using signature
 gene sets
 JOURNAL Patent: WO 0194629-A 8343 (3-DEC-2001);
 TITLE Avalon Pharmaceuticals
 FEATURES
 1..2370
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="genbank:8343" accession No. Y10032*
 BASE COUNT 636 a 517 c 513 g 704 t
 ORIGIN
 Alignment Scores: Length: 2370
 Pred. No.: 624.00 Matches: 119
 Score: 624.00
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Gaps: 0
 Query Match: 100.00% Indels: 0
 DBs: 6
 US-10-000-039a-2_COPY_313_431 (1-119) x AX337834 (1-2370)
 QY 1 ProLeuGlnLeuValSerGlyProAsnIleThrAsnSerAlaAargHisLeuGluGlyLeu 20
 Db 979 CTTCTCCAGCTGAACCAATATTCATATATTCCTCCAGACACTCTCTGGAGGCGCTCTG 1038
 QY 21 GlnValPheAsnValLeuValAspValLeuValAspPheMetGluIleYssSerHis 40
 Db 1039 CAGAGACAGACAGAACGGCTCGGGCCAGATGACTTCATGGAGATTAGAGTACT 1098
 QY 41 ValPhePheSerLeuIleAsnTrpAspAspLeuIleAsnLysLysIleThrProPhe 60
 Db 1099 GTCTCTCTCTCTTAATTAATCTGGGATCATCTCATTAAGAAGATTACTCCCTCTT 1158

QY 61 AsnProAsnValSerGlyProAsnGlnLeuValGlnHisPheAspProGluPheThrGlu 80
 Db 1159 AACCCAAATGTAGTGGGCGGACGAGCTACGGACTTCTACCCGCGAGTTTACGGAAG 1218
 QY 81 ProValProAsnSerIleGlyYssSerProAspSerValLeuValThrAlaSerVal 100
 Db 1219 CTGTCTCCCACTCCATCTGGCAAGTCCCTTACNACGGTCTCTCCACACGACGATG 1278
 QY 101 GluAlaAlaGlnAlaPheLeuGlyPheSerTrpAlaProProThrAspSerPheLeu 119
 Db 1279 GAACTCCGAGGCTTTCTTAGGCTTTCTTATGCGCTCTCCACGAGACTCTTTCTTC 1335
 RESULT 5
 LOCUS AX412131 3858 from Patent WO0229103.
 DEFINITION ACCSSION
 VERSION AX412131.1 GI:21443916
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM
 REFERENCES
 1 Ayres G., Norno D., Peres-de-Silva, S. and Vockley, J.G.
 Gene expression profiles in liver cancer
 JOURNAL Patent: WO 0229103-A 3858 11-APR-2002;
 TITLE GENE LOGIC INC (US)
 FEATURES
 1..3858
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="genbank:3858" accession No. Y10032*
 BASE COUNT 636 a 517 c 513 g 704 t
 ORIGIN
 Alignment Scores: Length: 3858
 Pred. No.: 624.00 Matches: 2370
 Score: 624.00
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Gaps: 0
 Query Match: 100.00% Indels: 0
 DBs: 6
 US-10-000-039a-2_COPY_313_431 (1-119) x AX412131 (1-2370)
 QY 1 ProLeuGlnLeuValSerGlyProAsnIleThrAsnSerAlaAargHisLeuGluGlyLeu 20
 Db 979 CTTCTCCAGCTGAACCAATATTCATATATTCCTCCAGACACTCTCTGGAGGCGCTCTG 1038
 QY 21 GlnValPheAsnValLeuValAspValLeuValAspPheMetGluIleYssSerHis 40
 Db 1039 CAGAGACAGACAGAACGGCTCGGGCCAGATGACTTCATGGAGATTAGAGTACT 1098
 QY 41 ValPhePheSerLeuIleAsnTrpAspAspLeuIleAsnLysLysIleThrProPhe 60
 Db 1099 GTCTCTCTCTCTTAATTAATCTGGGATCATCTCATTAAGAAGATTACTCCCTCTT 1158
 QY 61 AsnProAsnValSerGlyProAsnGlnLeuValGlnHisPheAspProGluPheThrGlu 80
 Db 1159 AACCCAAATGTAGTGGGCGGACGAGCTACGGACTTCTACCCGCGAGTTTACGGAAG 1218
 QY 81 ProValProAsnSerIleGlyYssSerProAspSerValLeuValThrAlaSerVal 100
 Db 1219 CTGTCTCCCACTCCATCTGGCAAGTCCCTTACNACGGTCTCTCCACACGACGATG 1278
 QY 101 GluAlaAlaGlnAlaPheLeuGlyPheSerTrpAlaProProThrAspSerPheLeu 119
 Db 1279 GAACTCCGAGGCTTTCTTAGGCTTTCTTATGCGCTCTCCACGAGACTCTTTCTTC 1335
 RESULT 6
 LOCUS HSRNASTPK

LOCUS H.sapiens mRNA 2370 bp mRNA linear PRI 16-MAY-1997

ACCESSION Y10032.1 GI:1834510

KEYWORDS serine/threonine protein kinase; spt gene.

ORGANISM Homo sapiens (human).

Bukariyola; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE Waldegger, S., Barth, P., Rober, G. and Lang, F.
Cloning and characterization of a putative human serine/threonine protein kinase transcriptionally modified during antiseptic and isocaine alterations of cell volume
J Biol Chem, 268(1), Acad. Sci. U.S.A. 94 (9), 4440-4445 (1997)

JOURNAL J972242

MEDLINE 9114008

PUBLISHED 2 (bases 1 to 2370)

REFERENCES Waldegger, S.
University of Tuebingen,
Physiology I, Gmelinstr. 5, D-72076 Tuebingen, FRG

AUTHORS TITLE Location/Qualifiers

JOURNAL "Homo sapiens"

FEATURES source /organism="Homo sapiens"
mol_type="mRNA"
db_xref="taxon:9606"
gene name="sgk"
cds 43..1138
ORIGIN 636 a 517 c 513 g 704 t

Alignment Scores:
Pred. No.: Length: 2370
Score: 215
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 0
Mismatches: 0
Indels: 0
Gaps: 0

US-10-000-039A-2_COPY_313_431 (1-119) x HSNWSTPK (1-2370)

QY 1 ProctuleinLeuysProasniethrAnserAlarqshileuLeuglyLeuLeu 20
Db CTCTCCAGCGTGGNCAATTCGAGCAGACTCTCGAGGCCCTCG 1038

QY 21 GlyLysAspArgThrtyrArgLeuGlyAlaylaspasPheMetCduIteLysSerHis 40
Db 1039 CAGAGGCACAGCACMACCGCCGCGGCCAGCATCTCTTGGAATTAGMGATCAT 1098

QY 41 ValPhePheSerLeuIleasantPasapleuIleasnlyslsylethrProPhe 60
Db 1099 GTCTTTCTCTTAATCACTGGGTGATCTCATATAAGAAGATTACTCCCCCTTT 1158

QY 61 AspProtsValserGlyProsnogluLeuarshisPheaspProclophehrLeu 80
Db 1159 ACACCAATGTGAAGGGCCCAACAGCACTTCAGCCGAGTTTACCGAAGAG 1218

LOCUS h.sapiens mRNA 2370 bp mRNA linear PRI 16-MAY-1997

ACCESSION Y10032.1 GI:1834510

KEYWORDS serine/threonine protein kinase; spt gene.

ORGANISM Homo sapiens (human).

Bukariyola; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE Waldegger, S., Barth, P., Rober, G. and Lang, F.
Cloning and characterization of a putative human serine/threonine protein kinase transcriptionally modified during antiseptic and isocaine alterations of cell volume
J Biol Chem, 268(1), Acad. Sci. U.S.A. 94 (9), 4440-4445 (1997)

JOURNAL J972242

MEDLINE 9114008

PUBLISHED 2 (bases 1 to 2370)

REFERENCES Waldegger, S.
University of Tuebingen,
Physiology I, Gmelinstr. 5, D-72076 Tuebingen, FRG

AUTHORS TITLE Location/Qualifiers

JOURNAL "Homo sapiens"

FEATURES source /organism="Homo sapiens"
mol_type="mRNA"
db_xref="taxon:9606"
gene name="sgk"
cds 43..1138
ORIGIN 636 a 517 c 513 g 704 t

Alignment Scores:
Pred. No.: Length: 2370
Score: 215
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 0
Mismatches: 0
Indels: 0
Gaps: 0

US-10-000-039A-2_COPY_313_431 (1-119) x HSNWSTPK (1-2370)

QY 1 ProctuleinLeuysProasniethrAnserAlarqshileuLeuglyLeuLeu 20
Db CTCTCCAGCGTGGNCAATTCGAGCAGACTCTCGAGGCCCTCG 1038

QY 21 GlyLysAspArgThrtyrArgLeuGlyAlaylaspasPheMetCduIteLysSerHis 40
Db 1039 CAGAGGCACAGCACMACCGCCGCGGCCAGCATCTCTTGGAATTAGMGATCAT 1098

QY 41 ValPhePheSerLeuIleasantPasapleuIleasnlyslsylethrProPhe 60
Db 1099 GTCTTTCTCTTAATCACTGGGTGATCTCATATAAGAAGATTACTCCCCCTTT 1158

QY 61 AspProtsValserGlyProsnogluLeuarshisPheaspProclophehrLeu 80
Db 1159 ACACCAATGTGAAGGGCCCAACAGCACTTCAGCCGAGTTTACCGAAGAG 1218

LOCUS h.sapiens mRNA 2370 bp mRNA linear PRI 16-MAY-1997

ACCESSION Y10032.1 GI:1834510

KEYWORDS serine/threonine protein kinase; spt gene.

ORGANISM Homo sapiens (human).

Bukariyola; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE Waldegger, S., Barth, P., Rober, G. and Lang, F.
Cloning and characterization of a putative human serine/threonine protein kinase transcriptionally modified during antiseptic and isocaine alterations of cell volume
J Biol Chem, 268(1), Acad. Sci. U.S.A. 94 (9), 4440-4445 (1997)

JOURNAL J972242

MEDLINE 9114008

PUBLISHED 2 (bases 1 to 2370)

REFERENCES Waldegger, S.
University of Tuebingen,
Physiology I, Gmelinstr. 5, D-72076 Tuebingen, FRG

AUTHORS TITLE Location/Qualifiers

JOURNAL "Homo sapiens"

FEATURES source /organism="Homo sapiens"
mol_type="mRNA"
db_xref="taxon:9606"
gene name="sgk"
cds 43..1138
ORIGIN 636 a 517 c 513 g 704 t

Alignment Scores:
Pred. No.: Length: 2370
Score: 215
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 0
Mismatches: 0
Indels: 0
Gaps: 0

US-10-000-039A-2_COPY_313_431 (1-119) x HSNWSTPK (1-2370)

QY 1 ProctuleinLeuysProasniethrAnserAlarqshileuLeuglyLeuLeu 20
Db CTCTCCAGCGTGGNCAATTCGAGCAGACTCTCGAGGCCCTCG 1038

QY 21 GlyLysAspArgThrtyrArgLeuGlyAlaylaspasPheMetCduIteLysSerHis 40
Db 1039 CAGAGGCACAGCACMACCGCCGCGGCCAGCATCTCTTGGAATTAGMGATCAT 1098

QY 41 ValPhePheSerLeuIleasantPasapleuIleasnlyslsylethrProPhe 60
Db 1099 GTCTTTCTCTTAATCACTGGGTGATCTCATATAAGAAGATTACTCCCCCTTT 1158

QY 61 AspProtsValserGlyProsnogluLeuarshisPheaspProclophehrLeu 80
Db 1159 ACACCAATGTGAAGGGCCCAACAGCACTTCAGCCGAGTTTACCGAAGAG 1218

LOCUS h.sapiens mRNA 2370 bp mRNA linear PRI 16-MAY-1997

ACCESSION Y10032.1 GI:1834510

KEYWORDS serine/threonine protein kinase; spt gene.

ORGANISM Homo sapiens (human).

Bukariyola; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE Waldegger, S., Barth, P., Rober, G. and Lang, F.
Cloning and characterization of a putative human serine/threonine protein kinase transcriptionally modified during antiseptic and isocaine alterations of cell volume
J Biol Chem, 268(1), Acad. Sci. U.S.A. 94 (9), 4440-4445 (1997)

JOURNAL J972242

MEDLINE 9114008

PUBLISHED 2 (bases 1 to 2370)

REFERENCES Waldegger, S.
University of Tuebingen,
Physiology I, Gmelinstr. 5, D-72076 Tuebingen, FRG

AUTHORS TITLE Location/Qualifiers

JOURNAL "Homo sapiens"

FEATURES source /organism="Homo sapiens"
mol_type="mRNA"
db_xref="taxon:9606"
gene name="sgk"
cds 43..1138
ORIGIN 636 a 517 c 513 g 704 t

Alignment Scores:
Pred. No.: Length: 2370
Score: 215
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 0
Mismatches: 0
Indels: 0
Gaps: 0

US-10-000-039A-2_COPY_313_431 (1-119) x HSNWSTPK (1-2370)

QY 1 ProctuleinLeuysProasniethrAnserAlarqshileuLeuglyLeuLeu 20
Db CTCTCCAGCGTGGNCAATTCGAGCAGACTCTCGAGGCCCTCG 1038

QY 21 GlyLysAspArgThrtyrArgLeuGlyAlaylaspasPheMetCduIteLysSerHis 40
Db 1039 CAGAGGCACAGCACMACCGCCGCGGCCAGCATCTCTTGGAATTAGMGATCAT 1098

QY 41 ValPhePheSerLeuIleasantPasapleuIleasnlyslsylethrProPhe 60
Db 1099 GTCTTTCTCTTAATCACTGGGTGATCTCATATAAGAAGATTACTCCCCCTTT 1158

QY 61 AspProtsValserGlyProsnogluLeuarshisPheaspProclophehrLeu 80
Db 1159 ACACCAATGTGAAGGGCCCAACAGCACTTCAGCCGAGTTTACCGAAGAG 1218

LOCUS h.sapiens mRNA 2370 bp mRNA linear PRI 16-MAY-1997

ACCESSION Y10032.1 GI:1834510

KEYWORDS serine/threonine protein kinase; spt gene.

ORGANISM Homo sapiens (human).

Bukariyola; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE Waldegger, S., Barth, P., Rober, G. and Lang, F.
Cloning and characterization of a putative human serine/threonine protein kinase transcriptionally modified during antiseptic and isocaine alterations of cell volume
J Biol Chem, 268(1), Acad. Sci. U.S.A. 94 (9), 4440-4445 (1997)

JOURNAL J972242

MEDLINE 9114008

PUBLISHED 2 (bases 1 to 2370)

REFERENCES Waldegger, S.
University of Tuebingen,
Physiology I, Gmelinstr. 5, D-72076 Tuebingen, FRG

AUTHORS TITLE Location/Qualifiers

JOURNAL "Homo sapiens"

FEATURES source /organism="Homo sapiens"
mol_type="mRNA"
db_xref="taxon:9606"
gene name="sgk"
cds 43..1138
ORIGIN 636 a 517 c 513 g 704 t

Alignment Scores:
Pred. No.: Length: 2370
Score: 215
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 0
Mismatches: 0
Indels: 0
Gaps: 0

US-10-000-039A-2_COPY_313_431 (1-1

[illegible]


```

Oy 41 ValPheSerLeuIleasn7rAspAspLeuIleAnlysIstlerProProPhe 60
Db 1066 GTCCTCTCTCTTAACTATGAGTGAAGTCTATGATAGAAAGATTAACGCTCTTTT 1125
Oy 61 AspProAsnValSerGlyProAsnGluLeuArgHisPheAspProGluPheThrGluGlu 80
Db 1126 AACCCAAATGTAGTGGTGGCCAGACACTACGCACTTTGACCCCGAGTTTACCGAAG 1185
Oy 81 ProValProAsnSerIleGlySerProAspSerValLeuValThrAlaSerValGly 100
Db 1186 CTTGCTCCGCACTCCATCTGCAAGTCCCTCCACAGCGCTCTCTCCACAGCGCTCAAG 1245
Oy 101 GluAlaAlaGluAlaPheGluGlyPheSerTyAlaProProThrAspSerPheLeu 119
Db 1246 GAGCTGCCGAGGCTTTCTAGGCTTTTCTGATATGGCTCCGACGAGACTCTTCTC 1302

RESULT 13
AX553549
LOCUS AX553549 2354 bp DNA linear PAT 27-NOV-2002
DEFINITION Sequence 1 from Patent WO2074987.
VERSION AX553549.1 GI:25897549
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1
Lang, F., Busjahn, A. and Luft, F.C.
Homo sapiens: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
AUTHORS
Lang, Florian (OE)
LOCATION/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/notes="unnamed protein product"
/feature_id="CD048123.1"
/translation="MTYKDAAGLTVSBMGQVAILIAFKPKNRINLPDIOKIAN
NSYKAGVQSGLKTOPPEPLNANNRSPPSQOIKNSPNHPKPSDFHLK
VTGSGSPFVKLARKAEVYAVKVLQKALIKKREKHSRWLVKYNKHPFLV
GLKSPFVKLARKAEVYAVKVLQKALIKKREKHSRWLVKYNKHPFLV
GLKSPFVKLARKAEVYAVKVLQKALIKKREKHSRWLVKYNKHPFLV
DVTMKGALVEMALVGLPPYSRINMDILINKITPPFNVSQNDLRHDFPFEZ
DVTMKGALVEMALVGLPPYSRINMDILINKITPPFNVSQNDLRHDFPFEZ
DVTMKGALVEMALVGLPPYSRINMDILINKITPPFNVSQNDLRHDFPFEZ
DVTMKGALVEMALVGLPPYSRINMDILINKITPPFNVSQNDLRHDFPFEZ"
variation
/notes="1. SNP (C in T), stumme Mutation, d.h. beide
Versionen des SNPs resultieren in der AMINO ACID Asp in
der AMINO ACID-Position 240"
BASE COUNT 613 a 518 c 513 g 710 t
ORIGIN
Alignment Scores:
Pred. No.: 8,91e-65 Length: 2354
Percent Similarity: 100.00% Conservative: 1
Mismatch: 0
Query Match: 99.52%
DB: 6 Gaps: 0

US-10-000-039a-2_COPY_313_431 (1-119) x AX553549 (1-2354)
Oy 1 ProLeuGluLeuAspGluLeuIleThrAsnSerAlaArgHisPheThrGluGlu 20
Db 979 CTTCTCCAGTCAACCAAAATATGATTAACAAATTCGACAGACCTCTCGAGGCTCTG 1038
Oy 21 GlnIleAspArgThrIlyArgLeuGluAlaIlyAlaIlyAspPheMetGluIleIlySerHis 40

```

```

Db 1039 GAGAGGACGACAAACCGCTCGGGCGGAGGATGATCTATGGAGATTAACGATCAT 1098
Oy 41 ValPheSerLeuIleasn7rAspAspLeuIleAnlysIstlerProProPhe 60
Db 1099 GTCCTCTCTCTTAACTATGAGTGAAGTCTATGATAGAAAGATTAACGCTCTTTT 1158
Oy 61 AspProAsnValSerGlyProAsnGluLeuArgHisPheAspProGluPheThrGluGlu 80
Db 1159 AACCCAAATGTAGTGGTGGCCAGACACTACGCACTTTGACCCCGAGTTTACCGAAG 1218
Oy 81 ProValProAsnSerIleGlySerProAspSerValLeuValThrAlaSerValGly 100
Db 1219 CTTGCTCCGCACTCCATCTGCAAGTCCCTCCACAGCGCTCTCTCCACAGCGCTCAAG 1278
Oy 101 GluAlaAlaGluAlaPheGluGlyPheSerTyAlaProProThrAspSerPheLeu 119
Db 1279 GAGCTGCCGAGGCTTTCTAGGCTTTTCTGATATGGCTCCGACGAGACTCTTCTC 1345

RESULT 14
AX098509
LOCUS AX098509 2364 bp mRNA linear PKI 15-JUN-2002
DEFINITION SERINE/THROMBIN-PROTEIN KINASE SKR (EC 2.7.1.-).
VERSION AX098509.1 GI:21759535
KEYWORDS Oligo capping; fis (full insert sequence).
SOURCE Homo sapiens (human)
ORGANISM Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1
Ishibashi, T., Kanehori, K., Yoshida, M., Matanabe, S., Ishida, S.,
Kato, Y., Hoshino, T., Matsuda, T., Tanabe, T., Tanai, H., Ishida, N.,
Kato, Y., Matanabe, S., Fujino, K., Tanai, H., Ishida, N.,
Yamashita, H., Chiba, Y., Suzuki, Y., Hata, H., Nakagawa, K., Mizuno, S.,
Mortenga, M., Kawamura, M., Sugiyama, T., Irie, R., Otsuki, T., Sato, H.,
Shinikawa, T., Saito, Y., Kawakami, S., Nagai, K., Isopai, T., and
Saito, Y.
NEO human cDNA sequencing project
Unpublished (bases 1 to 2364)
2,364 bp mRNA linear PKI 15-JUN-2002
Direct Submission
Submitted (08-JUL-2002) Sumio Sugano, Institute of Medical Science,
University of Tokyo, Laboratory of Genome Structure, Human Genome
Center, 4-6-1 Honcho, Komaba, Tokyo 153-8502, Japan
(E-mail: cdna@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
Fax:81-3-5449-5416)
COMMENT
NEO human cDNA sequencing project supported by Ministry of
Economic Trade and Industry, Japan.
Research Center for Biotechnology (RAB) cDNA library
construction and 5'-end one pass sequencing: Institute of Medical
Science, University of Tokyo, Laboratory of Genome Structure, Human
Genome Center; 3'-end one pass sequencing: RAB, clone selection for
full annotation/Qualifiers
1. 2364
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="STM07148"
/tissue_type="stomach mucosa"
/clone_11b="STM"
/annotation_vector: pHEBSFL3*
BASE COUNT 615 a 524 c 517 g 708 t
ORIGIN
Alignment Scores:
Pred. No.: 8.96e-65 Length: 2364
Percent Similarity: 621.00% Matches: 118
Conservative: 1
Mismatch: 0
Query Match: 100.00%
DB: 99.16% Mismatches: 1
Best Local Similarity: 99.16%

```

Query Match: 99.52% Idents: 0
 Un: 9 Gaps: 0

US-10-000-039a-2_COPY_313_431 (1-119) x AK098509 (1-2364)

Qy 1 ProLeuGluInLysProAnGluThrAnSerAlaArgGluLeuGluGlyLeuLeu 20
 Db 994 COTCTCCACGTGAACCAAAATATACAAATTCGACAGACACCTCTGGAGGCTCTG 1053

Qy 21 GlnLysAspAgThrLysArgLeuGluYAlaLysAspPheMetGluLysSerHis 40
 Db 1054 CAGAGACAGACGACAAAGCGGCTCGGGCCGACAGATGACTTCATGGAGATTAGAGCTCAT 1113

Qy 41 ValPheSerSerLeuGluLysThrProAspSerValLeuValThrAlaSerValProPhe 60
 Db 1114 GTCCTCTCTCTTAATTAAGTGGATGATCTCATTAATTAAGAAGTACTCCCTCTTT 1173

Qy 61 AsnProAsnValSerGluProAsnGluLeuArgHisPheAspProGluLysGluGlu 80
 Db 1174 AACCCAAATGTAGTGGCCCAAGCGACTACAGCGACTTGTACCCGAGATTACCGAAGG 1233

Qy 81 ProValProAsnSerLeuGluLysThrProAspSerValLeuValThrAlaSerValPro 100
 Db 1234 CTTCTGCCCACTCATTTGGCAAGTCCCTTGACAGCGCTCTGCTGACAGCAGGCTCAAG 1293

Qy 101 GluAlaGluAlaGluPheGluPheSerValThrLeuProGluPheAspSerPheLeu 119
 Db 1294 GAAGCTGCGAGGCTTTCTTAGGCTTTCTGATGCGCTGCCAGGACTCTCTCTC 1350

RESULT 15
 CDS 95609
 LOCUS 2382 bp mRNA linear PRI 28-JUN-1999
 DEFINITION Homo sapiens serine/threonine protein kinase sgk mRNA, complete
 CDS 51609
 ACCESSION AF153609.1 GI:5231142
 VERSION AF153609.1
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 1 (bases 1 to 2382) Seo J.M., Lee H.M., Chung H.J., Sohn M.Y.,
 Wang S.Y., Kim S.U., Jung E.J. and Kim J.C.
 TITLE A catalogue of genes in the human dermal papilla cells as
 identified by expressed sequence tags
 JOURNAL Exp Biol Med 238:1-10 (2003)
 REFERENCE
 AUTHORS Kim M.K., Kim Y.H., Suh J.M., Lee H.M., Chung H.J., Sohn M.Y.,
 Wang S.Y., Im S.U., Jung E.J. and Kim J.C.
 TITLE Direct Substrates of the Serine/Threonine Kinase SGK
 JOURNAL School of Medicine, 101 Dongin Dong, Kyungpook National University,
 School of Medicine, 101 Dongin Dong, Kyung Gu, Taegu 700-422,
 South Korea

FEATURES
 source Location/Qualifiers
 1..2382
 /codon_start=1
 /product=serine/threonine protein kinase sgk*
 /protein_id=AK091.1
 /db_xref="taxon:9606"
 /db_xref="GeneID:5231143"
 /db_xref="GI:5231143"
 /translation="MVTVEAKGTLTYSRHWAILAFKMRKGLAMDFQKIAN
 NSTACIKPEVDSILKISQPEPELMANPPSPSQIINAGSSNMRKPSRFLK
 GFLSTCAKLYLPIVDYINGEYFYLORKEFLRPFAYAEIASALGYLHSIANI
 VYDLAPENLIDSQHIVLDTGKLECNIEHNSITSTCTCPYLAPEYLRKPYDOR
 TVDMKIGAVILEYKMGAPPPYSRNTAYEMDINLMPDLQKNITNSARHLLEKOLLQ
 DTKLGLGARDUPPELASHWFTSLINWDLINKLITPPFNPNVSGPNDIARFDPEETEE

Alignment Scores:
 Pred. No.: 9,04e-65 Length: 2382
 Score: 621.00 Matches: 118
 Percent Similarity: 99.16% Mismatches: 0
 Query Match: 99.52% Indels: 0
 Db: 9 Gaps: 0

US-10-000-039a-2_COPY_313_431 (1-119) x AF153609 (1-2382)

Qy 1 ProLeuGluInLysProAnGluThrAnSerAlaArgGluLeuGluGlyLeuLeu 20
 Db 979 COTCTCCACGTGAACCAAAATATACAAATTCGACAGACACCTCTGGAGGCTCTG 1038

Qy 21 GlnLysAspAgThrLysArgLeuGluYAlaLysAspPheMetGluLysSerHis 40
 Db 1039 CAGAGACAGACGACAAAGCGGCTCGGGCCGACAGATGACTTCATGGAGATTAGAGCTCAT 1098

Qy 41 ValPheSerSerLeuGluLysThrProAspSerValLeuValThrAlaSerValProPhe 60
 Db 1099 GTCCTCTCTCTTAATTAAGTGGATGATCTCATTAATTAAGAAGTACTCCCTCTTT 1158

Qy 61 AsnProAsnValSerGluProAsnGluLeuArgHisPheAspProGluLysGluGlu 80
 Db 1159 AACCCAAATGTAGTGGCCCAAGCGACTACAGCGACTTGTACCCGAGATTACCGAAGG 1218

Qy 81 ProValProAsnSerLeuGluLysThrProAspSerValLeuValThrAlaSerValPro 100
 Db 1219 COTGTCGCCCACTCATTTGGCAAGTCCCTTGACAGCGCTCTGCTGACAGCAGGCTCAAG 1278

Qy 101 GluAlaGluAlaGluPheGluPheSerValThrLeuProGluPheAspSerPheLeu 119
 Db 1279 GAAGCTGCGAGGCTTTCTTAGGCTTTCTGATGCGCTGCCAGGACTCTCTCTC 1335

Search completed: August 11, 2003, 10:05:01
 Job time : 3340 secs

Percent Similarity: 98.08%
Best Local Similarity: 75.97%
Query Match: 25
Dbs: 1

Conservative: 7
Indels: 1
Gaps: 0

US-10-000-039a-2_COPY_313_431 (1-119) x AH95953 (1-433)

QY 17 GDIUYLEUENLINSYSPARGTHLYSARGLEUQIYALYSASPHEMETGLU 36
DB 13 GAGGCTCTCTCGAGAGACGACAGAGAGGCTGGCTCCGAGACTCTTTGAGG 72
QY 37 ILYASYSRHALVPEHPESERLEULEASNTIRASPASPENLEASLYSYSTLE 56
DB 73 ATTAGAGATGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 132
QY 57 THYPROTPHEASNTVALSERGLYPROASNDLEUAGHISPHASPPROGLU 76
DB 133 ACTGCT 192
QY 77 PHEHTIGLUUPEVALPROANSERLEUYSYSPRASPERSERVALEUVALTHR 96
DB 193 THGTGAGAGAGGCT 252
QY 0Y 4LSALSERVALYSGLICUALALPEHLEUGLYSPESERTYALAPRO-PROTHAS 116
DB 253 GCGAGCT 312
QY 116 PSEPHLEU 119
DB 313 CT 322

RESULT 15

AH95953

XX AH95953 standard; CONA; 1333 BP.

AC AH95953;

XX 16-OCT-2001 (first entry)

XX Human protein encoding cDNA sequence SEQ ID NO:370.

DE
XX Human cancer virus; HIV infection; Human immunodeficiency virus;
XX anti-inflammatory; antirheumatic; antiarthritic; immunosuppressive;
KW anti-HIV; fungicide; antimetagen; cardiant; central nervous system; virocidic;
KW neuroprotective; antidiabetic; antitumor; antineoplastic; antineoplastic;
KW neuroprotective; antidiabetic; antitumor; antineoplastic; antineoplastic;
KW immunostimulant; gene therapy; antitumor; antineoplastic; antineoplastic;
KW cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;
KW genetic disease; haematopoietic disorder; platelet disorder; asthma;
KW thrombocytopenia; osteoporosis; severe combined immunodeficiency;
KW Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;
KW neurological disorder; ss.

XX Homo sapiens.

XX W0200153455-A2.

XX 26-JUN-2001.

XX 22-DEC-2000; 2000W0-US35017.

XX 23-DEC-1999; 99US-0471275.

XX 21-JAN-2000; 2000US-0488725.

XX 25-APR-2000; 2000US-0552317.

XX (HISB-) HISBQ INC.

XX Tang YT, Liu C, Dmanac RT;

XX

DR

PF 2001-457607/49.

XX P-508; AH95953.

PT Isolated human polynucleotides encoding polypeptides, useful for the
PF treatment and diagnosis of e.g. cancer, ulcers and HIV infection.

PS Claim 1; Page 474; 1217pp; English.

XX AH95953 encode the human proteins given in AH95953 to
CC cells they are expressed in, such as: anti-inflammatory; antineoplastic;
CC antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant;
CC central nervous system; virocidic; anti-HIV; fungicide; antimetagen;
CC antitumor; osteoporosis; severe combined immunodeficiency;
CC Alzheimer's disease; Parkinson's disease; neurodegenerative and
CC neurologic disorder.

XX Sequence 1333 BP; 315 A; 383 C; 349 G; 286 T; 0 other;

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

/mol-type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:593863"
/feature="normal endometrium, mid-secretory phase,
cycle day 23"
/lab_host="DH10B (T1-resistant)"
/note="Organ: uterus; Vector: pcWV-SKORT6.1.cdb (Rescan,
Invitrogen Corporation); Site: 1: NotI; Site 2: EcoRV;
Cloned unidirectionally from microquantity amounts of mRNA
from the endometrium of a woman (100 ng total RNA, cycle
day 23). Average insert size 1.6 kb, library constructed
by Rescan (Invitrogen Corporation)."

BASE COUNT 153 a 167 c 169 t
ORIGIN
Alignment Scores:
Pred. No.: 1,346-65
Score: 621.00
Percent Similarity: 100.00%
Best Local Similarity: 99.52%
Query Match: 99.52%
Mismatches: 0
Indels: 0
Gaps: 0

US-10-000-039a-2_COPY_313_431 (1-119) x CB216592 (1-630)

QY 1 ProLeuGLuLeuLysProHnIeThrAnSerAlaArgHISLeuLeuLeu 20
DB 93 CDTCTCCCTCGTGAACCAATATTACAAATTCGACAGACACTCTGGAGCGCTCTG 152
QY 21 GlnLysAspArgThrValGLeuGLuValAlaLysAspAspPheMetCtLueLysSerHis 40
DB 153 CNGAGAGCGCGAGCAAGCGCTCGGCCCAAGGTGACTTCATCGAGATTAGAGTCAT 212
QY 41 ValPhePheSerLeuLeuAsnTPasAspLeuLeuLysLysLysIleThrProProPhe 60
DB 213 GTCCTCTCTCTCTATTACTGGGATGATCTCATTAAGAAGATTACTCCCTCTT 272
QY 61 AnpProAsnValSerGlyProAsnGluLeuValGHisPheAspProGluPheHrGLu 80
DB 273 ACCCAATATGTGATGGGCCGACGACCTGACGCTGACCTGACCTGACCTGACCTGAC 332
QY 81 ProvalProHnSerLleClyLysSerProAspSerValLeuValThAlaSerValLys 100
DB 333 CCGTCCGCTCCCACTGTGAGCATCTCTGACAGCTCTCTGACAGCTCTCTGACAG 392
QY 101 GlnAlaAlaGluAlaPheLeuGLuPheSerTyTAlaProThrAspSerPheLeu 119
DB 393 GAGCTGCGCGAGGACTTCTTGAGCTTTCTTGAGCTTTCTTGAGCTTTCTTGAGCT 449

RESULT 5
BG770190 571 bp mRNA linear EST 15-MAY-2001
DEFINITION 60274454FL NIH_MSC_49 Homo sapiens cDNA clone IMAGE:487085 5',
mRNA sequence.

ACCESSION BG770190
VERSION BG770190.1
KEYWORDS G1:14080843
SOURCE Homo sapiens
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 671)
NIH-MSC http://mhc.nci.nih.gov/
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS 1 (bases 1 to 671)
KEYWORDS Mammalian Gene Collection (MGC)
COMMENT Unpublished
Contact: Robert Strausberg, Ph.D.
Email: rgs@femail.nih.gov
NIH-MSC Genome Center, Bethesda, MD 20892
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMU)
DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LMU at:
http://image.llnl.gov k. cgm: 14
High quality sequence stop: 669.

FEATURES
source Location/Qualifiers
1..671
locus_tag="Homo sapiens"
mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:593863"
/feature="normal endometrium, mid-secretory phase,
cycle day 23"
/lab_host="DH10B (T1-resistant)"
/note="Organ: uterus; Vector: pcWV-SKORT6.1.cdb (Rescan,
Invitrogen Corporation); Site: 1: NotI; Site 2: EcoRV;
Cloned unidirectionally from microquantity amounts of mRNA
from the endometrium of a woman (100 ng total RNA, cycle
day 23). Average insert size 1.6 kb, library constructed
by Rescan (Invitrogen Corporation)."

BASE COUNT 160 a 171 c 152 g 188 t
ORIGIN
Alignment Scores:
Pred. No.: 1,456-65
Score: 621.00
Percent Similarity: 100.00%
Best Local Similarity: 99.52%
Query Match: 99.52%
Mismatches: 0
Indels: 0
Gaps: 0

US-10-000-039a-2_COPY_313_431 (1-119) x BG770190 (1-671)

QY 1 ProLeuGLuLeuLysProHnIeThrAnSerAlaArgHISLeuLeuLeu 20
DB 102 CDTCTCCCTCGTGAACCAATATTACAAATTCGACAGACACTCTGGAGCGCTCTG 161
QY 21 GlnLysAspArgThrValGLeuGLuValAlaLysAspAspPheMetCtLueLysSerHis 40
DB 152 CNGAGAGCGCGAGCAAGCGCTCGGCCCAAGGTGACTTCATCGAGATTAGAGTCAT 221
QY 41 ValPhePheSerLeuLeuAsnTPasAspLeuLeuLysLysLysIleThrProProPhe 60
DB 222 GTCCTCTCTCTCTATTACTGGGATGATCTCATTAAGAAGATTACTCCCTCTT 281
QY 61 AnpProAsnValSerGlyProAsnGluLeuValGHisPheAspProGluPheHrGLu 80
DB 282 ACCCAATATGTGATGGGCCGACGACCTGACGCTGACCTGACCTGACCTGACCTG 341
QY 81 ProvalProHnSerLleClyLysSerProAspSerValLeuValThAlaSerValLys 100
DB 342 CDTCTCCCTCGTGAACCAATATTACAAATTCGACAGACACTCTGGAGCGCTCTG 401
QY 101 GlnAlaAlaGluAlaPheLeuGLuPheSerTyTAlaProThrAspSerPheLeu 119
DB 402 GAGCTGCGCGAGGACTTCTTGAGCTTTCTTGAGCTTTCTTGAGCTTTCTTGAGCT 158

RESULT 6
BG778994 721 bp mRNA linear EST 15-MAY-2001
DEFINITION 60266150FL NIH_MSC_60 Homo sapiens cDNA clone IMAGE:480574 5',
mRNA sequence.

ACCESSION BG778994
VERSION BG778994.1
KEYWORDS G1:14049311
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 721)
NIH-MSC http://mhc.nci.nih.gov/
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS 1 (bases 1 to 721)
KEYWORDS Mammalian Gene Collection (MGC)
COMMENT Unpublished
Contact: Robert Strausberg, Ph.D.
Email: rgs@femail.nih.gov
NIH-MSC Genome Center, Bethesda, MD 20892
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMU)
DNA Sequencing by: Incyte Genomics, Inc.

81 Proctolobus... 100
 481 C... 540
 101 Glial... 119
 541 GAGCTCG... 597

RESULT 8
 B0212589 767594.0 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6052827
 5', mRNA sequence.

ACCESSION
 B0212589
 VERSION
 B0212589.1
 SOURCE
 Homo sapiens (human)

ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata, Vertebrata; Euteleostomi;
 Mammalia; Primates; Catarrhini, Nonhuman; Homo.

REFERENCE
 NIH-MGC <http://mml.nhl.gov/>,
 (bases 1 to 847)

AUTHORS
 Unpublished

JOURNAL
 COMMENT
 Contact: Robert Strausberg, Ph.D.
 Email: caspe@remail.nih.gov
 CDNA Library Prepared by: The I.M.A.G.E. Consortium (LML)
 cDNA sequence by the I.M.A.G.E. Consortium
 Cloned into the pMDC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LML at:
<http://image.llnl.gov> n. column: 20
 High quality sequence stop: 636
 Location/Qualifiers

FEATURES
 source

61 Anp... 80
 444 AACCA... 509
 81 Proctolobus... 509
 504 C... 564
 101 Glial... 119
 564 GAGCTCG... 620

RESULT 9
 B0680126 816937 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6263586
 5', mRNA sequence.

ACCESSION
 B0680126
 VERSION
 B0680126.1
 SOURCE
 Homo sapiens (human)

ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata, Vertebrata; Euteleostomi;
 Mammalia; Primates; Catarrhini, Nonhuman; Homo.

REFERENCE
 NIH-MGC <http://mml.nhl.gov/>,
 (bases 1 to 855)

AUTHORS
 Unpublished

JOURNAL
 COMMENT
 Contact: Robert Strausberg, Ph.D.
 Email: caspe@remail.nih.gov
 CDNA Library Prepared by: The I.M.A.G.E. Consortium (LML)
 cDNA sequence by the I.M.A.G.E. Consortium
 Cloned into the pMDC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LML at:
<http://image.llnl.gov> l. column: 19
 High quality sequence stop: 718
 Location/Qualifiers

FEATURES
 source

BASE COUNT
 ORIGIN

Alignment Scores:
 Pred. No.: 847
 Score: 621.00
 Percent Similarity: 100.00
 Query Match: 0
 DB: 0

US-10-000-039a-2_COPY_313_431 (1-119) x B0212589 (1-847)

Qy 1 Proctolobus... 20
 Db 264 C... 323
 Qy 21 Glial... 40
 Db 324 GAGCTCG... 383
 Qy 41 Val... 60
 Db 384 C... 413

BASE COUNT
 ORIGIN

Alignment Scores:
 Pred. No.: 859
 Score: 621.00
 Percent Similarity: 100.00
 Query Match: 0
 DB: 0

US-10-000-039a-2_COPY_313_431 (1-119) x B0680126 (1-855)

Qy 1 Proctolobus... 20
 Db 95 C... 154

REFERENCE 1. (bases 1 to 933)
 TITLE: Human cDNA library: NIH.gov/
 JOURNAL: National Institutes of Health, Mammalian Gene Collection (MGC)
 COMMENT: Unpublished
 Contact: Robert Strausberg, Ph.D.
 Email: rstraus@nih.gov
 Tissue Procurement: David N. Louis, M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 Comments: This MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: 4810890
 High quality: 1
 Location/Qualifiers
 FEATURES
 Source
 1..933
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4944552"
 /tissue_type="anaplastic oligodendroglioma with lp/19q
 /lab_host="DM10B (71 phage-resistant)"
 /clone_lib="NCI_CGAP_Bn67"
 Notes: Organ: Brain; Vector: pCMV-SPORT6; Site: 1; Note:
 Constructed by Life Technologies. Note: this is a NCI_CGAP Library.
 Average insert size 2.3 kb. Constructed by Life
 Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT 226 a 250 c 215 g 242 t
 ORIGIN
 Alignment Scores:
 Pred. No.: 215 c5
 Length: 933
 Mismatches: 113
 Percent Similarity: 100.00%
 Conservative: 1
 Best Local Similarity: 99.16%
 Query Match: 99.52%
 Mismatches: 0
 Indels: 0
 Gaps: 12

US-10-000-039A-2_COPY_313_431 (1-119) x BG911625 (1-933)
 Oy 1 pccacgclenclvypcbsenllhrbsenrlakrslslslencluclydenlen 20
 Db 204 cctctccacgtgaacacaaattatgacaaattccgcacagacacctctcgaggccctctg 263
 Oy 21 clatvcsescthrvskleuclylatvcsesgsheseculicvcsellu 40
 Db 264 cagagacacagacacacgctccggccacagatgactctatggatgattagagctat 323
 Oy 41 valpesherserlileasrhrpeshesrlllesstusvsllethrprpeshes 60
 Db 324 gtct 383
 Oy 61 aenprcsesvalserclvpcbsenclucenarhlshesepcccluphrshclucly 80
 Db 384 aaccacaaatgagtgccgccacagaccttgaccgccacttgaccgccagag 443
 Oy 83 pccalprbsenrlledvysersprbsenrlleulsheserlsheserlsheserlshes 100
 Db 444 cctctccac 503
 Oy 101 clalshlshlshlshlshlshlshlshlshlshlshlshlshlshlshlshlshlshlsh 119
 Db 504 gacgtccgcagagccttct 560

Search completed: August 11, 2003, 11:27:43
 Job time : 3829.23 secs

1

1

```

SEQUENCE CHARACTERISTICS:
LENGTH: 2370 base pairs
TYPE: nucleic acid
STANDARDS: single
STRANDS: 1 strand
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
ORIGIN: 43...1335
US-09-031-235-1

Alignment Scores:
Score: 7416-74
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Mismatches: 0
Gaps: 0
DB:

US-10-000-039a-2_COPY_313_431 (1-119) x US-09-031-235-1 (1-2370)
Qy 1 ProLeuGlnLeuLeuProAsnGluLeuThrAsnSerAlaGHisLeuLeuGluGlyLeuLeu 20
Db 979 CCGTCCGCTGAGAACCAATATATGAAATTCGCGAGACACCTCTCGAGGCGCTCGT 1038
Qy 21 GlnGlyAspArgThrGlyArgLeuGlyAlaGlyAspAspPheMetGluLeuLeuSerHis 40
Db 1039 CNGAGAGACGACGACAGGCGCTGGGCGCAGGATGATGATCTGAGCATTAAGATCAT 1098
Qy 41 ValPhePheSerLeuLeuAsnGlyPheAspLeuLeuLeuGlyLeuThrProPhe 60
Db 1099 GTCTCTCTCTCTCTTAATTAATGCGGATGATCTCATTAAGAGATTAATCTCCCTTT 1158
Qy 61 AsnProAsnValSerGlyProAsnGluLeuArgHisPheAspProGluPheThrGluGlu 80
Db 1159 AACCAAAATGTGGTGCGGCGCAGGAGCTAGGCACTTTGACCGCGATTTACGAGAG 1218
Qy 81 AsnProAsnValSerGlyProAsnGluLeuArgHisPheAspProGluPheThrGluGlu 100
Db 1219 CCGTCCGCTGAGAACCAATATATGAAATTCGCGAGACACCTCTCGAGGCGCTCGT 1278
Qy 101 GluAlaAlaGluAlaPheLeuGlyPheSerTyrAlaProPheThrAspSerPheLeu 119
Db 1279 GAGCTCGCGAGGCTTTCTTAGGCTTTTCTATGCGGCTCCGACGACTCTTCTCTC 1335

RESULT 2
US-08-712-709-6
Sequence 6, Application US/08712709
PATENT NUMBER: US 5853782
GENERAL INFORMATION:
APPLICANT: Au-Young, Janice
APPLICANT: Guegler, Karl J.
APPLICANT INVENTORS: Guegler, Karl J. & Au-Young, Janice
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Inocyte Pharmaceuticals, Inc.
STREET: 3174 Foster Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/712-709
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749

SEQUENCE CHARACTERISTICS:
LENGTH: 2370 base pairs
TYPE: nucleic acid
STANDARDS: single
STRANDS: 1 strand
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
ORIGIN: 43...1335
US-09-031-235-1

Alignment Scores:
Score: 7416-74
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Mismatches: 0
Gaps: 0
DB:

US-10-000-039a-2_COPY_313_431 (1-119) x US-08-712-709-6 (1-2370)
Qy 1 ProLeuGlnLeuLeuProAsnGluLeuThrAsnSerAlaGHisLeuLeuGluGlyLeuLeu 20
Db 945 CCGTCCGCTGAGAACCAATATATGAAATTCGCGAGACACCTCTCGAGGCGCTCGT 1005
Qy 21 GlnGlyAspArgThrGlyArgLeuGlyAlaGlyAspAspPheMetGluLeuLeuSerHis 40
Db 1006 CAGAGAGACGACGACGCGCTGGGCGCAGGATGATGATCTGAGCATTAAGATCAT 1065
Qy 41 ValPhePheSerLeuLeuAsnGlyPheAspLeuLeuLeuGlyLeuThrProPhe 60
Db 1066 GTCTCTCTCTCTCTTAATTAATGCGGATGATCTCATTAAGAGATTAATCTCCCTTT 1125
Qy 61 AsnProAsnValSerGlyProAsnGluLeuArgHisPheAspProGluPheThrGluGlu 80
Db 1126 AACCAAAATGTGGTGCGGCGCAGGAGCTAGGCACTTTGACCGCGATTTACGAGAG 1185
Qy 81 ProValProAsnValSerGlyProAsnGluLeuArgHisPheAspProGluPheThrGluGlu 100
Db 1186 CCGTCCGCTGAGAACCAATATATGAAATTCGCGAGACACCTCTCGAGGCGCTCGT 1245
Qy 101 GluAlaAlaGluAlaPheLeuGlyPheSerTyrAlaProPheThrAspSerPheLeu 119
Db 1246 GAGCTCGCGAGGCTTTCTTAGGCTTTTCTATGCGGCTCCGACGACTCTTCTCTC 1302

RESULT 3
US-09-111-444-6
Sequence 6, Application US/09111444
PATENT NUMBER: US 6357782
GENERAL INFORMATION:
APPLICANT: Au-Young, Janice
APPLICANT: Guegler, Karl J.
APPLICANT INVENTORS: Guegler, Karl J. & Au-Young, Janice
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Inocyte Pharmaceuticals, Inc.
STREET: 3174 Foster Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/111-444
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749

```



```

1  TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
2  IN HUMAN GENE EXPRESSION
3  NUMBER OF SEQUENCES: 1490
4  CORRESPONDENCE ADDRESS:
5  ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
6  STREET: 317 PORTER DRIVE
7  CITY: PALO ALTO
8  STATE: CALIFORNIA
9  COUNTRY: USA
10  ZIP: 94304
11  COMPUTER READABLE FORM:
12  MEDIUM TYPE: Floppy disk
13  COMPUTER: IBM PC compatible
14  SOFTWARE: IBM PC DOS
15  CURRENT APPLICATION DATA:
16  SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
17  APPLICATION NUMBER: US/09/016,434
18  PRIORITY NUMBER: 09/016,434
19  APPLICATION NUMBER:
20  PRIORITY APPLICATION NUMBER:
21  CLASSIFICATION:
22  ATTORNEY/AGENT INFORMATION:
23  NAME: seller, Karen J. 071
24  REFERENCE/DOCKET NUMBER: 9A-0002 US
25  TELECOMMUNICATION INFORMATION:
26  TELEPHONE: (650) 855-0555
27  INFORMATION FOR SEQ ID NO: 772:
28  SEQUENCE CHARACTERISTICS:
29  LENGTH: 2311 base pairs
30  STRAND: single
31  TYPE: nucleic acid
32  TOPOLOGY: linear
33  IMMEDIATE SOURCE:
34  CLONING VECTORS:
35  LIBRARY: GenBank
36  CLONE: 47243
37  US-09-016-434-772
38
39  Alignment Scores:
40  Score: 1,816-73 Length: 2311
41  Percent Similarity: 621.00 Matches: 118
42  Best Local Similarity: 100.00 Conservative: 1
43  Query Match: 99.16% Mismatches: 0
44  DB: 99.35% Gaps: 0
45  US-09-016-434-772
46
47  US-10-000-039a-2_COPY_313_431 (1-119) x US-09-016-434-772 (1-2311)
48
49  QY 1 ProlaundLeuYsProaSnlelThraSerAlaKrhSlouLeuGluclyLeu 20
50  QY 946 CTTCTCCCTGGAACCAATATACATATCTCCGACACACTCTCGAGAGGCTCTCG 1005
51  QY 22 GlnYsAspGhTrLysAspLeuGlyAlaYsAspPheMetGluLeuYsSerHis 40
52  QY 1006 CAGAGACAGCAGCAACCGCTCGGGCCAGAGGATCTCTGGAATTAAGATCAT 1065
53  QY 41 ValPheSerLeuLeuIleAsnTrpAspLeuLeuLeuYsIleThrProPhe 60
54  QY 1066 GTCCTCTCTCTTATTAATCTAGGATATCATATATAGAGATTAATCTCCCTTTT 1125
55  QY 81 AsnProaSnValSerGlyProaSnlelThraSerAlaKrhSlouLeuGlucly 80
56  QY 1126 AACCAATATGATGGTGGCCACAGCACTAGCAGCTATGACCCAGATTTACGAGAG 1185
57  QY 81 ProValProaSnlelThraSerProaSnlelThraSerValLeuValThAlaSerValYs 100
58  QY 1186 GTGTGCCCACTGACAGCTGACAGCTGACAGCTGACAGCTGACAGCTGACAGCTGAC 1245
59  QY 101 GlnValAlaCkulaPheLeuGlyPheSerValAlaProPheAspPheLeu 119
60  QY 1191 GTCCTCTCTCTTATTAATCTAGGATATCATATATAGAGATTAATCTCCCTTTT

```

```

1  DB 1246 GAGCTGGCGAGCGCTTCTCTAGGCTTCTCTATGCGCTCCCGAGCACTATTCTTC 1302
2  RESULT 6
3  US-08-700-575-4
4  Sequence 4, Application US/08700575
5  TITLE OF INVENTION: NOVEL HUMAN KINASE HOMOLOGS
6  CORRESPONDENCE ADDRESS:
7  ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
8  STREET: 317 PORTER DRIVE
9  CITY: PALO ALTO
10  STATE: CALIFORNIA
11  COUNTRY: USA
12  ZIP: 94304
13  COMPUTER READABLE FORM:
14  MEDIUM TYPE: Floppy disk
15  COMPUTER: IBM PC compatible
16  OPERATING SYSTEM: PC-DOS/MS-DOS
17  SOFTWARE: Patent In Release #1.0, Version #1.30
18  CURRENT APPLICATION DATA:
19  SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
20  CURRENT APPLICATION NUMBER: US/08/700,575
21  PRIORITY NUMBER:
22  FILING DATE:
23  CLASSIFICATION: 435
24  ATTORNEY/AGENT INFORMATION:
25  NAME: seller, Karen J. 071
26  REFERENCE/DOCKET NUMBER: 36749
27  TELECOMMUNICATION INFORMATION:
28  TELEPHONE: (415) 845-4166
29  INFORMATION FOR SEQ ID NO: 4:
30  SEQUENCE CHARACTERISTICS:
31  LENGTH: 257
32  STRAND: single
33  TYPE: nucleic acid
34  TOPOLOGY: linear
35  IMMEDIATE SOURCE:
36  CLONING VECTORS:
37  LIBRARY: TNP-1 Phorbol LPS
38  CLONE: 12702
39  US-08-700-575-4
40
41  Alignment Scores:
42  Score: 9,616-19 Length: 257
43  Percent Similarity: 75.29% Conservative: 3
44  Best Local Similarity: 71.76% Mismatches: 15
45  Query Match: 32.61% Indels: 10
46  DB: 1 Gaps: 4
47  US-10-000-039a-2_COPY_313_431 (1-119) x US-08-700-575-4 (1-257)
48
49  QY 12 AlaKrhSlouLeuGluclyLeuGluclyLeuGluclyLeuGluclyLeuGluclyLeu 31
50  QY 32 GAGAGACACTCTCGAGGGCTCTCTGAG-AGGACAGG---CAAGGGCTGGGCC-AAG 57
51  QY 32 AsnAspPheSerLeuLeuIleAsnTrpAspLeuLeuLeuYsIleThrProPhe 51
52  QY 58 GATGATCTCTGATGAGTATGAGTATGATG-TTCTCTCTCTTATTAATCTAGGATCATC 116
53  QY 57 ThraSerValLeuValThAlaSerValYsIleThrProPheAspPheLeu 71
54  QY 117 ATTAATAGAGATTAATCTCCCTTTTAC-CAATATGATGAGTGGCCGACGCTAC 172
55  QY 72 HisPheProIleThraSerValLeuIleProValProaSnlelThraSerValYs 88
56  QY 173 GGAGTTTGGCGAGTTTACGAGAGC---CTTCCTCCATCATGAGTGGCTCCGAG 229

```

Qy 89 SerProbserv 93
Db 230 GGTCTATACAGTC 244

RESULT 7
US-08-749-902-4
Sequence 4, Application US/08749902
Patent No. 5985635
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Goll, Surya K.
APPLICANT: Hillman, Jennifer L.
APPLICANT: Korman, SERINE/THREONINE
TITLE OF INVENTION: PROTEIN KINASES
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/749,902
PRIORITY DATA:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER:
ATTORNEY AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
TELEPHONE: 415-855-0555
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NOS: 4:
SEQUENCE LENGTH: 1607 base pairs
TYPE: nucleic acid
STANDARDS: single
IMMEDIATE SOURCE:
CLONE: Consensus

US-08-749-902-4 (1-1607)

Alignment Scores:
Pred. No.: Length: 1607
Score: 187.00
Matches: 42
Best Local Similarity: 36.21%
Query Match: 29.97%
Indels: 10
Gaps: 2

US-10-000-039a-2_COPY_313_431 (1-119) x US-08-749-902-4 (1-1607)

Qy 2 LeuGluLeuYsProbsanIerThraSerAlaArgHisLeuLeuGluLeuLeu 21
Db 965 CTGGACATCCCGCTACCTGACATGAGATGCCGAGACCTGTGCAAGATTTCTGANA 1024

Qy 22 LysAspArgThrYsArgLeu---GlyAlaYsAspAspPheMetGluIleYsSerHis 40
Db 1075 CGGATCCGACACGAGATGGGGGAGGCCAGCGGCTCTGCTGTTGTCAGAGACAT 1084

Qy 41 ValPhePheSerIleLeuAnrThraPaspLeuLeuYsLysIleThrProPhe 60
Db 1085 CCTTTTTCGCGACATGATATGAGACGCTTGTGGCTGGCGGTGTGGAGCCGCTTTC 1144

Qy 61 AppProbsanValSerGlyProLeuGluLeuArgGlyHisPheAspProGluPheThrLeuGlu 80
Db 1145 AGGCGCTCTCGATGATGAGAGAGAGGAGCGCTGAGCGGCTTGTGACCGCTCTGACAGGAG 1204

Qy 81 ---ProValProbsanSerIleGlyYsSerProbsanSerValLeuValThrAlaSerVal 99
Db 1205 AGCGCGGTG-----GACAGTCTCTGATGAC-----ACAGGCTCTGAC 1240

Qy 100 LysGluAlaAlaGluPheLeuGlyPheSerThrAlaProPheGlnr 115
Db 1241 GAGATGTCACACAGCGCTTCTGCGCTTCACATGAGTGGCGGCGCTCT 1288

RESULT 8
US-09-016-434-126
Sequence 126, Application US/09016434
Patent No. 6500938
GENERAL INFORMATION:
APPLICANT: Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: FLORPY disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: GENEX 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREWITH
PRIORITY DATA:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
AGENCY INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/POCKET NUMBER: PA-0002 US
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 126:
SEQUENCE LENGTH: 1607 base pairs
TYPE: nucleic acid
STANDARDS: single
IMMEDIATE SOURCE:
LIBRARY: COLNET02
CLONE: 1309709

US-09-016-434-126

Alignment Scores:
Pred. No.: Length: 1607
Score: 287.00
Matches: 42
Best Local Similarity: 36.21%
Query Match: 29.97%
Indels: 10
Gaps: 4

US-10-000-039a-2_COPY_313_431 (1-119) x US-09-016-434-126 (1-1607)

Qy 2 LeuGluLeuYsProbsanIerThraSerAlaArgHisLeuLeuGluLeu 21
Db 965 CTGGACATCCCGCTACCTGACATGAGATGCCGAGACCTGTGCAAGATTTCTGANA 1024

Oy 22 LysAspATgThryArlau---GlyAlaLeuAspAspPheMolGluLeuLysSerHis 40
 Db 1025 GGAATACCGGAGTGGGGTGGCCAGGAGCTCTGCTGATGTGCGAGACAT 1084
 Oy 41 ValPheSerLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 60
 Db 1085 CCGTCTTTTCGGGACATGAATTCGAGACGCTCTGCGCTGGCGTGGAGCCCTTC 1144
 Oy 61 AsnProAsnValSerGlyProMolGluLeuMarLysPheAspProGluPheThrGluGlu 80
 Db 1145 AGGCGCTGCTGCTGAGTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1204
 Oy 81 ---ProValProAsnSerLeuGlySerProAsnSerValLeuValValValSerVal 99
 Db 1205 AGCGCGGTG-----GACAGCTCTGATGATC-----ACAGCCCTCAGC 1240
 Oy 100 LysGluAlaLeuAlaPheLeuGluPheSerThrAlaProPheThr 115
 Db 1241 GAGAGTGGCAACAGCCCTCTCGGCTCTGATACAGTGGCGCGCTCT 1288

RESULT 9
 US-09-430-564-1
 ; Sequence 1, Application US/09430564
 ; Patent No. 6372467
 ; GENETIC INFORMATION
 ; APPLICANT: KOLB, Blenis
 ; APPLICANT: Key K. Lee-Fruman
 ; APPLICANT: Calvin J. Kuo
 ; TITLE OF INVENTION: SHANK AND BRISQK GUNES, PROTEINS
 ; FILE OF INVENTION: 00246/506002
 ; CURRENT APPLICATION NUMBER: US/09430564
 ; BEST LOCAL SIMILARITY: 36.2%
 ; Mismatches: 40
 ; Deletions: 4
 ; Gaps: 4
 ; PRIOR FILING DATE: 1998-10-29
 ; NUMBER OF SEQ ID NOS: 16
 ; SEQ ID NO: 1 FASTSEQ FOR Windows Version 4.0
 ; TYPE: DNA
 ; GENETIC INFORMATION
 ; APPLICANT: Homo sapiens
 ; US-09-430-564-1

Alignment Scores:
 No.: 2,376-15 Length: 1732
 Score: 187.90 Matches: 42
 Percent Similarity: 56.90 Conservative: 24
 Best Local Similarity: 36.2% Mismatches: 40
 Deletions: 4 Gaps: 4

US-10-000-039a-2_copy_313_431 (1-119) x US-09-430-564-1 (1-1732)
 Oy 2 LeuGluLeuProAsnLeuThrAsnSerAlaArgHisLeuLeuGluLeuLeuGlu 21
 Db 891 CCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 950
 Oy 22 LysAspATgThryArlau---GlyAlaLeuAspAspPheMolGluLeuLysSerHis 40
 Db 951 CGSANTCCGCGGAGTGGGGTGGGGTGGGGTGGGGTGGGGTGGGGTGGGGTGGGGTGGGG 1010
 Oy 41 ValPheSerLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 60
 Db 1011 CCGTCTTTTCGGGACATGAATTCGAGACGCTCTGCGCTGGCGTGGAGCCCTTC 1070
 Oy 61 AsnProAsnValSerGlyProMolGluLeuMarLysPheAspProGluPheThrGluGlu 80
 Db 1071 AGGCGCTGCTGCTGAGTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1130
 Oy 81 ---ProValProAsnSerLeuGlySerProAsnSerValLeuValValValSerVal 99
 Db 1131 AGCGCGGTG-----GACAGCTCTGATGAC-----ACAGCCCTCAGC 1166

Oy 100 LysGluAlaLeuAlaPheLeuGluPheSerThrAlaProPheThr 115
 Db 1167 GAGAGTGGCAACAGCCCTCTCGGCTCTGATACAGTGGCGCGCTCT 1214

RESULT 10
 US-09-842-307-1
 ; Sequence 1, Application US/09842307
 ; Patent No. 6562574
 ; GENETIC INFORMATION
 ; APPLICANT: Altshuler, David M.
 ; APPLICANT: Hirschhorn, Joel N.
 ; APPLICANT: Lander, Eric S.
 ; TITLE OF INVENTION: ASSOCIATION OF PROTEIN KINASE C ZETA
 ; FILE OF INVENTION: POLYMORPHISMS WITH DIABETES
 ; CURRENT APPLICATION NUMBER: US/09842307
 ; BEST LOCAL SIMILARITY: 36.2%
 ; Mismatches: 46
 ; Deletions: 4
 ; Gaps: 3
 ; PRIOR FILING DATE: 2000-04-25
 ; NUMBER OF SEQ ID NOS: 2
 ; SEQ ID NO: 1 FASTSEQ FOR Windows Version 4.0
 ; TYPE: DNA
 ; GENETIC INFORMATION
 ; APPLICANT: Homo sapiens
 ; US-09-842-307-1

Alignment Scores:
 No.: 7,846-15 Length: 2146
 Score: 184.90 Matches: 42
 Percent Similarity: 53.45% Conservative: 20
 Best Local Similarity: 36.2% Mismatches: 46
 Deletions: 4 Gaps: 3

US-10-000-039a-2_copy_313_431 (1-119) x US-09-842-307-1 (1-2146)
 Oy 1 ProLeuGluLeuProAsnLeuThrAsnSerAlaArgHisLeuLeuGluLeuLeu 20
 Db 1403 CCGATCCGAGTCCCGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1461
 Oy 21 GlyLysAspATgThryArlauGlyAlaLeuAspAsp-----PheMolGluLeuLys 38
 Db 1462 ATATGAGACCCCAAGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1521
 Oy 39 SerHisValPhePheSerLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 58
 Db 1522 TCCGCGCTGCTTCCCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1581
 Oy 59 ProPheAsnProAsnValSerGlyProMolGluLeuMarLysPheAspProGluPheThr 78
 Db 1582 CCGATCCGAGTCCCGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1641
 Oy 79 GluGluProValProAsnSerLeuGlySerProAsnSerValLeuValThraLysSer 98
 Db 1642 AGGAGCGCGCTGAG-----CTGAGCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1699
 Oy 99 ValGluAlaLeuAlaLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 114
 Db 1699 ATGACGACGTCA-----GAGTTCGAGGCTTTCGATGATCAACGCCA 1731

RESULT 11
 US-09-474-922A-2
 ; Sequence 2, Application US/09474922A
 ; Patent No. 6562574
 ; GENETIC INFORMATION
 ; APPLICANT: Brett P. Monla
 ; APPLICANT: Lex M. Cosset
 ; APPLICANT: David A. Rothstein
 ; TITLE OF INVENTION: RFS-0036
 ; FILE OF INVENTION: RFS-0036
 ; CURRENT APPLICATION NUMBER: US/09474922A

US-10-000-039a-2_COPY_313_431 (1-119) x US-09-256-465-1 (1-1599)

OY 1 ProleuGlnLeuysProkAnlethraAnseRAlaarghLeuLeuGlyLeuLeu 20
 DB 1195 CCGCCAGCTTCAGCC-----GAGCCAGCTCTCTCTCTCTCTCTCT 1242
 OY 21 GlnlyAspArgThrLysArgLeu--GlyAlaLysAspAspPheMetGlnLysSer 39
 DB 1243 AAGAGAGAGCCCAAGCAGAGGCTTGGTGGGGGCCCAAGCATCCAGAGAGGATTCAGAG 1302
 OY 40 HisValPhePheSerLeuLeaThrPaspArgLeuLeaLysLysLysLysLysLys 59
 DB 1303 CAGAGGCTCTCTCAGATCACTGGCAGAGAGTGGTCCAGAGAGCTCTCTCCACACC 1362
 OY 60 PheAsnProAsnValSerGlyProAsnGlnLeuArgHisPheAspProGlnPheThrGlu 79
 DB 1363 TTCAGAACTCAGAGCTACGCTCCAGCTGACACAGAGTACTTCGATGATGAATTACCGCC 1422
 OY 80 GluProVal 82
 DB 1423 CAGTCCATC 1431

RESULT 14
 US-09-167-322-3

/ Sequence 3, Application US/09167322
 / Patent No. 6385151 ONV;
 / GENE: APPLICATION: Allegheny University of the Health
 / Sciences, Halpern, Michael S.
 / England, James M.
 / NUMBER OF INVENTORS: 14
 / TITLE OF INVENTION: THE NEW VACCINE
 / CORRESPONDENCE ADDRESS:
 / ADDRESSES: Beltsville, Condo, Lavoie, & Monaco, P.C.
 / CITY: Philadelphia
 / STATE: PA
 / COUNTRY: USA
 / CONTRA: USA
 / COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 SOFTWARE: PATENT RELEASE #1.0, Version #1.30
 CURRENT APPLICATION DATA: US/09167,322
 PENDING DATE: 07-Oct-1998
 CLASSIFICATION: <unknown>

PRIOR APPLICATION DATA: NOT/0097/00582
 FILING DATE: <unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Monaco, Daniel A.
 ADDRESS: 1480
 REFERENCE/DOCKET NUMBER: 7933-33 PC
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (215) 568-0393
 FAX: (215) 568-3549

INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1599 base pairs
 STANDARD: Molecular Biology
 TOPOLOGY: linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Alignment Scores:
 Pred. No.: 1,31e-13 Length: 1599
 Score: 57,530 Matches: 12
 Best Local Similarity: 43.37% Mismatches: 12
 Query Match: 27.80% Indels: 5

DBs: 4 Gaps: 2

US-10-000-039a-2_COPY_313_431 (1-119) x US-09-167-322-3 (1-1599)
 OY 1 ProleuGlnLeuysProkAnlethraAnseRAlaarghLeuLeuGlyLeuLeu 20
 DB 1195 CCGCCAGCTTCAGCC-----GAGCCAGCTCTCTCTCTCTCTCTCT 1242
 OY 21 GlnlyAspArgThrLysArgLeu--GlyAlaLysAspAspPheMetGlnLysSer 39
 DB 1243 AAGAGAGAGCCCAAGCAGAGGCTTGGTGGGGGCCCAAGCATCCAGAGAGGATTCAGAG 1302
 OY 40 HisValPhePheSerLeuLeaThrPaspArgLeuLeaLysLysLysLysLysLys 59
 DB 1303 CAGAGGCTCTCTCAGATCACTGGCAGAGAGTGGTCCAGAGAGCTCTCTCCACACC 1362
 OY 60 PheAsnProAsnValSerGlyProAsnGlnLeuArgHisPheAspProGlnPheThrGlu 79
 DB 1363 TTCAGAACTCAGAGCTACGCTCCAGCTGACACAGAGTACTTCGATGATGAATTACCGCC 1422
 OY 80 GluProVal 82
 DB 1423 CAGTCCATC 1431

RESULT 15
 US-09-167-70

/ Sequence 70, Application US/09417197
 / Patent No. 6518021
 / GENERAL INFORMATION:
 / TITLE OF INVENTION: METHOD FOR EXTRACTING QUANTITATIVE INFORMATION RELATING TO
 / ARTICLES OF INVENTION: 09-417197
 / TITLE OF INVENTION: On A Cellular Response
 / FILE REFERENCE: 3759-0110P US/09417,197
 / CURRENT FILING DATE: 1998-10-07
 / NUMBER OF SEQ ID NOS: 143
 / SOFTWARE: PatentIn version 3.0
 / SEQ ID NO: 1
 / LENGTH: 201
 / TYPE: DNA
 / ORGANISM: Artificial Sequence
 / FEATURES:
 / OTHER INFORMATION: PKB-EGFP fusion
 / NAME/KEY: CDS
 / FEATURE:
 / CDS: 1..(2178)
 / US-09-417-197-70

Alignment Scores:
 Pred. No.: 8.3e-13 Length: 2181
 Score: 169,000 Matches: 45
 Percent Similarity: 50.00% Conservative: 16
 Best Local Similarity: 36.8% Mismatches: 47
 Query Match: 4.00% Indels: 4
 Caps: 4

US-10-000-039a-2_COPY_313_431 (1-119) x US-09-417-197-70 (1-2181)

OY 1 ProleuGlnLeuysProkAnlethraAnseRAlaarghLeuLeuGlyLeuLeu 20
 DB 1105 CCGCCAGCTCTGTGTC-----GAGCCAGCTCTCTCTCTCTCTCTCT 1152
 OY 21 GlnlyAspArgThrLysArgLeu--GlyAlaLysAspAspPheMetGlnLysSer 39
 DB 1153 AAGAGAGAGCCCAAGCAGAGGCTTGGTGGGGGCCCAAGCATCCAGAGAGGATTCAGAG 1212
 OY 40 HisValPhePheSerLeuLeaThrPaspArgLeuLeaLysLysLysLysLysLys 59
 DB 1213 CAGGCTCTCTCAGATCACTGGCAGAGAGTGGTCCAGAGAGCTCTCTCCACACC 1272
 OY 60 PheAsnProAsnValSerGlyProAsnGlnLeuArgHisPheAspProGlnPheThrGlu 79
 DB 1273 TTCAGAACTCAGAGCTACGCTCCAGCTGACACAGAGTACTTCGATGATGAATTACCGCC 1332

Oy 80 GluProValProAsnSerIleClyLysSerProAspSerValLeuValThrAlaSerVal 99
Db 1333 CAGATGATCACCATCAGCACCTGACCAAGATGACAGCATGGAGTGTGTGGACAGC --- 1389
Oy 100 LysGluAlaAlaGluAlaPheLeuGlyPheSerTyrAla----- 112
Db 1390 ---GAGCGAGGGCCCCACTTCCGCCAGTTCUUTATGTGGCCACAGCAGCGGCTCGGAT 1446
Oy 113 ProPro 114
Db 1447 CCGCCG 1452

Search completed, August 11, 2003, 11:30:24
Job time : 119.591 secs

score greater than or equal to the score of the result being printed.
and is derived by analysis of the total score distribution.

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 11, 2003, 12:13:37 : Search time 2015 Seconds
10171.375 Million cell updates/sec

Title: US-10-000-039a-1_COPY_980_1480

Perfect score: 501
Sequence: 1 CTTCTCCAGCTGAACCAANT.....TAGCAATCTATTGCAACT 501

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 2886711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 577422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Genbank :

1: gb_hg.*

2: gb_hg.*

3: gb_hg.*

4: gb_hg.*

5: gb_hg.*

6: gb_hg.*

7: gb_hg.*

8: gb_hg.*

9: gb_hg.*

10: gb_hg.*

11: gb_hg.*

12: gb_hg.*

13: gb_hg.*

14: gb_hg.*

15: gb_hg.*

16: gb_hg.*

17: gb_hg.*

18: gb_hg.*

19: gb_hg.*

20: gb_hg.*

21: gb_hg.*

22: gb_hg.*

23: gb_hg.*

24: gb_hg.*

25: gb_hg.*

26: gb_hg.*

27: gb_hg.*

28: gb_hg.*

29: gb_hg.*

30: gb_hg.*

31: gb_hg.*

32: gb_hg.*

33: gb_hg.*

34: gb_hg.*

35: gb_hg.*

36: gb_hg.*

37: gb_hg.*

38: gb_hg.*

39: gb_hg.*

40: gb_hg.*

41: gb_hg.*

Pred. No. is the number of results predicted by chance to have a

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	501	100.0	2370	6	ARI79441 Sequence
2	501	100.0	2370	6	AX002570 Sequence
3	501	100.0	2370	6	AX337834 Sequence
4	501	100.0	2370	6	AX337834 Sequence
5	501	100.0	2370	6	Y10032 H sapiens m
6	499.4	99.7	2281	6	AX017284 Sequence
7	499.4	99.7	2281	6	AX524988 Sequence
8	499.4	99.7	2281	6	BD114455 Sequence
9	499.4	99.7	2281	6	AX511590 Sequence
10	499.4	99.7	2311	6	AX270209 Sequence
11	499.4	99.7	2311	6	BD021928 Human pro
12	499.4	99.7	2354	6	AX533549 Sequence
13	499.4	99.7	2382	6	AX533549 Sequence
14	499.4	99.7	2382	6	AF153609 Homo sapi
15	499.4	99.7	2382	6	BC001263 Sequence
16	499.4	99.7	3196	6	AX713538 Sequence
17	499.4	99.7	3196	6	AX713538 Sequence
18	499.4	99.7	3196	6	AX713538 Sequence
19	359.9	71.7	1296	6	AX056374 Sequence
20	315.2	62.9	2429	10	AF139638 Mus muscu
21	314.2	62.7	1659	10	BC002222 Mus muscu
22	314.2	62.7	1659	10	BC002222 Mus muscu
23	314.2	62.7	2426	10	AF205855 Mus muscu
24	314.2	62.7	2432	6	AX056375 Sequence
25	303.1	62.1	1578	9	HSSCK
26	303.1	62.1	1578	9	HSSCK
27	299.4	59.8	2245	10	AX056375 Sequence
28	275.2	54.9	216056	2	AC103256 Sequence
29	254	50.7	694	6	AX201922 Sequence
30	244	48.7	193110	10	AC103256 Sequence
31	237.2	41.4	2319	5	BC052134
32	207.2	41.4	2319	5	BC052134
33	205	40.9	2470	5	SAC227115
34	205	40.9	3105	5	SAC227115
35	157.2	31.4	140519	2	AC112980
36	157.2	31.4	140519	2	AC112980
37	155.8	31.1	220150	2	AC107530
38	151.4	30.2	208405	2	AC114405
39	151.4	30.2	208405	2	AC114405
40	132.4	26.4	1346	6	AX056376 Sequence
41	132.4	26.4	1346	6	AX056376 Sequence
42	132.4	26.4	1812	6	AX399684 Sequence
43	132.4	26.4	1812	6	AX399684 Sequence
44	132.4	26.4	1812	6	BC014037 Homo sapi
45	132.4	26.4	1834	6	AX026166 Sequence

ALIGNMENTS

RESULT 1
LOCUS ARI79441
DEFINITION Sequence 1 from patent US 6326181.
ACCESSION ARI79441
VERSION ARI79441.1
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1. (Patent)
Lari and Walteger, S.
Cell volume-regulated human Kinase h-ask
Patent: US 6326181-A 1 04-DEC-2001;
FEATURES
Location/Qualifiers

Linear PAT 20-APR-2002

```

source 1..2370
BASE COUNT 636 a 517 c 513 g 704 t
ORIGIN
Query Match
Best Local Similarity 100.0%; Score 501; DB 6; Length 2370;
Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CTCCTCAGCTGAAACCAATATACAAATTCGCGAGACACTCTCTGAGGCGCTCTGC 60
DB 980 CTCCTCAGCTGAAACCAATATACAAATTCGCGAGACACTCTCTGAGGCGCTCTGC 1039
OY 61 AGAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
DB 1040 AGAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1099
OY 121 TCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 180
DB 1100 TCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1159
OY 181 ACCCAATCTGAGTGGCGCCCAAGAGCTTACAGCACTTGTACCGGAGTTTACGAGAGC 240
DB 1160 ACCCAATCTGAGTGGCGCCCAAGAGCTTACAGCACTTGTACCGGAGTTTACGAGAGC 1219
OY 241 CTCTGCCCACTTCCATTCGCAATCCCTTGACACGCTCTCTGACAGCAGAGCTCAAG 300
DB 1220 CTCTGCCCACTTCCATTCGCAATCCCTTGACACGCTCTCTGACAGCAGAGCTCAAG 1279
OY 361 AGCTCTGCGAGCTTCTGAGCTTCTGCTTCTGCTTCTGCTGCTGCTGCTGCTGCTG 360
DB 1380 AGCTCTGCGAGCTTCTGAGCTTCTGCTTCTGCTTCTGCTGCTGCTGCTGCTGCTG 1339
OY 361 CCGCTGTAGGCTTGGTTTAAAGAGTTTATGCTTGTGCTGCTGCTGCTGCTGCTG 420
DB 1340 CCGCTGTAGGCTTGGTTTAAAGAGTTTATGCTTGTGCTGCTGCTGCTGCTGCTG 1399
OY 421 TTTGCTGAGCGCCGACGCTACAGAGCATCTTACAGAGAAATTGCGATCTCTGAGAGC 480
DB 1400 TTTGCTGAGCGCCGACGCTACAGAGCATCTTACAGAGAAATTGCGATCTCTGAGAGC 1459
OY 481 TTACGAATCTTATTCACACT 501
DB 1460 TTACGAATCTTATTCACACT 1480

RESULT 3
AX337834 2370 bp DNA linear PAT 09-JAN-2002
SEQUENCE 8343 from Patent WO0194629.
ACCESSION AX337834
VERSION 1
AUTHORS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
YOUNG, P. E., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,
Horrigan, S., Soppet, D.R. and Weaver, Z.
Cancer gene determination and therapeutic screening using signature
Patent: WO 0194629-A 8343 13-DEC-2001;
Avalon Pharmaceuticals (US)
FEATURES
Location/Qualifiers
Source
/organism="Homo sapiens"
/mol-type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 636 a 517 c 513 g 704 t
ORIGIN
Query Match
Best Local Similarity 100.0%; Score 501; DB 6; Length 2370;
Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CTCCTCAGCTGAAACCAATATACAAATTCGCGAGACACTCTCTGAGGCGCTCTGC 60
DB 980 CTCCTCAGCTGAAACCAATATACAAATTCGCGAGACACTCTCTGAGGCGCTCTGC 1039
OY 61 AGAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
DB 1040 AGAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1099
OY 121 TCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 180
DB 1100 TCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1159
OY 181 ACCCAATCTGAGTGGCGCCCAAGAGCTTACAGCACTTGTACCGGAGTTTACGAGAGC 240
DB 1160 ACCCAATCTGAGTGGCGCCCAAGAGCTTACAGCACTTGTACCGGAGTTTACGAGAGC 1219
OY 241 CTCTGCCCACTTCCATTCGCAATCCCTTGACACGCTCTCTGACAGCAGAGCTCAAG 300
DB 1220 CTCTGCCCACTTCCATTCGCAATCCCTTGACACGCTCTCTGACAGCAGAGCTCAAG 1279
OY 361 AGCTCTGCGAGCTTCTGAGCTTCTGCTTCTGCTTCTGCTGCTGCTGCTGCTGCTG 360
DB 1380 AGCTCTGCGAGCTTCTGAGCTTCTGCTTCTGCTTCTGCTGCTGCTGCTGCTGCTG 1339
OY 361 CCGCTGTAGGCTTGGTTTAAAGAGTTTATGCTTGTGCTGCTGCTGCTGCTGCTG 420
DB 1340 CCGCTGTAGGCTTGGTTTAAAGAGTTTATGCTTGTGCTGCTGCTGCTGCTGCTG 1399
OY 421 TTTGCTGAGCGCCGACGCTACAGAGCATCTTACAGAGAAATTGCGATCTCTGAGAGC 480
DB 1400 TTTGCTGAGCGCCGACGCTACAGAGCATCTTACAGAGAAATTGCGATCTCTGAGAGC 1459
OY 481 TTACGAATCTTATTCACACT 501
DB 1460 TTACGAATCTTATTCACACT 1480

RESULT 2
AX002570 2370 bp DNA linear PAT 10-MAR-2000
LOCUS AX002570
DEFINITION Sequence 1 from Patent EP0861896.
ACCESSION AX002570
VERSION 1
AUTHORS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Lang, P.P. and Maldeger, S.D.
"Strain-Caucasian"
Patent: EP 0861896-A 1 02-SEP-1998.
DADE BEHRING WARBURG GMBH (DE)
FEATURES
Location/Qualifiers
Source
/organism="Homo sapiens"
/mol-type="genomic DNA"
/strain="CAUCASIAN"
/db_xref="taxon:9606"
/db_xref="HSMASNP"
BASE COUNT 636 a 517 c 513 g 704 t
ORIGIN
Query Match
Best Local Similarity 100.0%; Score 501; DB 6; Length 2370;
Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CTCCTCAGCTGAAACCAATATACAAATTCGCGAGACACTCTCTGAGGCGCTCTGC 60
DB 980 CTCCTCAGCTGAAACCAATATACAAATTCGCGAGACACTCTCTGAGGCGCTCTGC 1039

```

[illegible]

BASE COUNT 636 a 317 c 313 g 704 t
 ORIGIN PVPMSIGISGPOSVLTVMSKEMAGANLFTSAPTFDSFL*

Query Match 100.0%; Score 501; DB 9; Length 2370;
 Best Local Similarity 99.8%; Pred. NO. 1e-136;
 Matches 501; Conservative 0; Mismatches 0; Gaps 0;

QY 1 CTCCTCAGCTGAACCAAAATTTACAAATTCGCGACAGCTCTCGAGGCGCTCTGC 60
 DB 880 CTCCTCAGCTGAACCAAAATTTACAAATTCGCGACAGCTCTCGAGGCGCTCTGC 939
 QY 61 AGAGACAGCAGCAAGAGCTCGGGGCGACAGATGCTCATGAGATTAAGATCATG 120
 DB 940 AGAGACAGCAGCAAGAGCTCGGGGCGACAGATGCTCATGAGATTAAGATCATG 999
 QY 121 TCTCTCTCTCTTAATTAAGTGGATGATCTCATTAATTAAGAGATTAAGTCTCTTTA 180
 DB 1000 TCTCTCTCTCTTAATTAAGTGGATGATCTCATTAATTAAGAGATTAAGTCTCTTTA 1059
 QY 181 ACCCAATCTCCATTTGCAAGCTCGGCTGACAGCTCTTGACCGAGATTTACGAGAGC 240
 DB 1060 ACCCAATCTCCATTTGCAAGCTCGGCTGACAGCTCTTGACCGAGATTTACGAGAGC 1119
 QY 241 CTGTGCCCACTCCATTTGCAAGCTCGGCTGACAGCTCTTGACCGAGATTTACGAGAGC 300
 DB 1120 CTGTGCCCACTCCATTTGCAAGCTCGGCTGACAGCTCTTGACCGAGATTTACGAGAGC 1179
 QY 301 AGCTCGCGAGCTCTTCTAGGCTTTCTAGGCTTTCTAGGCTTTCTAGGCTTTCTAGGCT 360
 DB 1180 AGCTCGCGAGCTCTTCTAGGCTTTCTAGGCTTTCTAGGCTTTCTAGGCTTTCTAGGCT 1239
 QY 361 CCTGTAGGCTTTCTAGGCTTTCTAGGCTTTCTAGGCTTTCTAGGCTTTCTAGGCTTT 420
 DB 1240 CCTGTAGGCTTTCTAGGCTTTCTAGGCTTTCTAGGCTTTCTAGGCTTTCTAGGCTTT 1299
 QY 421 TTGTGGAGCGCGACGCTGACAGACATTTAGTGTCTTTGCGAATTTTGTAGTCAAGC 480
 DB 1300 TTGTGGAGCGCGACGCTGACAGACATTTAGTGTCTTTGCGAATTTTGTAGTCAAGC 1359
 QY 481 TTAGCAATCTTATTCACACT 501
 DB 1360 TTAGCAATCTTATTCACACT 1380

RESULT 7

AX524988 2281 bp DNA Linear PAT 21-MW-2002
 Sequence 39 from Patent BP126799.
 AX524988
 AX524988.1 GI:25170070
 VERSION
 KEYWORDS Homo sapiens (human)
 SOURCE
 ORGANISM Homo sapiens (human)
 BUKARYOTA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 Rosenthal, A.; Specht, T.; Hinzmann, B.; Schmitt, A.; Piliarsky, C.; Dahl, E. and
 Rosenthal, A.; acid sequences derived from breast tumor tissue
 Patent: EP 126799-A 30 04 SEP 2002;
 metagen Pharmacuticals GmbH (DE)
 Location/Qualifiers
 1..2281 "Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 BASE COUNT 601 a 498 c 494 g 688 t
 ORIGIN

FEATURES

Query Match 99.7%; Score 499.4; DB 6; Length 2281;
 Best Local Similarity 99.8%; Pred. NO. 1e-136;
 Matches 500; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CTCCTCAGCTGAACCAAAATTTACAAATTCGCGACAGCTCTCGAGGCGCTCTGC 60
 DB 880 CTCCTCAGCTGAACCAAAATTTACAAATTCGCGACAGCTCTCGAGGCGCTCTGC 939

BASE COUNT 636 a 317 c 313 g 704 t
 ORIGIN PVPMSIGISGPOSVLTVMSKEMAGANLFTSAPTFDSFL*

Query Match 100.0%; Score 501; DB 9; Length 2370;
 Best Local Similarity 99.8%; Pred. NO. 1e-136;
 Matches 501; Conservative 0; Mismatches 0; Gaps 0;

QY 1 CTCCTCAGCTGAACCAAAATTTACAAATTCGCGACAGCTCTCGAGGCGCTCTGC 60
 DB 880 CTCCTCAGCTGAACCAAAATTTACAAATTCGCGACAGCTCTCGAGGCGCTCTGC 939
 QY 61 AGAGACAGCAGCAAGAGCTCGGGGCGACAGATGCTCATGAGATTAAGATCATG 120
 DB 940 AGAGACAGCAGCAAGAGCTCGGGGCGACAGATGCTCATGAGATTAAGATCATG 999
 QY 121 TCTCTCTCTCTTAATTAAGTGGATGATCTCATTAATTAAGAGATTAAGTCTCTTTA 180
 DB 1000 TCTCTCTCTCTTAATTAAGTGGATGATCTCATTAATTAAGAGATTAAGTCTCTTTA 1059
 QY 181 ACCCAATCTCCATTTGCAAGCTCGGCTGACAGCTCTTGACCGAGATTTACGAGAGC 240
 DB 1060 ACCCAATCTCCATTTGCAAGCTCGGCTGACAGCTCTTGACCGAGATTTACGAGAGC 1119
 QY 241 CTGTGCCCACTCCATTTGCAAGCTCGGCTGACAGCTCTTGACCGAGATTTACGAGAGC 300
 DB 1120 CTGTGCCCACTCCATTTGCAAGCTCGGCTGACAGCTCTTGACCGAGATTTACGAGAGC 1179
 QY 301 AGCTCGCGAGCTCTTCTAGGCTTTCTAGGCTTTCTAGGCTTTCTAGGCTTTCTAGGCT 360
 DB 1280 AGCTCGCGAGCTCTTCTAGGCTTTCTAGGCTTTCTAGGCTTTCTAGGCTTTCTAGGCT 1339
 QY 361 CCTGTAGGCTTTCTAGGCTTTCTAGGCTTTCTAGGCTTTCTAGGCTTTCTAGGCTTT 420
 DB 1340 CCTGTAGGCTTTCTAGGCTTTCTAGGCTTTCTAGGCTTTCTAGGCTTTCTAGGCTTT 1299
 QY 421 TTGTGGAGCGCGACGCTGACAGACATTTAGTGTCTTTGCGAATTTTGTAGTCAAGC 480
 DB 1400 TTGTGGAGCGCGACGCTGACAGACATTTAGTGTCTTTGCGAATTTTGTAGTCAAGC 1459
 QY 481 TTAGCAATCTTATTCACACT 501
 DB 1460 TTAGCAATCTTATTCACACT 1480

Query Match 99.7%; Score 499.4; DB 6; Length 2281;

[illegible]

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

ON nucleic - nucleic search, using sw model

Run on: August 11, 2003, 11:27:55 ; Search time 249 Seconds
(without alignments)
3431.399 Million cell updates/sec

Title: US-10-000-039a-1_copy_980_1480

Perfect score: 501

Sequence: 1 CTCCTCCAGTCGAAACCCAT.....TACGACCTCTATTGCACACT 501

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : K Genesets 13jun03.4

1: /SIDSI/gcgdata/geneset/geneset-emb/NA1980.DAT.*
2: /SIDSI/gcgdata/geneset/geneset-emb/NA1981.DAT.*
3: /SIDSI/gcgdata/geneset/geneset-emb/NA1982.DAT.*
4: /SIDSI/gcgdata/geneset/geneset-emb/NA1983.DAT.*
5: /SIDSI/gcgdata/geneset/geneset-emb/NA1984.DAT.*
6: /SIDSI/gcgdata/geneset/geneset-emb/NA1985.DAT.*
7: /SIDSI/gcgdata/geneset/geneset-emb/NA1986.DAT.*
8: /SIDSI/gcgdata/geneset/geneset-emb/NA1987.DAT.*
9: /SIDSI/gcgdata/geneset/geneset-emb/NA1988.DAT.*
10: /SIDSI/gcgdata/geneset/geneset-emb/NA1989.DAT.*
11: /SIDSI/gcgdata/geneset/geneset-emb/NA1990.DAT.*
12: /SIDSI/gcgdata/geneset/geneset-emb/NA1991.DAT.*
13: /SIDSI/gcgdata/geneset/geneset-emb/NA1992.DAT.*
14: /SIDSI/gcgdata/geneset/geneset-emb/NA1993.DAT.*
15: /SIDSI/gcgdata/geneset/geneset-emb/NA1994.DAT.*
16: /SIDSI/gcgdata/geneset/geneset-emb/NA1995.DAT.*
17: /SIDSI/gcgdata/geneset/geneset-emb/NA1996.DAT.*
18: /SIDSI/gcgdata/geneset/geneset-emb/NA1997.DAT.*
19: /SIDSI/gcgdata/geneset/geneset-emb/NA1998.DAT.*
20: /SIDSI/gcgdata/geneset/geneset-emb/NA1999.DAT.*
21: /SIDSI/gcgdata/geneset/geneset-emb/NA2000.DAT.*
22: /SIDSI/gcgdata/geneset/geneset-emb/NA2001A.DAT.*
23: /SIDSI/gcgdata/geneset/geneset-emb/NA2001B.DAT.*
24: /SIDSI/gcgdata/geneset/geneset-emb/NA2002.DAT.*
25: /SIDSI/gcgdata/geneset/geneset-emb/NA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	501	100.0	2370	19	AAV48311
2	501	100.0	2370	20	Human cell-volume
3	501	100.0	2370	21	Human cell-volume
4	501	100.0	2370	24	ABL70096
5	501	100.0	2370	24	Pancreas cancer re
6	499.4	99.7	2281	20	Human breast tumor
7	499.4	99.7	2311	19	Human protein kinase
8	499.4	99.7	2311	19	Human protein kinase
8	499.4	99.7	2343	23	Human CDNA sequenc

Human skk DNA - Ho	9	499.4	99.7	2346	20	AAV74150
Novel protein kina	10	359	71.7	1256	22	AAV44639
DNA encoding a rat	11	314.2	62.7	2432	22	AAV44640
Novel protein kina	12	299.4	59.8	2365	41	AAV46592
Bovine hst associ	13	299.4	59.8	2365	41	AAV46592
Nucleotide sequen	14	286.2	57.0	404	25	AAK2226
Mouse ischaemic co	15	254	50.7	694	22	AAH2835
Human protein kina	16	140.6	28.1	431	24	ABT99409
Human protein kina	17	132.4	26.4	1332	22	AAH2835
Human protein kina	18	132.4	26.4	1332	22	AAH2835
Human protein kina	19	132.4	26.4	1332	22	AAH2835
Human protein kina	20	132.4	26.4	1332	22	AAH2835
Human serum and gl	21	132.4	26.4	1332	22	AAH2835
Human serum and gl	22	132.4	26.4	1332	22	AAH2835
Human serum and gl	23	132.4	26.4	1332	22	AAH2835
Human serum and gl	24	132.4	26.4	1332	22	AAH2835
Human serum and gl	25	132.4	26.4	1332	22	AAH2835
Human serum and gl	26	132.4	26.4	1332	22	AAH2835
Human serum and gl	27	132.4	26.4	1332	22	AAH2835
Human serum and gl	28	132.4	26.4	1332	22	AAH2835
Human serum and gl	29	132.4	26.4	1332	22	AAH2835
Human serum and gl	30	132.4	26.4	1332	22	AAH2835
Human serum and gl	31	132.4	26.4	1332	22	AAH2835
Human serum and gl	32	132.4	26.4	1332	22	AAH2835
Human serum and gl	33	132.4	26.4	1332	22	AAH2835
Human serum and gl	34	132.4	26.4	1332	22	AAH2835
Human serum and gl	35	132.4	26.4	1332	22	AAH2835
Human serum and gl	36	103	20.6	423	21	AAV16425
Human serum and gl	37	97.2	19.4	336	24	AAV86932
Human serum and gl	38	97.2	19.4	336	24	AAV86932
Human serum and gl	39	87	17.4	264	24	ABT9517
Human serum and gl	40	81.8	16.3	3872	24	ABT9517
Human serum and gl	41	76.4	15.2	615	24	ABV96134
Human serum and gl	42	76.4	15.2	615	24	ABV96134
Human serum and gl	43	68.4	13.7	2425	23	ABT28011
Human serum and gl	44	68.4	13.7	3712	25	ABT28011
Human serum and gl	45	60	12.0	60	24	ABN35464

ALIGNMENTS

RESULT 1
ID AAV48311 standard; CDNA: 2370 BP.

XX AAV48311;

DT 16-NOV-1998 (first entry)

XX Human cell-volume regulating kinase h-sgk.

XX ss: human; cell-volume: kinase; h-sgk; diabetes mellitus;
XX renal insufficiency; Inflammation; Alzheimer's disease.

OS Homo sapiens.

FW Key Location/Qualifiers

FF CDS /start=336

FF /product="Kinase h-sgk"

XX EP961896-A2.

XX PD 02-SEP-1998.

XX 27-JAN-1998; 98EP-0101338.

XX 28-FEB-1997; 97DE-1008173.

XX (DADB-) ONDE BEHRING HAMBURG GMBH.

XX Lang F, Waldeger S.

[illegible]

XX Human: cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
 KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
 KW cytostatic; gene therapy; antineoplastic; Hla's tumour; adenocarcinoma;
 KW gene; ds.
 OS Homo sapiens.
 XX
 XX W0300194629-A2.
 PD PD
 XX 30-MAY-2001; 2001MO-US0838.
 PF PF
 PR 05-JUN-2000; 2000US-209473P.
 PR 05-JUN-2000; 2000US-209531P.
 PR 18-SEP-2000; 2000US-23133P.
 PR 18-SEP-2000; 2000US-23133P.
 PR 20-SEP-2000; 2000US-234009P.
 PR 20-SEP-2000; 2000US-234034P.
 PR 20-SEP-2000; 2000US-234032P.
 PR 22-SEP-2000; 2000US-234567P.
 PR 25-SEP-2000; 2000US-234572P.
 PR 25-SEP-2000; 2000US-234077P.
 PR 25-SEP-2000; 2000US-235082P.
 PR 25-SEP-2000; 2000US-235134P.
 PR 26-SEP-2000; 2000US-235637P.
 PR 26-SEP-2000; 2000US-235638P.
 PR 27-SEP-2000; 2000US-235711P.
 PR 27-SEP-2000; 2000US-235840P.
 PR 27-SEP-2000; 2000US-235840P.
 PR 28-SEP-2000; 2000US-236028P.
 PR 28-SEP-2000; 2000US-236033P.
 PR 28-SEP-2000; 2000US-236034P.
 PR 28-SEP-2000; 2000US-236109P.
 PR 28-SEP-2000; 2000US-236842P.
 PR 29-SEP-2000; 2000US-236842P.
 PR 02-OCT-2000; 2000US-237172P.
 PR 02-OCT-2000; 2000US-237278P.
 PR 02-OCT-2000; 2000US-237295P.
 PR 02-OCT-2000; 2000US-237294P.
 PR 03-OCT-2000; 2000US-237425P.
 PR 03-OCT-2000; 2000US-237598P.
 PR 03-OCT-2000; 2000US-237604P.
 PR 03-OCT-2000; 2000US-237608P.
 PR 01-NOV-2000; 2000US-244867P.
 PR 01-NOV-2000; 2000US-245081P.
 XX (AVALON) AVALON PHARM.
 XX
 XX Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
 PI Soppel DR, Weaver L;
 XX WPI: 2002-188264/24.
 DR
 XX Screening for anti-neoplastic agent involves exposing cells to a
 XX chemical agent to be tested for anti-neoplastic activity and
 XX determining a change in expression of a gene of a signature gene set
 XX
 XX Claim 1: SEQ ID 8343; 44pp; English.
 XX The present invention describes a method (M1) for screening for an
 XX anti-neoplastic agent. The method involves exposing cells to a chemical
 XX agent to be tested for anti-neoplastic activity, determining a change in

CC expression of at least one gene (1) of a signature gene set, where (1)
 CC is a sequence selected from 847 sequences (given in AML1664
 CC to AML20110), or is at least 9% identical to (8), where a change in
 CC expression is indicative of anti-neoplastic activity. (1) has cytostatic
 CC activity and is useful for screening for anti-neoplastic agents.
 CC is an anti-neoplastic agent, and can be used for producing a product which
 CC is the data collected with respect to the anti-neoplastic agent as a
 CC result of M1, and the data is sufficient to convey the chemical
 CC structure and/or properties of the agent, and the agent is useful for
 CC screening for anti-neoplastic agents. The agent is selected from the group
 CC consisting of: ovarian, kidney, prostate or pancreatic cancer,
 CC oesophageal, adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,
 CC adenocarcinoma, carcinoma, squamous cell carcinoma, neuroendocrine
 CC carcinoma, papillary carcinoma and Wilms' tumour.
 XX
 XX Sequence 2370 BP: 636 A: 517 C: 513 G: 704 T: 0 other:
 XX
 XX Query Match 100.0% Score 501; Dh 24; Length 2370;
 XX Best Local Similarity 100.0%; Prod. No. 5,2e-153;
 XX Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX 1 CTCTCGACCTCAAGCAAAATATTAATTCATATTCGCAAGACCTCTCGAGGCTCTCTCTC 60
 XX 980 CTCTCGACCTCAAGCAAAATATTAATTCATATTCGCAAGACCTCTCGAGGCTCTCTC 1039
 XX
 XX 61 AGAAGGACGAGCAAGACGCGCTCGGGCCAGAGTACTCTCGAGGCTCTCTCTC 120
 XX
 XX 1040 AGAAGGACGAGCAAGACGCGCTCGGGCCAGAGTACTCTCGAGGCTCTCTCTC 1099
 XX
 XX 121 TCT 180
 XX
 XX 1100 TCT 1159
 XX
 XX 181 ACCCAATGTGAGTGGGCGCCACGAGCTTGGACCGAGCTTGGACCGAGCTTGGACCG 240
 XX
 XX 1160 ACCCAATGTGAGTGGGCGCCACGAGCTTGGACCGAGCTTGGACCGAGCTTGGACCG 1219
 XX
 XX 241 CTGTCGCCCACTCCATTCGCAAGTCCCTCGACAGCTTGGACCGAGCTTGGACCGAG 300
 XX
 XX 1220 CTGTCGCCCACTCCATTCGCAAGTCCCTCGACAGCTTGGACCGAGCTTGGACCGAG 1279
 XX
 XX 301 AAGTCGCGAGGCTTCTCTAGCTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 360
 XX
 XX 1280 AAGTCGCGAGGCTTCTCTAGCTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1419
 XX
 XX 361 CCGCTGTGAGGCTTCTCTAGGAAATATATATGAGTCTCGAGGCTTCTCTCTCTCTCT 440
 XX
 XX 1340 CCGCTGTGAGGCTTCTCTAGGAAATATATGAGTCTCGAGGCTTCTCTCTCTCTCT 1499
 XX
 XX 421 TTGCTGTGAGGCTTCTCTAGGAAATATATGAGTCTCGAGGCTTCTCTCTCTCTCTCT 480
 XX
 XX 1400 TTGCTGTGAGGCTTCTCTAGGAAATATATGAGTCTCGAGGCTTCTCTCTCTCTCT 1459
 XX
 XX 481 TTGCAATCTTATTCGCAACT 501
 XX
 XX 1460 TTGCAATCTTATTCGCAACT 1480
 XX
 XX RESULT 5
 XX AML23647
 XX ID AML23647 standard; CDNA; 2281 BP.
 XX AC AML23647;
 XX
 XX 08-DEC-1999 (first entry)
 XX DE
 XX Human breast tumour-associated EST 37.
 XX
 XX Expressed sequence tag; EST; human; breast; cancer; gene therapy;
 XX treatment; tumour; cytostatic; medicament; ds.
 XX Homo sapiens.
 XX

DE19813839-A1.
 21-SEP-1999.
 20-MAR-1998; 98DE-1013839.
 20-MAR-1998; 98DE-1013839.
 (META-) METACEN GENOMFORSCHUNG MBH.
 Specht T, Hinzmann B, Schmitt A, Pilsarsky C, Dahl E, Rosenthal A;
 US 7,199,520,901/45.
 P-FSDB; RA148573.
 Human nucleic acid sequences and protein products from tumor breast
 tissue, useful for breast cancer therapy -
 Claim 1a: 116-117; 188pp; German.
 This invention describes novel human nucleic acid sequences from tumor
 tissue which have catalytic activity. The nucleic acid sequences
 can be used to produce and isolate full-length gene sequences. They can
 be used to express proteins, which can be used as tools to find a
 activity against breast cancer. The sequences can be used to enhance or
 suppress the expression of the sequences. The sequences can be used in
 therapy to treat breast cancer. AA23611-248617 represents expressed
 sequence tags described in the method of the invention.

Query Match 99.7%; Score 499.4; DB 20; Length 2281;
 Best Local Similarity 99.8%; Pred. No. 1.7e-152;
 Matches 500; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 1 CTCTCCAGCTGAACCAAAATATGAAATTCGGAAGACATCTCTGGAGGCTCTGCG 60
 880 CTCTCCAGCTGAACCAAAATATGAAATTCGGAAGACATCTCTGGAGGCTCTGCG 939
 51 AGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 120
 940 AGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 999
 121 TCT 180
 1000 TCT 1059
 181 ACCCAATATGATGGTGGGCGGACAGCAGTATGAGCAGTATGAGCAGCAGCAGC 240
 1060 ACCCAATATGATGGTGGGCGGACAGCAGTATGAGCAGTATGAGCAGCAGCAGC 1119
 241 CTGTCCCAATCTGATGCAATCTCTGACAGCAGTCTCTGACAGCAGCAGCAGCAG 300
 1120 CTGTCCCAATCTGATGCAATCTCTGACAGCAGTCTCTGACAGCAGCAGCAGCAG 1179
 301 AGCTGGCAGGAGCTCTTACGAGTCTTCTTACGAGTCTTCTTACGAGTCTTCTT 360
 1180 AGCTGGCAGGAGCTCTTACGAGTCTTCTTACGAGTCTTCTTACGAGTCTTCTT 1239
 361 CCGTGTGAGGAGCTGGTGTAAAGAGTATGATGGTGTGAGGAGTGTGAGTGTAG 420
 1240 CCGTGTGAGGAGCTGGTGTAAAGAGTATGATGGTGTGAGGAGTGTGAGTGTAG 1299
 421 TTGTGGTGAAGCAGCAGTACAGCAGTCTTACAGAGAGTATGCAATCTCTGAGC 480
 1300 TTGTGGTGAAGCAGCAGTACAGCAGTCTTACAGAGAGTATGCAATCTCTGAGC 1359
 481 TAGCAATCTTATGCACT 501
 1360 TAGCAATCTTATGCACT 1360

RESULT 6

AY233833
 ID AY233833 Standard; CDM: 2311 NP.
 AC AY233833;
 DT AY233833;
 31-JUL-1998 (first entry)
 Human protein kinase HKK-3 coding sequence.
 Protein kinase: human; HKK; signalling cascade; kinase expression;
 Alzheimer's disease; cancer; anti-inflammatory agent; immunosuppressant;
 asthma; multiple sclerosis; rheumatoid arthritis; lymphocytic leukaemia;
 lymphoma; therapy; ss.
 KW
 KW
 KW Homo sapiens.
 OS
 Key
 Key
 CDS 379, 1080
 Location/Qualifiers
 /Laq_a
 MO581234-A2.
 19-MAR-1998.
 10-SEP-1997; 97NO-US15923.
 12-SEP-1996; 96US-0712709.
 (INCY-) INCYTE PHARM INC.
 AU-Young J, Guegler KJ, Hawkins PK;
 WPI: 1998-207394/18.
 P-FSDB; RAW54205.
 New diagnosis and treatment of e.g. Alzheimer's disease, cancers,
 asthma, multiple sclerosis or rheumatoid arthritis
 Claim 25; Fig 3; 75pp; English.
 This sequence encodes a human protein kinase (HKK) of the invention. The
 HKK protein can be used to develop products for studying signalling
 cascades in various cells and tissues, diagnosing disease and selecting
 inhibitors or drugs with the potential to intervene in various disorders
 and diseases. The HKK protein can be used to develop products for the
 products can be used to e.g. reverse memory loss, such as due to
 Alzheimer's disease, for cancer treatment or to provide anti-inflammatory
 and immunosuppressive effects in the treatment of e.g. asthma, multiple
 sclerosis as well as certain cancers, e.g.
 Lymphocytic leukaemias or lymphomas.
 Sequence 2311 BP: 604 A; 506 C; 652 T; 1 other;
 Query Match 99.7%; Score 499.4; DB 19; Length 2311;
 Best Local Similarity 99.8%; Pred. No. 1.7e-152;
 Matches 500; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 1 CTCTCCAGCTGAACCAAAATATGAAATTCGGAAGACATCTCTGGAGGCTCTGCG 60
 947 CTCTCCAGCTGAACCAAAATATGAAATTCGGAAGACATCTCTGGAGGCTCTGCG 1006
 61 AGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 120
 1007 AGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 1066
 121 TCT 180
 1067 TCT 1126
 181 ACCCAATATGATGGTGGGCGGACAGCAGTATGAGCAGTATGAGCAGCAGCAGC 240
 1127 ACCCAATATGATGGTGGGCGGACAGCAGTATGAGCAGTATGAGCAGCAGCAGC 1186

OY 241 CTCTCCCACTGATTCGCACTCCCTGACAGCTCTCTGTCAGCCAGCTCAGG 300
 CC CC
 DB 1187 CTGTGTCGCAACTGCAATTCGCAAGTCTCTGACAGCTCTCTGTCAGCCAGCTCAGG 1246
 CC CC
 OY 301 AAGCTGCGCACTGCAATTCGCAAGTCTCTGACAGCTCTCTGTCAGCCAGCTCAGG 360
 CC CC
 DB 1247 AAGCTGCGCACTGCAATTCGCAAGTCTCTGACAGCTCTCTGTCAGCCAGCTCAGG 1306
 CC CC
 OY 361 CCGCTGTCGCACTGCAATTCGCAAGTCTCTGACAGCTCTCTGTCAGCCAGCTCAGG 420
 CC CC
 DB 1307 CCGCTGTCGCACTGCAATTCGCAAGTCTCTGACAGCTCTCTGTCAGCCAGCTCAGG 1366
 CC CC
 OY 421 TTTGCTGTCGCACTGCAATTCGCAAGTCTCTGACAGCTCTCTGTCAGCCAGCTCAGG 480
 CC CC
 DB 1367 TTTGCTGTCGCACTGCAATTCGCAAGTCTCTGACAGCTCTCTGTCAGCCAGCTCAGG 1426
 CC CC
 OY 481 TTGAGCAATCTTATTGCACT 501
 CC CC
 DB 1427 TTGAGCAATCTTATTGCACT 1447
 CC CC
 RESULT 7
 ACAS6174
 ID ACA56174 standard; cDNA; 2311 bp.
 AC ACAS6174;
 XX 06-JUN-2003 (first entry)
 DT DT
 DB Human signalling pathway polynucleotide probe SEQ ID NO 772.
 XX
 XX Human; probe; ss; array element; Parkinson's disease; Leukemia;
 KW signalling pathway polynucleotide; Parkinson's disease; Leukemia;
 KW immunogenity; AIDS; Schen; neuropathy; Alzheimer's disease; Microarray.
 XX
 XX Homo sapiens.
 XX US8500938-B1.
 XX 31-DEC-2002.
 PD PD
 XX 30-JAN-1998; 98US-0016434.
 XX 30-JAN-1998; 98US-0016434.
 PR PR
 XX (INC-) INCYTE GENOMICS INC.
 XX
 PI Au-Young J, Seilhamer JJ;
 XX WPI; 2003-352189/33.
 XX
 XX Combination of polynucleotide probes, useful as array elements in a
 PT microarray for monitoring the expression of a number of target
 PR polynucleotides.
 XX
 XX Claim 1; SEQ ID NO 772; 65pp; English.
 ES ES
 XX The invention relates to a combination which comprises a number of
 CC polynucleotide probes comprising a sequence selected from one of the 1490
 CC sequences mentioned in the specification. The combination is useful as an
 CC array element in a microarray for monitoring the expression of a number
 CC of genes. The combination is useful for the diagnosis and treatment of
 CC cancer and immunopathology and neuropathology.
 CC The microarray is useful in diagnostics and treatment regimens, drug
 CC discovery and development, toxicological and carcinogenicity studies,
 CC monitoring progression of diseases and for developing sophisticated
 CC profiles for the effects of currently available therapeutic drugs. The
 CC combination is also useful for purifying a subpopulation of mRNAs, cDNAs
 CC and genomic fragments and in research and diagnostic applications. The
 CC combination is also useful for identifying genes and for identifying
 CC different signalling pathway populations which can be used to diagnose

CC various diseases including cancer e.g. adenocarcinoma and lymphoma,
 CC immunopathies e.g. AIDS and asthma, neuropathies e.g. Alzheimer's disease
 CC and Parkinson's disease. The present sequence represents a polynucleotide
 CC probe of the invention. For this patent did not form part of the claimed
 CC invention, but was obtained in electronic format directly from USPTO
 CC at seqdata.uspto.gov/sequence.html?docId=06500938B1.
 OY Sequence 2311 bp; 604 A; 508 C; 506 G; 692 T; 1 other;
 Query Match 99.7%; Score 499.4; DB 25; Length 2411;
 Best Local Similarity 99.8%; Pred. No. 1.7e-152;
 Matches 500; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 1 CTCCTGCACTGCAATTCGCAAGTCTCTGACAGCTCTCTGTCAGCCAGCTCAGG 60
 CC CC
 DB 947 CTGTGTCGCAACTGCAATTCGCAAGTCTCTGACAGCTCTCTGTCAGCCAGCTCAGG 1006
 CC CC
 OY 61 AAGAGGAGGAGCAAAAGGCTCTGACAGCTCTCTGTCAGCCAGCTCAGG 120
 CC CC
 DB 1007 AAGAGGAGGAGCAAAAGGCTCTGACAGCTCTCTGTCAGCCAGCTCAGG 1066
 CC CC
 OY 121 TCTCTTCTCTTAAATTAATGAGATGATCTCAATTAAGAGATTAAGTCTCTCTTAA 180
 CC CC
 DB 1067 TCTCTTCTCTTAAATTAATGAGATGATCTCAATTAAGAGATTAAGTCTCTCTTAA 1126
 CC CC
 OY 181 ACCCAATGTCAGTGGTGGGCAAGCTCTGACAGCTCTCTGTCAGCCAGCTCAGG 240
 CC CC
 DB 1127 ACCCAATGTCAGTGGGCAAGCTCTGACAGCTCTCTGTCAGCCAGCTCAGG 1186
 CC CC
 OY 241 CTCTCCCACTGATTCGCACTCCCTGACAGCTCTCTGTCAGCCAGCTCAGG 300
 CC CC
 DB 1187 CTGTGTCGCAACTGCAATTCGCAAGTCTCTGACAGCTCTCTGTCAGCCAGCTCAGG 1246
 CC CC
 OY 301 AAGCTGCGCACTGCAATTCGCAAGTCTCTGACAGCTCTCTGTCAGCCAGCTCAGG 360
 CC CC
 DB 1247 AAGCTGCGCACTGCAATTCGCAAGTCTCTGACAGCTCTCTGTCAGCCAGCTCAGG 1306
 CC CC
 OY 361 CCGCTGTCGCACTGCAATTCGCAAGTCTCTGACAGCTCTCTGTCAGCCAGCTCAGG 420
 CC CC
 DB 1307 CCGCTGTCGCACTGCAATTCGCAAGTCTCTGACAGCTCTCTGTCAGCCAGCTCAGG 1366
 CC CC
 OY 421 TTTGCTGTCGCACTGCAATTCGCAAGTCTCTGACAGCTCTCTGTCAGCCAGCTCAGG 480
 CC CC
 DB 1367 TTTGCTGTCGCACTGCAATTCGCAAGTCTCTGACAGCTCTCTGTCAGCCAGCTCAGG 1426
 CC CC
 OY 481 TTGAGCAATCTTATTGCACT 501
 CC CC
 DB 1427 TTGAGCAATCTTATTGCACT 1447
 CC CC
 RESULT 8
 ABX74395
 ID ABX74395 standard; cDNA; 234 bp.
 AC ABX74395;
 XX 21-MAR-2003 (first entry)
 DT DT
 DB Human cDNA sequence 16 up-regulated in non-aggressive CC-NOC.
 XX
 XX Human; microarray; solid surface; immobilised probe; CC-NOC;
 KW microarray; solid surface; immobilised probe; CC-NOC;
 KW non-aggressive CC-NOC; tumor type; clear cell renal carcinoma;
 KW gene expression profiling; tumor tissue; gene; ss.
 XX
 XX Homo sapiens.
 XX NC000279411-A2.
 PN NC000279411-A2.
 XX 10-OCT-2002.
 PD PD
 XX 29-MAR-2002; 2002NC00059576.
 PF

XX 29-MAR-2001; 2001US-279411P.
 PR (VAND-) VAN ANDEL INST.
 PA Haab B, Rhodes D, Teh BT, Takashi M;
 PI WPI; 2003-040679/03.
 DA
 XX New microarray, comprising a matrix of cDNA probes from a set of probes
 XX that had a defined surface in predetermined order, useful in the
 XX prognosis of patients with clear cell renal carcinoma
 XX
 XX Claim 1, Page 79-80; 179pp; English.
 CC The present invention relates to a microarray comprising a matrix of
 CC at least one cDNA probe from a set of probes immobilised to a solid
 CC surface, and a defined surface in predetermined order, useful in the
 CC prognosis of patients with clear cell renal carcinoma
 CC
 CC complementary to nucleic acid sequences that are expressed
 CC differentially in aggressive as compared to non-aggressive types of
 CC renal cell carcinoma (RCC). The microarray is useful for the
 CC prognosis of patients with RCC, wherein aggressive and
 CC non-aggressive CC-RCC tumour types are characterised by differential
 CC expression of genes. The microarray is useful for gene
 CC expression profiling of tumour and normal tissues. The present
 CC sequence represents a human cDNA sequence up-regulated in
 CC non-aggressive CC-RCC phenotypes.
 XX
 XX Sequence 2343 BP; 612 A; 517 G; 511 G; 703 T; 0 other;
 XX
 XX Query Match 99.7%; Score 499.4; DB 25; Length 2343;
 XX Best Local Similarity 99.8%; Pred. No. 1.7e-152;
 XX Matches 500; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CTCTCCGCGCAACCAATATACAAATTCGCAACGACCTCTCGAGGCGTCTCGC 60
 DB 973 CTCTCCGCGCAACCAATATACAAATTCGCAACGACCTCTCGAGGCGTCTCGC 1032
 QY 61 AGAAGGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 120
 DB 1033 AGAAGGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 1092
 QY 121 NGVGTCT 180
 DB 1093 TCT 1152
 QY 181 ACCCAATATGAGTGGGCGGCAACGACCTCTCGAGGCGTCTCGC 240
 DB 1153 ACCCAATATGAGTGGGCGGCAACGACCTCTCGAGGCGTCTCGC 1212
 QY 241 CTCTCCGCGCAACCAATATACAAATTCGCAACGACCTCTCGAGGCGTCTCGC 300
 DB 1213 CTCTCCGCGCAACCAATATACAAATTCGCAACGACCTCTCGAGGCGTCTCGC 1272
 QY 301 AGTCT 360
 DB 1273 AGCT 1332
 QY 361 CCCT 420
 DB 1333 CCCT 1392
 QY 421 TTGCT 480
 DB 1393 TTGCT 1452
 QY 481 TTGCT 501
 DB 1453 TTGCT 1473

RESULT 9
 ANV74190
 ID ANV74190 standard; DNA; 2346 bp.
 XX
 XX ANV71190.
 DT 15-MAR-1999 (first entry)
 XX
 XX Human sgk DNA.
 XX
 XX Serum glucocorticoid regulated kinase; sgk; human; treatment: inhibitor;
 XX serine/threonine protein kinase family; antagonist; diabetic nephropathy;
 XX chronic renal failure; inflammation; Alzheimer's disease; aging; etc.
 XX
 XX Homo sapiens.
 OS
 XX Location/units/ifiers
 XX Key 45..1340
 XX CDS /*tag- a
 XX /product- "sgk"
 XX /trans_cacopt- (pub:1185..1187, aa:sgk)
 XX
 XX EF887081-A2.
 XX
 XX 30-DEC-1998.
 XX
 XX 27-MAY-1998; 98pp-0304189.
 XX
 XX 27-JUN-1997; 9705-0051124.
 XX
 XX (SMK) SMITHKLINE BEECHAM CORP.
 PA
 XX Kumar JM;
 XX P-FSDB: AW90139.
 DR
 XX WPI: 1995-047627/05.
 XX
 XX Treating chronic renal failure, diabetic nephropathy and Alzheimer's
 XX disease by administration of nucleic acids and antagonists which
 XX inhibit activity or expression of human serum glucocorticoid
 XX regulated kinase (sgk), a serine/threonine protein kinase
 XX
 XX disclosure; Page 14-15; 17pp; English.
 XX
 XX This sequence encodes a novel human serum glucocorticoid regulated kinase
 XX (sgk) protein which is a member of the serine/threonine protein kinase
 XX family. This protein is used for the treatment of a subject having need
 XX to inhibit/antagonise activity or expression of human sgk polypeptide
 XX chain. The sequence encodes a novel human serum glucocorticoid
 XX regulated kinase (sgk), a serine/threonine protein kinase
 XX
 XX inflammation, Alzheimer's disease and wounds.
 XX
 XX Sequence 2346 BP; 608 A; 520 C; 518 G; 700 T; 0 other;
 XX
 XX Query Match 99.7%; Score 499.4; DB 20; Length 2346;
 XX Best Local Similarity 99.8%; Pred. No. 1.7e-152;
 XX Matches 500; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CTCTCCGCGCAACCAATATACAAATTCGCAACGACCTCTCGAGGCGTCTCGC 60
 DB 982 CTCTCCGCGCAACCAATATACAAATTCGCAACGACCTCTCGAGGCGTCTCGC 1041
 QY 61 AGAAGGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 120
 DB 1042 AGAAGGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 1101
 QY 121 TCT 180
 DB 1102 TCT 1163
 QY 181 ACCCAATATGAGTGGGCGGCAACGACCTCTCGAGGCGTCTCGC 240
 DB 1162 ACCCAATATGAGTGGGCGGCAACGACCTCTCGAGGCGTCTCGC 1221

PT treating immune-related diseases and disorders, cardiovascular disease,
 XT neurodegenerative diseases and/or cancers -
 PS Disclosure: Fig 2: 310pp; English.

XX The present sequence encodes a novel protein kinase, the nucleic acid
 CC sequences of which are disclosed herein. The present sequence encodes a
 CC protein kinase that may be used in the treatment and
 CC diagnosis of diseases associated with inappropriate kinase expression
 CC such as immune-related diseases and disorders, cardiovascular disease,
 CC neurodegenerative diseases and/or cancers -
 CC Disclosure: The present sequence may also be used as DNA probes in diagnostic
 CC assays. The kinase polypeptides may be used as antigens in the production
 CC of antibodies of kinase expression and activity. Anti-kinase antibodies
 CC and kinase antagonists may be used in the treatment of diseases
 CC and kinase antagonists may be used in the treatment of diseases
 CC activity include rheumatoid arthritis, atherosclerosis, autoimmune
 CC disorders, complications of organ transplantation, myocardial infarction,
 CC oxidative stress-related disorders, chronic inflammatory bowel disease,
 CC chronic inflammatory pelvic disease, multiple sclerosis, asthma,
 CC osteoarthritis, psoriasis, rhinitis, autoimmunity, diabetes, cancers and
 CC reproductive disorders.

XX Sequence 2432 BP: 586 A; 586 G; 560 G; 699 T; 1 other:

Query Match 63.7%; Score 314.2; DB 22; Length 2432;
 Best Local Similarity 81.7%; Pred. No. 7; 1e-92;
 Matches 401; Conservative 0; Mismatches 83; Indels 7; Gaps 3;

UY 1 CTTGCGCGTGAACCAACCAATTTTCAGATTCGCGAGCAGCTCTGCGAGCGCTCTGCG 60
 DB 1009 CTCTTCGATTTGAACCAATTTTCAGATTCGCGAGCAGCTCTGCGAGCGCTCTGCG 1068
 GY 61 AGAGCG 120
 DB 1069 AGAGCG 1128
 GY 121 CCGTCT 180
 DB 1129 TTTTCT 188
 GY 181 AGCGAATTCG 240
 DB 1189 ACCCAATTCG 1248
 GY 241 CCGTCT 300
 DB 1249 CGGTCT 1308
 GY 301 AGCGAATTCG 360
 DB 1309 AGCGAATTCG 1368
 GY 361 CCGTCT 419
 DB 1369 TGC-TCCGCGGATTCG 1426
 GY 420 TTTTCT 479
 DB 1427 CTTCG 490
 GY 480 CTTCG 490
 DB 1483 CTTCG 1493

RESULT 12

ID AA46592

AC AA46592 standard; DNA: 2365 BP.

XX AA46592;

XX 25-SEP-2000 (first entry)

XX DNA encoding a rat serum and glucocorticoid induced protein kinase.
 XX
 XX Protein kinase: Pkl1; Pkl2; Yrk1; Yrk2; protein kinase B-alpha;
 KW serum and glucocorticoid induced protein kinase B-alpha; Pkl1;
 KW Yrk1; Yrk2; protein kinase B-alpha; Pkl1; Yrk1; Yrk2; protein kinase
 KW thru; cancer; diabetes; obesity; antifungal; Candida infection; ss.
 XX
 XX Rattus sp.
 OS
 ES key
 ES CDS
 FF /cds- "serum and glucocorticoid induced protein
 FF /cds- "serum and glucocorticoid induced protein
 FF /transcript- "serum and glucocorticoid induced protein
 FF /note- "the codon encoding Met at position 1 and
 XX /note- "Pro at position 318 are not given"

PM MO2000036135-A2.

XX 23-JUN-2000.

XX 14-DEC-1999; 99NOV04228.

XX 14-DEC-1998; 98NOV-0112114.

XX (MEDI-) MEDICAL RES COUNCIL.

PA (MEDC) UNIV CALIFORNIA.

XX Thorner JW, Alessi DR, Torrance PD, Casamayor A;

XX WP1: 2000-44239J/28.

XX P-F006; AA493530.

PT Screening method identifying compounds which modulate protein kinase

XX activity for use in treating fungal infections and cancer -

XX Disclosure: Fig 12: 155pp; English.

XX The present sequence encodes a rat serum and glucocorticoid induced
 CC protein kinase (SKK) which modulates the activity of protein kinases
 CC from different sources, using host yeast cells. The method is used to
 CC identify a compound which modulates (inhibits) the activity of a
 CC protein kinase B-alpha (Pkl1) or a protein kinase C-alpha (Pkc).
 CC SKK or protein kinase B-alpha (Pkl1) is used to phosphorylate-dependent
 CC protein kinase-1 (PK1) is used to phosphorylate and activate Yrk1 and
 CC Yrk2 or SKK but not Pkl1alpha or P70S kinase. Compounds identified by
 CC yeast cancer to treat cancer, the compounds inhibit PK1, PK1 or the
 CC activation of PK1 by Pkl1. Compounds which activate PK1 or PK1 can be
 CC used in the treatment of diabetes or obesity, and compounds which
 CC inhibit PK1 or PK1 can be used in the treatment of diabetes or obesity.
 CC (Yrk1 or Yrk2) can be used as an antifungal agent to treat Candida
 CC infections, e.g. thrush.

XX Sequence 2365 BP: 591 A; 580 G; 518 G; 676 T; 0 other;

XX Query Match 59.8%; Score 299.4; DB 21; Length 2365;

XX Best Local Similarity 78.4%; Pred. No. 4; 9e-8;

XX Matches 371; Conservative 0; Mismatches 101; Indels 1; Gaps 1;

UY 17 AAATATTACAAATTTCCGACACACTCTCTGAGCGCGCTCTGACAGAGACGACAA 76

DB 946 AAATATCAACACTCTGAGCGCGCTCTGAGCGCGCTCTGAGAGAGCGCGACAA 1005

UY 77 CGCGCTCGCGCGCGAGGAGTCTCTGAGAGATTAGAGATCATGCTCTCTCTCTTAT 136

DB 1006 GAGCTCGGCTCGCGCGAGTCTCTGAGAGATTAGAGATCATGCTCTCTCTCTTAT 1665

UY 137 TACTCGGATGATCTATATATGAGGATTAATCCCTCTCTCTCTCTCTCTCTCTCT 196

QY 308 CGAGGCTTCTAGGCTTTTCTATGCGCCTCCACAGGACTCTTTCTCTGAACCTGTT 367
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 111 CGAGGCTTCTAGGCTTTTCTATGCGCCTCCACAGGACTCTTTCTCTGAACCTGTT 170
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 368 AGGCTTGGTTTAAAGGATTTATGTGTTCGGAATGTTTAGTTACCTTTTGGTG 427
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 171 AGGCTTGGTTTAAAGGATTTATGTGTTCGGAATGTTTAGTTACCTTTTGGTG 230
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 428 GAGCCCGAGCTGACAGGACATCTTACAGAGAAATTGCACATCTCTGGAAGCTTAGCA 487
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 231 GAGCCCGAGCTGACAGGACATCTTACAGAGAAATTGCACATCTCTGGAAGCTTAGCA 290
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 488 TCTTATTGCACACT 501
Db ||||||||||||||||||
QY 291 TCTTATTGCACACT 304
Db ||||||||||||||||||

Search completed: August 11, 2003, 13:51:06
Job time : 253 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OH nucleic - nucleic search, using sw model

Run on: August 11, 2003, 13:40:45, Search time 2064 Seconds
(without alignments)
5993,468 Million cell updates/sec

Title: US-10-000-039a-l_copy_980_1480

Perfect score: 501

Sequence: 1 CTCCTCCAGTGAACCAAAAT.....TAGCAGCTCTATTCAGCACT 501

Scoring Table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 4562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%

Maximum Match 10%

Listing first 45 summaries

Database : 1287

1: em_estha:*

2: em_estha:*

3: em_estha:*

4: em_estha:*

5: em_estha:*

6: em_estha:*

7: em_estha:*

8: em_estha:*

9: em_estha:*

10: gb_est2:*

11: gb_est2:*

12: gb_est3:*

13: gb_est3:*

14: gb_est3:*

15: em_estfun:*

16: em_estfun:*

17: em_estfun:*

18: em_estfun:*

19: em_estfun:*

20: em_estfun:*

21: em_estfun:*

22: em_estfun:*

23: em_estfun:*

24: em_estfun:*

25: em_estfun:*

26: em_estfun:*

27: em_estfun:*

28: gb_gsl1:*

29: gb_gsl2:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query	Length	DB	ID	Description
1	496.4	99.7	608	14	CB216184	CB216184 NISC_nq02
2	496.4	99.7	630	14	CB216182	CB216182 NISC_nq06
3	496.4	99.7	630	14	CB216182	CB216182 NISC_nq06
4	499.4	99.7	755	12	BG763506	BG763506 602735901

5	499.4	99.7	859	14	HU680126	
6	499.4	99.7	873	10	RG756781	
7	499.4	99.7	912	13	RG756781	
8	495.6	98.3	895	12	RG756781	
9	495.6	98.3	895	12	RG756781	
10	492.4	98.3	905	12	RG762465	
11	489.8	97.8	561	14	CH14488	
12	488.4	97.5	757	9	AV13155	
13	488.4	97.5	757	9	AV13155	
14	482.4	96.3	912	10	BE710437	
15	480.4	95.9	847	13	B0212889	
16	479.4	95.7	731	12	B0212889	
17	479.4	95.7	731	12	B0212889	
18	469.4	93.7	530	12	B0212889	
19	469.4	93.7	530	12	B0212889	
20	460.8	92.0	586	12	B1003243	
21	458.4	91.8	586	12	B1003243	
22	452.4	90.3	1068	13	B0151460	
23	438.6	87.5	909	12	B0006359	
24	435.2	86.9	898	13	B0087193	
25	416.4	81.9	1087	10	BE088131	
26	416.4	81.9	1087	10	BE088131	
27	407.4	81.3	557	12	BM705333	
28	405.2	80.9	458	14	CB114428	
29	396.2	79.3	921	13	BX291132	
30	396.2	79.3	921	13	BX291132	
31	378.8	75.6	834	12	BL135545	
32	374.2	74.7	876	10	BE178455	
33	364.2	72.7	565	12	BE070499	
34	364.2	72.7	565	12	BE070499	
35	354.8	70.8	663	10	BE178469	
36	350.6	70.0	659	10	BE178455	
37	347.4	69.3	365	12	BE070499	
38	347.4	69.3	365	12	BE070499	
39	338.4	67.5	906	10	BG032094	
40	336.8	67.2	661	10	BE178442	
41	335.2	66.9	736	10	BE075335	
42	335.2	66.9	736	10	BE075335	
43	327.4	65.3	424	14	NA9311	
44	325.4	65.0	620	10	BF503042	
45	318.4	63.6	337	14	N33832	

ALIGNMENTS

CH216184 608 bp mRNA linear EST 06-FEB-2003
NISC_nq02c07.yl NICHID_HS_022 Homo sapiens cDNA clone IMAGE:5937781
Sequence:
CB216184
CB216184.1 GI:28264376
EST, sapiens (human)
Homo sapiens
Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCI-CCAP http://www.ncbi.nlm.nih.gov/nciccap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Contact: Robert Strausberg, Ph.D.
Email: cysab@femail.nih.gov

cDNA Library Preparation:
RNA Library Arrayed by: The I.M.A.G.E. Consortium/ILM
Fundamental Biology Institutes of Health Intramural
Sequencing Center (NISC)
Clone distribution: NCI-CCAP clone distribution information can be
found through the I.M.A.G.E. Consortium/ILM at:
http://www.ncbi.nlm.nih.gov/nciccap/seq/seq9801480.html
Plate: LHAM13165 row: E column: 14

Seq primer: M13p1 reverse primer (Abi).
 Location/Qualifiers
 1..608
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5937781"
 /tissue_type="normal endometrium, mid-secretory phase, cycle day 23"
 /lab_host="DH10B (T1-resistant)"
 /clone_lib="M13CH15_U2"
 /vector="pGV-SPO16.1.cdb (ResGen, Invitrogen Corporation); Site 1: Not; Site 2: EcoRV; Cloned unidirectionally from microquantity amounts of mRNA from normal endometrial tissue (mid-secretory phase, cycle day 23) by ResGen (Invitrogen Corporation)." Library constructed by ResGen (Invitrogen Corporation)."
 BASE COUNT 151 a 164 c 132 g 161 t
 ORIGIN
 Query Match 99.7% Score 499.4; DB 14; Length 608;
 Best Local Similarity 99.8%; Pred. No. 2,5e-134;
 Matches 500; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CTCCTCCGCTGAAACCAANTATACAAATTCGCCAGACACTCTCTGGAGGCTCTCC 60
 DB 60 CTCCTCCGCTGAAACCAANTATACAAATTCGCCAGACACTCTCTGGAGGCTCTCC 119
 QY 61 AGACGACGACGACGACGCTCGGGCCAGAGTACTCTATGAGATTAAGAGTCATG 120
 DB 61 AGACGACGACGACGACGCTCGGGCCAGAGTACTCTATGAGATTAAGAGTCATG 120
 QY 120 AGAAGACGACGACGACGCTCGGGCCAGAGTACTCTATGAGATTAAGAGTCATG 179
 DB 120 AGAAGACGACGACGACGCTCGGGCCAGAGTACTCTATGAGATTAAGAGTCATG 179
 QY 121 TCTCTCTCTCTCTTAACTTAACTGGATGATCTCTTATTAAGAGATTAATCTCC 180
 DB 121 TCTCTCTCTCTCTTAACTTAACTGGATGATCTCTTATTAAGAGATTAATCTCC 180
 QY 180 TCTCTCTCTCTTAACTTAACTGGATGATCTCTTATTAAGAGATTAATCTCC 239
 DB 180 TCTCTCTCTCTTAACTTAACTGGATGATCTCTTATTAAGAGATTAATCTCC 239
 QY 181 ACCCAATCTGAGTGGGCCCAACAGACTACGCCACTTGGACCGAGTTTACGAGAGC 240
 DB 181 ACCCAATCTGAGTGGGCCCAACAGACTACGCCACTTGGACCGAGTTTACGAGAGC 240
 QY 240 ACCCAATCTGAGTGGGCCCAACAGACTACGCCACTTGGACCGAGTTTACGAGAGC 299
 DB 240 ACCCAATCTGAGTGGGCCCAACAGACTACGCCACTTGGACCGAGTTTACGAGAGC 299
 QY 241 CTCTCCGCTCACTCTATGAGTGGGCCCAACAGACTACGCCACTTGGACCGAGTT 300
 DB 241 CTCTCCGCTCACTCTATGAGTGGGCCCAACAGACTACGCCACTTGGACCGAGTT 300
 QY 300 CTCTCCGCTCACTCTATGAGTGGGCCCAACAGACTACGCCACTTGGACCGAGTT 359
 DB 300 CTCTCCGCTCACTCTATGAGTGGGCCCAACAGACTACGCCACTTGGACCGAGTT 359
 QY 360 AAGCTCTGGAGGCTTCTAGGCTTCTATGAGTGGGCCCAACAGACTACGCCAGT 419
 DB 360 AAGCTCTGGAGGCTTCTAGGCTTCTATGAGTGGGCCCAACAGACTACGCCAGT 419
 QY 361 CCGCTCTAGGCTTCTAGGCTTCTATGAGTGGGCCCAACAGACTACGCCAGTCT 420
 DB 361 CCGCTCTAGGCTTCTAGGCTTCTATGAGTGGGCCCAACAGACTACGCCAGTCT 420
 QY 420 CCGCTCTAGGCTTCTAGGCTTCTATGAGTGGGCCCAACAGACTACGCCAGTCT 479
 DB 420 CCGCTCTAGGCTTCTAGGCTTCTATGAGTGGGCCCAACAGACTACGCCAGTCT 479
 QY 421 TTGCTGTCGAGGCTTCTAGGCTTCTATGAGTGGGCCCAACAGACTACGCCAGT 480
 DB 421 TTGCTGTCGAGGCTTCTAGGCTTCTATGAGTGGGCCCAACAGACTACGCCAGT 480
 QY 480 TTGCTGTCGAGGCTTCTAGGCTTCTATGAGTGGGCCCAACAGACTACGCCAGT 539
 DB 480 TTGCTGTCGAGGCTTCTAGGCTTCTATGAGTGGGCCCAACAGACTACGCCAGT 539
 QY 481 TTAGCACTATTATGCACT 501
 DB 481 TTAGCACTATTATGCACT 501
 QY 540 TTAGCACTATTATGCACT 560
 DB 540 TTAGCACTATTATGCACT 560

FEATURES
 source
 1..630
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:593863"
 /sex="female"
 /tissue_type="normal endometrium, mid-secretory phase, cycle day 23"
 /lab_host="DH10B (T1-resistant)"
 /clone_lib="M13CH15_U2"
 /vector="pGV-SPO16.1.cdb (ResGen, Invitrogen Corporation); Site 1: Not; Site 2: EcoRV; Cloned unidirectionally from microquantity amounts of mRNA from normal endometrial tissue (mid-secretory phase, cycle day 23) by ResGen (Invitrogen Corporation)." Library constructed by ResGen (Invitrogen Corporation)."
 BASE COUNT 153 a 167 c 141 g 169 t
 ORIGIN
 Query Match 99.7% Score 499.4; DB 14; Length 630;
 Best Local Similarity 99.8%; Pred. No. 2,5e-134;
 Matches 500; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CTCCTCCGCTGAAACCAANTATACAAATTCGCCAGACACTCTCTGGAGGCTCTCC 60
 DB 94 CTCCTCCGCTGAAACCAANTATACAAATTCGCCAGACACTCTCTGGAGGCTCTCC 153
 QY 61 AGACGACGACGACGACGCTCGGGCCAGAGTACTCTATGAGATTAAGAGTCATG 120
 DB 61 AGACGACGACGACGACGCTCGGGCCAGAGTACTCTATGAGATTAAGAGTCATG 120
 QY 154 AGACGACGACGACGACGCTCGGGCCAGAGTACTCTATGAGATTAAGAGTCATG 213
 DB 154 AGACGACGACGACGACGCTCGGGCCAGAGTACTCTATGAGATTAAGAGTCATG 213
 QY 121 TCTCTCTCTCTTAACTTAACTGGATGATCTCTTATTAAGAGATTAATCTCC 180
 DB 121 TCTCTCTCTCTTAACTTAACTGGATGATCTCTTATTAAGAGATTAATCTCC 180
 QY 214 TCTCTCTCTCTTAACTTAACTGGATGATCTCTTATTAAGAGATTAATCTCC 273
 DB 214 TCTCTCTCTCTTAACTTAACTGGATGATCTCTTATTAAGAGATTAATCTCC 273
 QY 181 ACCCAATCTGAGTGGGCCCAACAGACTACGCCACTTGGACCGAGTTTACGAGAGC 240
 DB 181 ACCCAATCTGAGTGGGCCCAACAGACTACGCCACTTGGACCGAGTTTACGAGAGC 240
 QY 241 CTCTCCGCTCACTCTATGAGTGGGCCCAACAGACTACGCCACTTGGACCGAGTT 300
 DB 241 CTCTCCGCTCACTCTATGAGTGGGCCCAACAGACTACGCCACTTGGACCGAGTT 300
 QY 300 CTCTCCGCTCACTCTATGAGTGGGCCCAACAGACTACGCCACTTGGACCGAGTT 359
 DB 300 CTCTCCGCTCACTCTATGAGTGGGCCCAACAGACTACGCCACTTGGACCGAGTT 359
 QY 361 AGCTGCGGAGGCTTCTAGGCTTCTATGAGTGGGCCCAACAGACTACGCCAGT 360
 DB 361 AGCTGCGGAGGCTTCTAGGCTTCTATGAGTGGGCCCAACAGACTACGCCAGT 360
 QY 394 AGCTGCGGAGGCTTCTAGGCTTCTATGAGTGGGCCCAACAGACTACGCCAGT 453
 DB 394 AGCTGCGGAGGCTTCTAGGCTTCTATGAGTGGGCCCAACAGACTACGCCAGT 453
 QY 361 CCGCTCTAGGCTTCTAGGCTTCTATGAGTGGGCCCAACAGACTACGCCAGTCT 420
 DB 361 CCGCTCTAGGCTTCTAGGCTTCTATGAGTGGGCCCAACAGACTACGCCAGTCT 420
 QY 454 CCGCTCTAGGCTTCTAGGCTTCTATGAGTGGGCCCAACAGACTACGCCAGTCT 513
 DB 454 CCGCTCTAGGCTTCTAGGCTTCTATGAGTGGGCCCAACAGACTACGCCAGTCT 513
 QY 421 TTGCTGTCGAGGCTTCTAGGCTTCTATGAGTGGGCCCAACAGACTACGCCAGTCT 480
 DB 421 TTGCTGTCGAGGCTTCTAGGCTTCTATGAGTGGGCCCAACAGACTACGCCAGTCT 480
 QY 514 TTGCTGTCGAGGCTTCTAGGCTTCTATGAGTGGGCCCAACAGACTACGCCAGTCT 573
 DB 514 TTGCTGTCGAGGCTTCTAGGCTTCTATGAGTGGGCCCAACAGACTACGCCAGTCT 573

REFERENCE
 1 (bases 1 to 630)
 Authors
 Title
 Journal
 Comment
 Contact: Robert Stromstedt, Ph.D.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished
 CDNA Library Preparation:
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
 DNA Sequencing by: National Institutes of Health Intramural
 Sequencing Facility
 Sample Distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 info@img.llnl.gov
 Plate: 114M1316 row: N column: 20
 Seq primer: M13p1 reverse primer (Abi).
 Location/Qualifiers
 1..630
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:593863"
 /sex="female"
 /tissue_type="normal endometrium, mid-secretory phase, cycle day 23"
 /lab_host="DH10B (T1-resistant)"
 /clone_lib="M13CH15_U2"
 /vector="pGV-SPO16.1.cdb (ResGen, Invitrogen Corporation); Site 1: Not; Site 2: EcoRV; Cloned unidirectionally from microquantity amounts of mRNA from normal endometrial tissue (mid-secretory phase, cycle day 23) by ResGen (Invitrogen Corporation)." Library constructed by ResGen (Invitrogen Corporation)."
 BASE COUNT 151 a 164 c 132 g 161 t
 ORIGIN
 Query Match 99.7% Score 499.4; DB 14; Length 608;
 Best Local Similarity 99.8%; Pred. No. 2,5e-134;
 Matches 500; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CTCCTCCGCTGAAACCAANTATACAAATTCGCCAGACACTCTCTGGAGGCTCTCC 60
 DB 60 CTCCTCCGCTGAAACCAANTATACAAATTCGCCAGACACTCTCTGGAGGCTCTCC 119
 QY 61 AGACGACGACGACGACGCTCGGGCCAGAGTACTCTATGAGATTAAGAGTCATG 120
 DB 61 AGACGACGACGACGACGCTCGGGCCAGAGTACTCTATGAGATTAAGAGTCATG 120
 QY 120 AGAAGACGACGACGACGCTCGGGCCAGAGTACTCTATGAGATTAAGAGTCATG 179
 DB 120 AGAAGACGACGACGACGCTCGGGCCAGAGTACTCTATGAGATTAAGAGTCATG 179
 QY 121 TCTCTCTCTCTTAACTTAACTGGATGATCTCTTATTAAGAGATTAATCTCC 180
 DB 121 TCTCTCTCTCTTAACTTAACTGGATGATCTCTTATTAAGAGATTAATCTCC 180
 QY 180 TCTCTCTCTCTTAACTTAACTGGATGATCTCTTATTAAGAGATTAATCTCC 239
 DB 180 TCTCTCTCTCTTAACTTAACTGGATGATCTCTTATTAAGAGATTAATCTCC 239
 QY 181 ACCCAATCTGAGTGGGCCCAACAGACTACGCCACTTGGACCGAGTTTACGAGAGC 240
 DB 181 ACCCAATCTGAGTGGGCCCAACAGACTACGCCACTTGGACCGAGTTTACGAGAGC 240
 QY 240 ACCCAATCTGAGTGGGCCCAACAGACTACGCCACTTGGACCGAGTTTACGAGAGC 299
 DB 240 ACCCAATCTGAGTGGGCCCAACAGACTACGCCACTTGGACCGAGTTTACGAGAGC 299
 QY 241 CTCTCCGCTCACTCTATGAGTGGGCCCAACAGACTACGCCACTTGGACCGAGTT 300
 DB 241 CTCTCCGCTCACTCTATGAGTGGGCCCAACAGACTACGCCACTTGGACCGAGTT 300
 QY 300 CTCTCCGCTCACTCTATGAGTGGGCCCAACAGACTACGCCACTTGGACCGAGTT 359
 DB 300 CTCTCCGCTCACTCTATGAGTGGGCCCAACAGACTACGCCACTTGGACCGAGTT 359
 QY 360 AAGCTCTGGAGGCTTCTAGGCTTCTATGAGTGGGCCCAACAGACTACGCCAGT 419
 DB 360 AAGCTCTGGAGGCTTCTAGGCTTCTATGAGTGGGCCCAACAGACTACGCCAGT 419
 QY 361 CCGCTCTAGGCTTCTAGGCTTCTATGAGTGGGCCCAACAGACTACGCCAGTCT 420
 DB 361 CCGCTCTAGGCTTCTAGGCTTCTATGAGTGGGCCCAACAGACTACGCCAGTCT 420
 QY 420 CCGCTCTAGGCTTCTAGGCTTCTATGAGTGGGCCCAACAGACTACGCCAGTCT 479
 DB 420 CCGCTCTAGGCTTCTAGGCTTCTATGAGTGGGCCCAACAGACTACGCCAGTCT 479
 QY 421 TTGCTGTCGAGGCTTCTAGGCTTCTATGAGTGGGCCCAACAGACTACGCCAGT 480
 DB 421 TTGCTGTCGAGGCTTCTAGGCTTCTATGAGTGGGCCCAACAGACTACGCCAGT 480
 QY 480 TTGCTGTCGAGGCTTCTAGGCTTCTATGAGTGGGCCCAACAGACTACGCCAGT 539
 DB 480 TTGCTGTCGAGGCTTCTAGGCTTCTATGAGTGGGCCCAACAGACTACGCCAGT 539
 QY 481 TTAGCACTATTATGCACT 501
 DB 481 TTAGCACTATTATGCACT 501
 QY 540 TTAGCACTATTATGCACT 560
 DB 540 TTAGCACTATTATGCACT 560

RESULTS 2
 LOCUS CB216592
 DEFINITION N15C_inq06g10.y1 N15C_inq12 Homo sapiens cDNA clone IMAGE:593863
 5' UTR mRNA sequence.
 ACCESSION CB216592.1
 VERSION 1
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 TISSUE Chordata; Craniata; Vertebrata; Euteleostomi;
 Embryophyta; Metazoa;

1 CTCTCCAGCTGAACCAATATTACAAATTCGCAAGACGACTCTCTGGAGCGCTCTCC 60
 Db 242 CTCTCTCTAGCTGACCAATATTACAAATTCGCAAGACGACTCTCTGGAGCGCTCTCC 301
 Qy 61 AGAAGACAGACCAAGCGCTGGGGCAAGAGTACTCATGAGAGATTAGAGTCATG 120
 Db 302 AGAAGACAGACCAAGCGCTGGGGCAAGAGTACTCATGAGAGATTAGAGTCATG 361
 Qy 121 CT 180
 Db 362 CT 421
 Qy 181 ACCCAAAATGAGTGGGGCCAGACGACTACGCACTTTGACCGCGATTACCGAGAGC 240
 Db 422 ACCCAAAATGAGTGGGGCCAGACGACTACGCACTTTGACCGCGATTACCGAGAGC 481
 Qy 241 CTCTCCCAAGCT 300
 Db 482 CTCTCCCAAGCT 541
 Qy 301 AAGCTCCAGAGCT 360
 Db 542 AAGCTCCAGAGCT 601
 Qy 361 CCGCTGATGAGGCT 420
 Db 602 CCGCTGATGAGGCT 661
 Qy 421 TTGCTGGTGGCGCCAGCTGACAGACATCTCTCAAGAGATTTCGCATCTCGAAGC 480
 Db 662 TTGCTGGTGGCGCCAGCTGACAGACATCTCTCAAGAGATTTCGCATCTCGAAGC 721
 Qy 481 TTGAGCAATCTTATGCACT 501
 Db 722 TTGAGCAATCTTATGCACT 742

RESULT 5
 B0680126
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

B0680126 859 bp mRNA linear EST J5-JUL-2002
 NCENCOU87_8196937 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6263586
 sequence.
 B0680126
 B0680126.1 G1:21792805
 EST
 Homo sapiens (human)
 Chondrin

CONTACT: Robert Strausberg, Ph.D.
 Tissue Procurement: DCTD/DPV
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 Vectors: pTZ19, pTZ19.1, pTZ19.2, pTZ19.3, pTZ19.4, pTZ19.5
 Cloned through the I.M.A.G.E. Consortium/LLNL information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Note: L102427 was a false positive.
 High quality sequence stop file.

1. 859
 Location/Qualifiers
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:6263586"
 /tissue_type="melanotic melanoma, cell line"
 /lab_host="mouse melanoma, resistant"
 /lab_host="NIH_MGC_112"

FEATURES
 source

/note="Origin: skin. Vector: pOT87. Site: 1. What: slice 2. How: EPCR/NotI slice using the following 5' adaptor: GCGACAG(G). Library constructed by Linda Hone in the laboratory of Gerald K. Rubin (University of California, Berkeley) using standard techniques (Life Technologies). Note: this is a NIH_MGC library."

BASE COUNT 206 a 211 c 201 g 241 t

Query Match 99.7% Score 499.4; DB 13; Length 459;
 Best Local Similarity 99.8%; Pred. No. 2.8e-134;
 Matches 500; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CTCTCCAGCTGAACCAATATTACAAATTCGCAAGACGACTCTCTGGAGCGCTCTCC 60
 Db 96 CTCTCCAGCTGAACCAATATTACAAATTCGCAAGACGACTCTCTGGAGCGCTCTCC 155
 Qy 61 AGAAGACAGACCAAGCGCTGGGGCAAGAGTACTCATGAGAGATTAGAGTCATG 120
 Db 156 AGAAGACAGACCAAGCGCTGGGGCAAGAGTACTCATGAGAGATTAGAGTCATG 215
 Qy 121 CT 180
 Db 216 CT 275
 Qy 181 ACCCAAAATGAGTGGGGCCAGACGACTACGCACTTTGACCGCGATTACCGAGAGC 240
 Db 276 ACCCAAAATGAGTGGGGCCAGACGACTACGCACTTTGACCGCGATTACCGAGAGC 335
 Qy 241 CTCTCCCAAGCT 300
 Db 336 CTCTCCCAAGCT 395
 Qy 301 AAGCTCCAGAGCT 360
 Db 396 AAGCTCCAGAGCT 455
 Qy 361 CCGCTGATGAGGCT 420
 Db 456 CCGCTGATGAGGCT 515
 Qy 421 TTGCTGGTGGCGCCAGCTGACAGACATCTCTCAAGAGATTTCGCATCTCGAAGC 480
 Db 516 TTGCTGGTGGCGCCAGCTGACAGACATCTCTCAAGAGATTTCGCATCTCGAAGC 575
 Qy 481 TTGAGCAATCTTATGCACT 501
 Db 576 TTGAGCAATCTTATGCACT 596

B0756781
 G027102541 NIH_MGC_48 Homo sapiens cDNA linear EST J5-MAY-2001
 mRNA sequence.
 B0756781
 B0756781.1 G1:14067434
 EST
 Homo sapiens (human)
 Chondrin

CONTACT: Robert Strausberg, Ph.D.
 Tissue Procurement: DCTD/DPV
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 Vectors: pTZ19, pTZ19.1, pTZ19.2, pTZ19.3, pTZ19.4, pTZ19.5
 Cloned through the I.M.A.G.E. Consortium/LLNL information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Note: L102427 was a false positive.
 High quality sequence stop file.

1. 859
 Location/Qualifiers
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:6263586"
 /tissue_type="melanotic melanoma, cell line"
 /lab_host="mouse melanoma, resistant"
 /lab_host="NIH_MGC_112"

FEATURES
 source


```

421 TTGTGTGAGCGCCCACTGACGACGACATCTTACAAAGAGANTTGCACATCTCGAAGC 480
Db 516 TTGTGTGAGCGCCCACTGACGACGACATCTTACAAAGAGANTTGCACATCTCGAAGC 575
Qy 481 TTGACATCTTATTGCACACT 501
Db 576 TTGACATCTTATTGCACACT 596

RESULT 8
BU838753
LOCUS      BU838753
DEFINITION      AGNC000T_8210094 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6258012
5', mRNA sequence.
ACCESSION      BU838753
VERSION        BU838753.1
DBSOURCE       BU838753.1 GI:24023148
ORGANISM       Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE      NIH-MGC http://mgs.nci.nih.gov/
1 (bases 1 to 918)
AUTHORS        National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE          Contact: Robert Strausberg, Ph.D.
COMMENT        Tissue Procurement: DCTD/DP
Email: cagabs-remail.nih.gov
Accession: BU838753
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone Distribution: by Agencourt Bioscience Corporation
Found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L10H413 row: d column: 13
High quality sequence stop: 524.
Location/Qualifiers
1 .899
/organism="Homo sapiens"
/mol_type="mRNA"
/ab_xref="taxon:9606"
/ab_xref="IMAGE:6258012"
/tissue_type="melanotic melanoma, cell line"
/clone_lib="NIH-MGC_48"
/ab_host="DH10B (phase-resistant)"
/clone_lib="NIH-MGC_48"
Note: cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGAG(G). Library constructed by Ling Hong in the
Berkeley YAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH-MGC library."
BASE COUNT      214 a 289 c 218 g 197 t
ORIGIN
Query Match      98.7% Score 494.6; DB 13; Length 918;
Best Local Similarity 99.2% Pred No. 7,2e-133;
Matches 497; Conservative 4; Indels 0; Gaps 0;
Qy 1 CTTCTCCAGCTGAACCAAAATATACAAATCTCCGACAGACTCTCTGGAGGGCTCTCTCC 60
96 CTTCTCCAGCTGAACCAAAATATACAAATCTCCGACAGACTCTCTGGAGGGCTCTCTCC 155
Db 61 AGAAGACAGCAAAAGGGCTCTGGGGCGACAGATGATCTTATGGAGTAAAGAGTCATG 120
Qy 156 AGAAGACAGCAAAAGGGCTCTGGGGCGACAGATGATCTTATGGAGTAAAGAGTCATG 215
Db 156 AGAAGACAGCAAAAGGGCTCTGGGGCGACAGATGATCTTATGGAGTAAAGAGTCATG 215
Qy 121 TCTCTCTCTCTCTTAACTCGGATGATCTTATTAAGAGAGTAACTCCGCTTTTA 180
Db 216 TCTCTCTCTCTCTTAACTCGGATGATCTTATTAAGAGAGTAACTCCGCTTTTA 275

```

```

181 ACCCAATGTGAGTGGGCCCAAGCACTACGGCACTTTGACCGGCACTTACCAAGAC 240
Db 276 ACCCAATGTGAGTGGGCCCAAGCACTACGGCACTTTGACCGGCACTTACCAAGAC 315
Qy 241 CTGTCCCAACTGCAATGCAAGTCCCTGACAGCTCTCTGTCACAGAGCGGTGACAG 390
Db 336 CTGTCCCAACTGCAATGCAAGTCCCTGACAGCTCTCTGTCACAGAGCGGTGACAG 405
Qy 301 CAGTCGCGAGAGCTCTTACGACTTTTCTGATGCGCTCCGACGGAGCTTTCTTGA 360
Db 396 CAGTCGCGAGAGCTCTTACGACTTTTCTGATGCGCTCCGACGGAGCTTTCTTGA 455
Qy 361 CCCTGTGTAGAGCTCTGTTTAAAGAGATTTATGTGTGTTCGGAATGTTTACTAGCT 420
Db 456 CCCTGTGTAGAGCTCTGTTTAAAGAGATTTATGTGTGTTCGGAATGTTTACTAGCT 515
Qy 421 TTGTGTGAGCGCCCACTGACGACGACATCTTACAAAGAGANTTGCACATCTCGAAGC 480
Db 516 TTGTGTGAGCGCCCACTGACGACGACATCTTACAAAGAGANTTGCACATCTCGAAGC 575
Qy 481 TTGACATCTTATTGCACACT 501
Db 576 TTGACATCTTATTGCACACT 596

RESULT 9
BU8769533
LOCUS      BU8769533
DEFINITION      AGNC001 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:5477546.5.
5', mRNA sequence.
ACCESSION      BU8769533
VERSION        BU8769533.1
DBSOURCE       BU8769533.1 GI:14080186
ORGANISM       Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE      NIH-MGC http://mgs.nci.nih.gov/
1 (bases 1 to 999)
AUTHORS        National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE          Contact: Robert Strausberg, Ph.D.
COMMENT        Tissue Procurement: ATCC/DCTD/DP
Email: cagabs-remail.nih.gov
Accession: BU8769533
DNA Sequencing by: Invitrogen Genomics, Inc.
Clone Distribution: MGC clone distribution information (see below)
Found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L10H413 row: d column: 05
High quality sequence stop: 822.
Location/Qualifiers
1 .899
/organism="Homo sapiens"
/mol_type="mRNA"
/ab_xref="taxon:9606"
/clone_lib="IMAGE:5477546"
/ab_host="DH10B (phase-resistant)"
/clone_lib="NIH-MGC_48"
Note: Organ: skin; Vector: pORF9; Site: 2.
Note: cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGAG(G). Size selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
and the NIH-MGC. Note: this is a NIH-MGC
Library."
BASE COUNT      203 a 216 c 216 g 264 t
ORIGIN

```


21C Frontier Korean EST Project 2001
 Unpublished
 Contact: Kim YS Center
 Korea Research Institute of Bioscience & Biotechnology
 52 Eoan-dong Yuseong-gu, Daejeon 305-333, South Korea
 Tel.: +82-42-860-4470
 Fax: +82-42-860-4470
 E-mail: ykangsu@gmail.kr, ykbb.re.kr
 Plate: 27 row: D column: 05
 High quality sequence stop: 561.
 Location/Qualifiers
 1..561
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /sex="M"
 /lab_host="Toplite"
 /clone_lib="B2807048"
 /site_2="N61; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then deacetylated with tabacco acid pyrophosphatase (TAP). The deacetylated RNA was ligated with a 5'-phosphorylated EcoRI linker. The EcoRI site was treated with 74 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was circularized with E. coli DNA ligase after digestion of EcoRI. This site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA were used for transformation of E. coli. The cDNA libraries were constructed by this method are full-length enriched cDNA library."

BASE COUNT 144 a 147 c 123 g 147 t

Query Match
 Best Local Similarity 97.88; Score 489.8; DB 14; Length 561;
 Matches 494; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy 1 CTCCTCAGCTGAACCAATATATACAAATTCGCGACAGACCTCTCGAGGCGCTCTGC 60
 Db 50 CTCCTCAGCTGAACCAATATATACAAATTCGCGACAGACCTCTCGAGGCGCTCTGC 109
 Oy 61 AGACAGACAGCAACAGCGCTCGCGGCGACGATCTTCAGAGATTAAGATCATG 120
 Db 110 AGACAGACAGCAACAGCGCTCGCGGCGACGATCTTCAGAGATTAAGATCATG 169
 Oy 121 TCTCTCTCTCTTAACTGGGATGATCTCATTAATGAAGAGATTAAGATCATG 180
 Db 290 TCTCTCTCTCTTAACTGGGATGATCTCATTAATGAAGAGATTAAGATCATG 229
 Oy 181 ACCCAATGTGATGGCGCCAGACGATAGCGACATTTGACCGGAGTTCACGACGAG 240
 Db 230 ACCCAATGTGATGGCGCCAGACGATAGCGACATTTGACCGGAGTTCACGACGAG 289
 Oy 241 CTCTCCCACTTCATGCAATGCTCGCTGAGAGCGCTCTCTGACAGCGGCTCAAG 300
 Db 290 CTCTCCCACTTCATGCAATGCTCGCTGAGAGCGCTCTCTGACAGCGGCTCAAG 349
 Oy 301 AGTCGCGAGGCTTCTAGGCTGATTCCTATGGGCTCTCCAGAGATCTCTCTCTGAA 360
 Db 350 AGTCGCGAGGCTTCTAGGCTGATTCCTATGGGCTCTCCAGAGATCTCTCTCTGAA 409
 Oy 361 CCCTGTAAGCGTGGTTTAAAGGATTAATGAGCTGTTTCCGAGATTTATGATAGGCT 420
 Db 410 CCCTGTAAGCGTGGTTTAAAGGATTAATGAGCTGTTTCCGAGATTTATGATAGGCT 469
 Oy 421 TTGGTGGAGCGCGCGATCTGACAGAGATCTTACAGAGAGATTTGCACTCTCGAGAC 480

Db 470 TTTCCTGGAGCGCCACTGACAGACATCTTACAGAGAGATTTGCACTCTCGAGAC: 529
 Oy 481 TTACAGATTAATGAGCTGATGCT: 501
 Db 530 TTACAGATTAATGAGCTGATGCT: 550

RESULT 12
 B0691213
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens (human)
 B0691213.1 GI:21816529
 EST.
 REFERENCE
 TITLE
 JOURNAL
 COMMENT
 Contact: Robert Strausberg, Ph.D.
 Tissue Procurement: ATCC
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILIN)
 cDNA Distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: LINC2386 row: b column: 04
 High quality sequence stop: 715.
 Location/Qualifiers
 1..997
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone_lib="IMAGE:624758"
 /tissue_type="Ductal carcinoma, cell line"
 /cell_line="MDA-MB-231 (resistant)"
 /clone_lib="NIH-MGC:310"
 /note="Torgan; pancreas; Vector: pOT87; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. In the following 5' adaptor: GCGCAGG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using 2AP-cDNA synthesis kit (Life Technologies). Note: this is a NIH-MGC library." 1 others

BASE COUNT 243 a 255 c 233 g 265 t

Query Match
 Best Local Similarity 97.5%; Score 488.4; DB 13; Length 997;
 Matches 500; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Oy 1 CTCCTCAGCTGAACCAATATATACAAATTCGCGACAGACCTCTCGAGGCGCTCTGC 60
 Db 295 CTCCTCAGCTGAACCAATATATACAAATTCGCGACAGACCTCTCGAGGCGCTCTGC 354
 Oy 61 AGACAGACAGCAACAGCGCTCGCGGCGACGATCTTCAGAGATTAAGATCATG 120
 Db 355 AGACAGACAGCAACAGCGCTCGCGGCGACGATCTTCAGAGATTAAGATCATG 414
 Oy 121 TCTCTCTCTCTTAACTGGGATGATCTCATTAATGAAGAGATTAAGATCATG 180
 Db 415 TCTCTCTCTTAACTGGGATGATCTCATTAATGAAGAGATTAAGATCATG 474
 Oy 181 ACCCAATGTGATGGCGCCAGACGATAGCGACATTTGACCGGAGTTCACGAGAC 240

the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

227 a 206 g 231 t

BASE COUNT

ONTIN

Query Match 95.3%; Score 482.4; DB 10; Length 912;
Best Local Similarity 95.6%; Pred. No. 9.6e-129;
Matches 494; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

OY 1 CTCCTCAGCTGAACCAAAATATTACAAATTCGCCAGACACTCTCTCGAGGCTCTCG 59
DDB 210 CTCCTCAGCTGAACCAAAATATTACAAATTCGCCAGACACTCTCTCGAGGCTCTCG 269
OY 60 CAGAAGCAGGACGAGGAGGCTCTCGGCGCAGAGTACTCTCTGAGATTAAGAGCAT 119
DDB 220 CAGAAGCAGGACGAGGAGGCTCTCGGCGCAGAGTACTCTCTGAGATTAAGAGCAT 329
OY 120 CTCCT 179
DDB 330 CTCCT 389
OY 180 AACCCAAATGTGAGGCT 239
DDB 340 AACCCAAATGTGAGGCT 449
OY 240 CTCCT 299
DDB 450 CTCCT 509
OY 300 GAGCTGAGGAGGCT 359
DDB 630 GAGCTGAGGAGGCT 569
OY 360 ACCCTGTGAGGCT 419
DDB 570 ACCCTGTGAGGCT 629
OY 420 TTTTGTGAGGCT 479
DDB 630 TTTTGTGAGGCT 689
OY 480 CTTAGCAATCTATTG 495
DDB 690 CTTAGCAATCTATTG 705

RESULT 15

B0212589

LOCUS B0212589

DEFINITION 5', mRNA sequence.

ACCESSION B0212589

VERSION B0212589.1

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Homo sapiens

REFERENCE 1. B0212589

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)

TITLE Unpublished

JOURNAL Unpublished

COMMENT Contact: Robert Strassburg, Ph.D.
Tissue Procurement: ATCC/DC/PTP
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMML)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LMML at:
http://image.llnl.gov
Plate: LMML3368 row: n column: 20

High quality sequence stop: 636.

Location/Qualifiers

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:6093827"

/lab_host="DH10B (phage-resistant)"

/note="Organ: Skin; Vector: pGW-SPORE6; Site: 1. Melt; Average insert size: 2 kb. Library constructed by Life Technologies."

BASE COUNT 194 a 247 c 190 g 216 t

ORIGIN

Query Match 95.9%; Score 480.4; DB 13; Length 847;
Best Local Similarity 95.6%; Pred. No. 9.6e-129;
Matches 495; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

OY 1 CTCCTCAGCTGAACCAAAATATTACAAATTCGCCAGACACTCTCTCGAGGCTCTCG 60
DDB 265 CTCCTCAGCTGAACCAAAATATTACAAATTCGCCAGACACTCTCTCGAGGCTCTCG 324
OY 61 AGAGGACGACGAGGAGGCT 120
DDB 325 AGAGGACGACGAGGAGGCT 184
OY 121 CTCCT 180
DDB 385 CTCCT 444
OY 181 ACCCAAAATGTGAGGCT 240
DDB 445 ACCCAAAATGTGAGGCT 504
OY 241 CTCCTCAGCT 500
DDB 505 CTCCTCAGCT 564
OY 301 MACTGTGAGGCT 600
DDB 565 MACTGTGAGGCT 624
OY 361 CTCCTGTGAGGCT 419
DDB 625 CTCCTGTGAGGCT 684
OY 420 TTTTGTGAGGCT 479
DDB 685 TTTTGTGAGGCT 744
OY 480 CTTAGCAATCTATTG 501
DDB 745 CTTAGCAATCTATTG 766

Search completed: August 11, 2003, 14:59:33

Job time: 2'007 secs


```

Oy 1 CTCCTCAGCTGAAACCAAAATTAATTAATTCGCGAGACAGCTCTCTGAGGCGCTCTGCG 60
Db 980 CTCCTCAGCTGAAACCAAAATTAATTAATTCGCGAGACAGCTCTCTGAGGCGCTCTGCG 1039
Oy 61 AGAGAGCAGACAGACAGCGCTCGGCGCAGAGATCTCATTAAGAGTAAGTCAATG 120
Db 1040 AGAGAGCAGACAGACAGCGCTCGGCGCAGAGATCTCATTAAGAGTAAGTCAATG 1039
Oy 121 TCTCTCTCTCTTAATTAAGTGGAGTCTCATTAATTAAGAGAGATTAATCTCCCTTTTA 180
Db 1100 TCTCTCTCTCTTAATTAAGTGGAGTCTCATTAATTAAGAGAGATTAATCTCCCTTTTA 1159
Oy 181 ACCCAATATGAGTGCGGCGCAGAGAGTCTCTGAGAGCTTTTGACCGAGGTTTACCGAGAGC 240
Db 1160 ACCCAATATGAGTGCGGCGCAGAGAGTCTCTGAGAGCTTTTGACCGAGGTTTACCGAGAGC 1219
Oy 241 CTGCTCCCAACTCATGTCGAAGTCCCTGAGAGCGCTCTCTGACAGCGAGTTCACAGCGAGGTCAGG 300
Db 1220 CTGCTCCCAACTCATGTCGAAGTCCCTGAGAGCGCTCTCTGACAGCGAGTTCACAGCGAGGTCAGG 1279
Oy 301 AGCTGCGGAGGCTTCTAGAGCTTTTCTATGATGGGCTCTGCGCAGAGAGCTCTCTCTCGAA 360
Db 1380 AGCTGCGGAGGCTTCTAGAGCTTTTCTATGATGGGCTCTGCGCAGAGAGCTCTCTCTCGAA 1339
Oy 361 CCTGTATAGGCGTGGTTTAAAGAGTTTATGATGGTTCCTGAGAGTCTTTAGTACGCT 420
Db 1340 CCTGTATAGGCGTGGTTTAAAGAGTTTATGATGGTTCCTGAGAGTCTTTAGTACGCT 1399
Oy 421 TTGCTGAGGCGCGAGCTGACAGAGATCTTACAGAGAGATTTGACAGATCTGAGAGC 480
Db 1400 TTGCTGAGGCGCGAGCTGACAGAGATCTTACAGAGAGATTTGACAGATCTGAGAGC 1459
Oy 481 TTAGCAATCTATTGCAACT 501
Db 1460 TTAGCAATCTATTGCAACT 1480

```

RESULT 2
US-08-712-709-6
Sequence 6, Application US/08712709
Patent No. 6045792

GENERAL INFORMATION:

```

APPLICANT: Au-Young, Janice
APPLICANT: Guegler, Karl J.
TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304

```

COMPUTER READABLE FORM:

```

MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA: US/08712709
FILLING COLOR NUMBER: 1
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
TELEPHONE: 415-855-0555
TELECOMMUNICATION INFORMATION:
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE LENGTH: 2311 base pairs

```

```

TYPE: nucleic acid
STRANDEDNESS: single
MOLECULE TYPE: cDNA
IMMEDIATE SOURCE:
LIBRARY:
CLONE: Consensus
US-08-712-709-6

```

Query Match

```

Best local Similarity 99.7%: Score 499.4; DB 2: Length 2311;
Matches 500; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 1 CTCCTCAGCTGAAACCAAAATTAATTAATTCGCGAGACAGCTCTCTGAGGCGCTCTGCG 60
Db 980 CTCCTCAGCTGAAACCAAAATTAATTAATTCGCGAGACAGCTCTCTGAGGCGCTCTGCG 1006
Oy 61 AGAGAGCAGACAGACAGCGCTCGGCGCAGAGATCTCATTAAGAGTAAGTCAATG 120
Db 947 CTCCTCAGCTGAAACCAAAATTAATTAATTCGCGAGACAGCTCTCTGAGGCGCTCTGCG 1066
Oy 121 TCTCTCTCTCTTAATTAAGTGGAGTCTCATTAATTAAGAGAGATTAATCTCCCTTTTA 180
Db 1007 AGAGAGCAGACAGACAGCGCTCGGCGCAGAGATCTCATTAAGAGTAAGTCAATG 1066
Oy 181 ACCCAATATGAGTGCGGCGCAGAGAGTCTCTGAGAGCTTTTGACCGAGGTTTACCGAGAGC 240
Db 1127 ACCCAATATGAGTGCGGCGCAGAGAGTCTCTGAGAGCTTTTGACCGAGGTTTACCGAGAGC 1186
Oy 241 CTGCTCCCAACTCATGTCGAAGTCCCTGAGAGCGCTCTCTGACAGCGAGTTCACAGCGAGGTCAGG 300
Db 1187 CTGCTCCCAACTCATGTCGAAGTCCCTGAGAGCGCTCTCTGACAGCGAGTTCACAGCGAGGTCAGG 1246
Oy 301 AGCTGCGGAGGCTTCTAGAGCTTTTCTATGATGGGCTCTGCGCAGAGAGCTCTCTCTCGAA 360
Db 1247 AGCTGCGGAGGCTTCTAGAGCTTTTCTATGATGGGCTCTGCGCAGAGAGCTCTCTCTCGAA 1306
Oy 361 CCTGTATAGGCGTGGTTTAAAGAGTTTATGATGGTTCCTGAGAGTCTTTAGTACGCT 420
Db 1307 CCTGTATAGGCGTGGTTTAAAGAGTTTATGATGGTTCCTGAGAGTCTTTAGTACGCT 1466
Oy 421 TTGCTGAGGCGCGAGCTGACAGAGATCTTACAGAGAGATTTGACAGATCTGAGAGC 480
Db 1367 TTGCTGAGGCGCGAGCTGACAGAGATCTTACAGAGAGATTTGACAGATCTGAGAGC 1426
Oy 481 TTAGCAATCTATTGCAACT 501
Db 1427 TTAGCAATCTATTGCAACT 1447

```

RESULT 3

```

US-09-111-444-6
Sequence 6, Application US/0911444
Patent No. 6045792
GENERAL INFORMATION:
APPLICANT: Au-Young, Janice
APPLICANT: Guegler, Karl J.
APPLICANT: Hawkins, Phillip R.
TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:

```

? APPLICATION NUMBER: US/09/111,444
 ? FILING DATE: 1998-01-14
 ? PRIORITY DATA: 08/712,709
 ? APPLICATION NUMBER: 08/712,709
 ? FILING DATE:
 ? ATTORNEY/AGENT INFORMATION:
 ? NAME: J. A. G. S.
 ? REGISTRATION NUMBER: 36,749
 ? REFERENCE/DOCKET NUMBER: PF-0118 US
 ? TELECOMMUNICATION INFORMATION:
 ? TELEPHONE: 415-851-0555
 ? TELEFAX: 415-845-4166
 ? INFORMATION FOR SEQ ID NO: 6:
 ? SEQUENCE CHARACTERISTICS:
 ? LENGTH: 2311 base pairs
 ? MOLECULE TYPE: single
 ? STRANDEDNESS: single
 ? TOPOLOGY: linear
 ? IMMEDIATE SOURCE: cDNA
 ? CLONE: Consensus
 ?

US-09-111-444-6
 Query Match 99.78; Score 499.4; DB 3; Length 2311;
 Best Local Similarity 99.88; Prod. No. 5.8e-161;
 Matches 500; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 ?
 ? 1 CTCTCCAGCTGAAACCAATATTACAAATTCGCGAGACACCTCTCGAGGAGCTCTGCG 60
 Db 947 CTCTCCAGCTGAAACCAATATTACAAATTCGCGAGACACCTCTCGAGGAGCTCTGCG 1006
 ?
 ? 61 AGAGAGACAGACGAAAGCGCTCGGGCGAAGATGACTTCATGAGAGATTAAGCATG 120
 Db 1007 AGAGAGACAGACGAAAGCGCTCGGGCGAAGATGACTTCATGAGAGATTAAGCATG 1066
 ?
 ? 121 TCTCTCTCTCTTAATTAAGTGGATGATCTCATTAATGAAGAGATTAAGCATG 180
 Db 1067 TCTCTCTCTCTTAATTAAGTGGATGATCTCATTAATGAAGAGATTAAGCATG 1126
 ?
 ? 181 ACCGAAATGAGATGAGCGGACAGAGGAGAGGAGATTTGACCGGAGTTACCAAGAG 240
 Db 1127 ACCGAAATGAGATGAGCGGACAGAGGAGAGGAGATTTGACCGGAGTTACCAAGAG 1186
 ?
 ? 241 CTGTGTCCCACTTCATTTGGCAAGTCCCTGACAGCGCTCTGTCACGAGAGGTCAAG 300
 Db 1187 CTGTGTCCCACTTCATTTGGCAAGTCCCTGACAGCGCTCTGTCACGAGAGGTCAAG 1246
 ?
 ? 301 AGCTCTCGAGAGCTTTCTTAGGCTTTTCTATGCGGCTCCACAGGAGTCTTCTCTGAA 360
 Db 1247 AGCTCTCGAGAGCTTTCTTAGGCTTTTCTATGCGGCTCCACAGGAGTCTTCTCTGAA 1306
 ?
 ? 361 CCGTGTGAGAGCTTGGTTTAAAGAGTTTATGATGTGTTTCCGAGTTGTTTATGAGCT 420
 Db 1307 CCGTGTGAGAGCTTGGTTTAAAGAGTTTATGATGTGTTTCCGAGTTGTTTATGAGCT 1366
 ?
 ? 421 TTGTGGTGAAGCCGACCTACAGAGACATCTACAGAGAGATTTGCACATCTCTGGAGC 480
 Db 1367 TTGTGGTGAAGCCGACCTACAGAGACATCTACAGAGAGATTTGCACATCTCTGGAGC 1426
 ?
 ? 481 TTAGCAATCTTAATGACACT 501
 Db 1427 TTAGCAATCTTAATGACACT 1447

RESULT 4
 US-09-541-228-6
 ? Sequence 6, Application US/09541228
 ? Patent No. 625707
 ? GENERAL INFORMATION:
 ? APPLICANT: Au-Young, Janice
 ? APPLICANT: Guejler, Karl J.
 ? APPLICANT: HawkIns, Phillip R.

? TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES
 ? NUMBER OF SEQUENCES: 9
 ? CORRESPONDENCE ADDRESS:
 ? STREET: 3174 Porter Drive
 ? CITY: Palo Alto
 ? STATE: CA
 ? ZIP: 94304
 ? COMPUTER READABLE FORM:
 ? MEDIUM TYPE: Diskette
 ? COMPUTER: IBM Compatible
 ? SOFTWARE: FASTSEQ Version 1.5
 ? CURRENT APPLICATION DATA:
 ? APPLICATION NUMBER: US/09/541,228
 ? PRIORITY DATA:
 ? PRIOR APPLICATION NUMBER: 08/712,709
 ? FILING DATE:
 ? ATTORNEY/AGENT INFORMATION:
 ? REGISTRATION NUMBER: 36,749
 ? REFERENCE/DOCKET NUMBER: PF-0118 US
 ? TELECOMMUNICATION INFORMATION:
 ? TELEPHONE: 415-851-0555
 ? TELEFAX: 415-845-4166
 ? INFORMATION FOR SEQ ID NO: 6:
 ? SEQUENCE CHARACTERISTICS:
 ? LENGTH: 2311 base pairs
 ? MOLECULE TYPE: single
 ? STRANDEDNESS: single
 ? TOPOLOGY: linear
 ? IMMEDIATE SOURCE: cDNA
 ? CLONE: Consensus

US-09-541-228-6
 Query Match 99.78; Score 499.4; DB 3; Length 2311;
 Best Local Similarity 99.88; Prod. No. 5.8e-161;
 Matches 500; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 ?
 ? 1 CTCTCCAGCTGAAACCAATATTACAAATTCGCGAGACACCTCTCGAGGAGCTCTGCG 60
 Db 947 CTCTCCAGCTGAAACCAATATTACAAATTCGCGAGACACCTCTCGAGGAGCTCTGCG 1006
 ?
 ? 61 AGAGAGACAGACGAAAGCGCTCGGGCGAAGATGACTTCATGAGAGATTAAGCATG 120
 Db 1007 AGAGAGACAGACGAAAGCGCTCGGGCGAAGATGACTTCATGAGAGATTAAGCATG 1066
 ?
 ? 121 TCTCTCTCTCTTAATTAAGTGGATGATCTCATTAATGAAGAGATTAAGCATG 180
 Db 1067 TCTCTCTCTCTTAATTAAGTGGATGATCTCATTAATGAAGAGATTAAGCATG 1126
 ?
 ? 181 ACCGAAATGAGATGAGCGGACAGAGGAGAGGAGATTTGACCGGAGTTACCAAGAG 240
 Db 1127 ACCGAAATGAGATGAGCGGACAGAGGAGAGGAGATTTGACCGGAGTTACCAAGAG 1186
 ?
 ? 241 CTGTGTCCCACTTCATTTGGCAAGTCCCTGACAGCGCTCTGTCACGAGAGGTCAAG 300
 Db 1187 CTGTGTCCCACTTCATTTGGCAAGTCCCTGACAGCGCTCTGTCACGAGAGGTCAAG 1246
 ?
 ? 301 AGCTCTCGAGAGCTTTCTTAGGCTTTTCTATGCGGCTCCACAGGAGTCTTCTCTGAA 360
 Db 1247 AGCTCTCGAGAGCTTTCTTAGGCTTTTCTATGCGGCTCCACAGGAGTCTTCTCTGAA 1306
 ?
 ? 361 CCGTGTGAGAGCTTGGTTTAAAGAGTTTATGATGTGTTTCCGAGTTGTTTATGAGCT 420
 Db 1307 CCGTGTGAGAGCTTGGTTTAAAGAGTTTATGATGTGTTTCCGAGTTGTTTATGAGCT 1366
 ?
 ? 421 TTGTGGTGAAGCCGACCTACAGAGACATCTACAGAGAGATTTGCACATCTCTGGAGC 480

Db 1367 TTGTGGAGGCCAGCTGACAGACATCTTACAGAGANTTTCACATCTCTGGAGC 1426
 Oy 481 TTAGCAATCTATTGCACT 501
 Db 1427 TTAGCAATCTATTGCACT 1447

RESULT 5
 US-09-016-434-772

; Sequence 772, Application US/09016434
 ; Patent No. 6500938
 ; GENERAL INFORMATION:
 ; APPLICANT: 3MCS Au-Young
 ; APPLICANT: Jeffrey J. Sellhammer
 ; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
 ; NAME OF INVENTOR: JAMES E. FARMY GENE EXPRESSION
 ; NUMBER OF SEQUENCES: 149
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
 ; STREET: 1774 PORTER DRIVE
 ; CITY: PALO ALTO
 ; STATE: CALIFORNIA
 ; COUNTRY: USA
 ; ZIP: 94304
 ; COMMUNICATION INFORMATION:
 ; MEDIUM TYPE: FLOPPY disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PATENT RELEASE 6.1 for Windows/MS-DOS 6.2
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/016,434
 ; FILING DATE: HEREWITH
 ; CLASSIFICATION: DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; CLASSIFICATION:
 ; NAME: 3MCS Au-Young
 ; NAME: Jeffrey J. Sellhammer
 ; REGISTRATION NUMBER: 37,071
 ; REFERENCE/DOCKET NUMBER: PA-0002 US
 ; TELEPHONE: (650) 955-0555
 ; TELEFAX: (650) 845-4166
 ; INFORMATION FOR SEQ ID NO: 772:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2311 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; IMMEDIATE SOURCE:
 ; LIBRARY: MCLR20701
 ; CLONE: 477245
 ; US-09-016-434-772

Query Match 99.7%; Score 499.4; DB 4; Length 2311;
 Best Local Similarity 99.8%; Pred. No. 5.8e-161;
 Matches 500; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Oy 1 CTCCTCCAGCTGAACCAATATACAAATTCGGACAGCACTCTCGAGGGCTCTCGC 60
 Db 947 CTCCTCCAGCTGAACCAATATACAAATTCGGACAGCACTCTCGAGGGCTCTCGC 1006
 Oy 61 AGAGAGCAGCAGCAGCAGCCTCGGGCCAGAGATGACTCTCATGTGATTAAGCATCTG 120
 Db 1007 AGAGAGCAGCAGCAGCAGCCTCGGGCCAGAGATGACTCTCATGTGATTAAGCATCTG 1066
 Oy 121 TCTCTCTCTCTTAATACGCGAGATCTCTTAATAGAGATTAAGTCCGCTTTTA 180
 Db 1067 TCTCTCTCTCTTAATACGCGAGATCTCTTAATAGAGATTAAGTCCGCTTTTA 1126
 Oy 181 AGCAATAGTGTGAGTGGGCCAGCAGCTTADGGAGCTTTGACCCCGAGTTTACGAGAGC 240

Db 1127 ACCCAATGTGATGTGGCCAGCACTTACGAGCATTTGACCCGCGAGTTTACGAGAGC 1186
 Oy 241 CTGTGCCCACTCTCATTTGCAAGTCCCTGACAGAGCTCTCTGTGACAGCAGAGTTCAG 300
 Db 1187 CTGTGCCCACTCTCATTTGCAAGTCCCTGACAGAGCTCTCTGTGACAGCAGAGTTCAG 1246
 Oy 301 AGCTCCGAGGAGCTTTCTTAGCTTTCTTATGTGGCTCCGAGAGCTCTTCTCTCTGAA 360
 Db 1247 AGCTCCGAGGAGCTTTCTTAGCTTTCTTATGTGGCTCCGAGAGCTCTTCTCTCTGAA 1306
 Oy 361 CCTGTGTAAGGGCTTTGTTTAAAGATTTTATGTGTGTTTCGAGATGTTTATTTAGCT 420
 Db 1307 CCTGTGTAAGGGCTTTGTTTAAAGATTTTATGTGTGTTTCGAGATGTTTATTTAGCT 1366
 Oy 421 TTTGTGGAGGCCCACTGACAGACATCTTACAGAGAGATTTTCACATCTCTCGAGC 480
 Db 1367 TTTGTGGAGGCCCACTGACAGACATCTTACAGAGAGATTTTCACATCTCTCGAGC 1426
 Oy 481 TTAGCAATCTATTGCACT 501
 Db 1427 TTAGCAATCTATTGCACT 1447

RESULT 6
 US-08-700-575-4
 ; Sequence 4, Application US/08700575
 ; Patent No. 5817479
 ; GENERAL INFORMATION:
 ; APPLICANT: Au-Young, Janice
 ; APPLICANT: Phillip K.
 ; APPLICANT: Hawkins, Phillip K.
 ; APPLICANT: Wilde, Craig G.
 ; TITLE OF INVENTION: NOVEL HUMAN KINASE HOMOLOGS
 ; NUMBER OF SEQUENCES: 45
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
 ; STREET: 3174 PORTER DRIVE
 ; CITY: PALO ALTO
 ; STATE: CALIFORNIA
 ; COUNTRY: USA
 ; ZIP: 94304
 ; COMMUNICATION INFORMATION:
 ; MEDIUM TYPE: FLOPPY disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/700,575
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; NAME: AU-YOUNG, JANICE
 ; NAME: HAWKINS, PHILIP J.
 ; REGISTRATION NUMBER: 36749
 ; REFERENCE/DOCKET NUMBER: SP-100 US
 ; TELEPHONE: US-455-0555
 ; TELEFAX: 415-845-4166
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1453 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; IMMEDIATE SOURCE: cDNA
 ; LIBRARY: T1P-1 Phorbol 1PS
 ; CLONE: 12702
 ; US-08-700-575-4

Query Match 22.4%; Score 112; DB 1; Length 257;
 Best Local Similarity 93.1%; Pred. No. 1.3e-28;
 Matches 162; Conservative 0; Mismatches 5; Indels 7; Gaps 4;

```

Qy 31 CCGCAAGACAGCTCTGGAGCGCTCTGGAGAGAGAGACAGCAAGCGCTGGGGCCA 90
Db 1 CCGCAAGACAGCTCTGGAGCGCTCTGGAGAGAGAGACAGCAAGCGCTGGGGCCA 55
Qy 91 AGATGAGCTCTGTGGAGATTAAGCATGCTCTCTCTCTTAATTAAGTGGGATGATC 150
Db 56 AGATGAGCTCTGTGGAGATTAAGCATGCTCTCTCTCTTAATTAAGTGGGATGATC 114
Qy 151 TCATTAAATGAAGAGATTACTCCCGCTTTTAACTCCCAATGTAGTGGGCCCAAG 204
Db 115 TCATTAAATGAAGAGATTACTCCCGCTTTTAACTCCCAATGTAGTGGGCCCAAG 167

RESULT 7
US-09-474-922A-2
; Sequence 70, Application US/09474922A
; Patent No. 6187586
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; INVENTOR: Lex M. Cowsett
; APPLICANT: Richard A. Rolin
; TITLE OF INVENTION: ANTISENSE MODULATION OF AAT-3 EXPRESSION
; FILE REFERENCE: RTS-0036
; CURRENT APPLICATION NUMBER: US/09/474,922A
; CURRENT FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 2
; LENGTH: 387
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-474-922A-2

```

```

Query Match
Best Local Similarity 9.6%; Score 48.2; DB 3; Length 387;
Matches 89; Conservative 0; Mismatches 68; Indels 0; Gaps 0;
Qy 93 GATGACTGTGAGAGATTAGCATGATGCTCTCTCTTAATTAAGTGGGATGATC 152
Db 219 GATGACGCAAGAAGATTATGAGACAGAGTCTCTCTGTGATTAAGTGGGATGATC 278
Qy 153 ATTATTAAGAGATTACTCCCGCTTTTAACTCCCAATGTAGTGGGCCCAAGTACGG 212
Db 279 ATTATTAAGAGATTACTCCCGCTTTTAACTCCCAATGTAGTGGGCCCAAGTACGA 338
Qy 213 CACTTTCGCCCGAGTTTACCGAGAGCGCTGTCGCCCA 249
Db 339 TATTATTGAAGATTATGCTGACATCTTACACA 375

```

```

RESULT 8
US-09-417-197-70
; Sequence 70, Application US/09417197
; Patent No. 6518021
; GENERAL INFORMATION:
; APPLICANT: Oligo Therapeutics, et al.
; TITLE OF INVENTION: A Method For Extracting Quantitative Information Relating To An
; FILE REFERENCE: 3759-0110P
; CURRENT APPLICATION NUMBER: US/09/417,197
; CURRENT FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 1
; LENGTH: 231
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: PKB-EKFP fusion
; NAME/KEY: COS
; LOCATION: (1)..(2178)
; LOCATOR: Lex M. Cowsett
US-09-417-197-70

```

```

Query Match
Best Local Similarity 9.6%; Score 48; DB 4; Length 2181;
Matches 114; Conservative 0; Mismatches 110; Indels 0; Gaps 0;
Qy 54 CTCCTCGAGAGACAGACAGCAAGCGCTGGGGCCCAAGAGTACTGCTCATGAGATTAAG 114
Db 1150 CTCGAAGAGACCCCAAGCAAGCAAGCTTTGGCGGGGCTCGAGAGAGCCCAAGAAATCATG 1209
Qy 114 ATGATGCTGCTCTCTCTCTCTTAATTAAGTGGGATGATCTTAATTAAGAAATTAAGTCC 173
Db 1210 CAGCATTCCTCTTTGGCCCGTATCTGTGTGGACAGCGGTGACGAGAGAACTTACACCA 1269
Qy 174 CTTTATTAACCAAAATGTGATGTGGGCGCAAGAGCTACGAGCACTTCACTCCCAATTAAG 233
Db 1270 CCGCTTCAGGCCCAAGGTACATCTCGAGACTGACACAGCTATTTGATGAGATTTACG 1329
Qy 234 GAGAGCGCTGCGCCCAAGCACTCTGTGTGAGTATCCCTGTGAGAGCGT 277
Db 1330 GCCCAGATGATCACCATCACACACCACTGACCAAGATGACAGCAT 1773

```

```

RESULT 9
US-09-417-197-138
; Sequence 138, Application US/09417197
; Patent No. 6518021
; GENERAL INFORMATION:
; APPLICANT: Oligo Therapeutics, et al.
; TITLE OF INVENTION: A Method For Extracting Quantitative Information Relating To A
; FILE REFERENCE: 3759-0110P
; CURRENT APPLICATION NUMBER: US/09/417,197
; CURRENT FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 138
; LENGTH: 2184
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: EGFP-PKB fusion
; NAME/KEY: COS
; LOCATION: (1)..(2181)
; LOCATOR: Lex M. Cowsett
US-09-417-197-138

```

```

Query Match
Best Local Similarity 9.6%; Score 48; DB 4; Length 2184;
Matches 114; Conservative 0; Mismatches 110; Indels 0; Gaps 0;
Qy 54 CTCCTCGAGAGACAGACAGCAAGCGCTGGGGCCCAAGAGTACTGCTCATGAGATTAAG 113
Db 1891 CTCGAAGAGACCCCAAGCAAGCAAGCTTTGGCGGGGCTCGAGAGAGCCCAAGAAATCATG 1950
Qy 114 AGTCACTGCTCTCTCTCTCTTAATTAAGTGGGATGATCTTAATTAAGAAATTAAGTCC 173
Db 1951 CAGCATGCTCTCTTTGGCCCGTATCTGTGTGGACAGCGGTGACGAGAGAACTTACACCA 2010
Qy 174 CTTTATTAACCAAAATGTGATGTGGGCGCAAGAGCTACGAGCACTTCACTCCCAATTAAG 233
Db 2011 CCGCTTCAGGCCCAAGGTACATCTCGAGACTGACACAGCTATTTGATGAGATTTACG 2070
Qy 234 GAGAGCGCTGCGCCCAAGCACTCTGTGTGAGTATCCCTGTGAGAGCGT 277
Db 2071 GCCCAGATGATCACCATCACACACCGCTGACCAAGATGACAGCAT 2114

```

```

RESULT 10
US-09-212-771-1
; Sequence 1, Application US/09212771
; Patent No. 6518021
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowsett
US-09-212-771-1

```

; TITLE OF INVENTION: ANTISENSE MODULATION OF AKT-1 EXPRESSION

; FILE REFERENCE: RTS-0034

; CURRENT APPLICATION NUMBER: US/09/212.771

: CURRENT FILING DATE: 1998-12-16
 : CURRENT AFFIDAVIT NUMBER: 03/0

: CURRENT FILING DATE: 1998-12-10
 : NUMBER OF SEQ ID NOS: 47

; NUMBER OF SEQ
; SEQ ID NO 1

```

; SEQ ID NO 1
: LENGTH: 3610

```

; LENGTH: 2610

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

```

CURRENT APPLICATION DATA:
  FILING DATE: 07-OCT-1998
  CLASSIFICATION: <unknown>
  PRIOR APPLICATION DATA:
    FILING DATE: 07-OCT-1998
    CLASSIFICATION: <unknown>
    FILING DATE: 07-OCT-1998
    CLASSIFICATION: <unknown>
  ATTORNEY/AGENT INFORMATION:
    NAME: Monaco, Daniel
    ADDRESS: 30, 480
    TELECOMMUNICATION INFORMATION:
      REFERENCE/DOCKET NUMBER: 7933-33 PC
      TELEPHONE: (215) 568-8383
      TELEFAX: (215) 568-8349
    INFORMATION FOR SEQ ID NO: 3:
      SEQUENCE CHARACTERISTICS:
        LENGTH: 1599 base pairs
        MOLECULE TYPE: single
        STANDARDS: single
        TOPOLOGY: linear
      SEQUENCE DESCRIPTION: SEQ ID NO: 3:
        US-09-167-1222-3
          Query Match
          Best Local Similarity 52.5%; Pred. No. 1.4e-05;
          Matches 126; Conservative 0; Mismatches 111; Indels 3; Gaps 1;
          QY 41 CTCCTCTGGAGGCGCTCTCGAAGCAGGAGCAGCAAGCGCT--CGGGCGCAAGATCA 97
          DB 1224 CTCCTCTGGAGGCGCTCTCGAAGCAGGAGCAGCAAGCGCTGGTGGGGGCCACAC 1283
          QY 98 CTCGATGGAGATTAAGATCATGTCTCTCTCTTAATCTACTGGGATGATCTATTAA 157
          DB 1284 CTCGATGGAGATTAAGATCATGTCTCTCTCTTAATCTACTGGGATGATCTATTAA 1343
          QY 158 TAAGAGATTAAGATCATGTCTCTCTCTTAATCTACTGGGATGATCTATTAA 217
          DB 1344 TAAGAGATTAAGATCATGTCTCTCTCTTAATCTACTGGGATGATCTATTAA 1403
          QY 218 TGACCGGAGTTTACGAGAGCGCTGTCCCACTCTCACTCTGCTGCTGCTGCTGCTGCT 277
          DB 1404 TGACCGGAGTTTACGAGAGCGCTGTCCCACTCTCACTCTGCTGCTGCTGCTGCTGCT 1463
          RESULT 14
          US-08-474-379C-25
          Sequence 25, Application US/08474379C
          Patent No. 6069240
          APPLICANT: Wiegler, Michael H.
          APPLICANT: Wiegler, Michael H.
          TITLE OF INVENTION: CLONING BY COMPLEMENTATION AND RELATED PROCESSES
          NUMBER OF SEQUENCES: 88
          CORRESPONDENCE ADDRESS:
            ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borum
            STREET: 233 South Wacker Drive/6300 Sears Tower
            CITY: Chicago
            STATE: Illinois
            COUNTRY: United States of America
            ZIP: 60606-6402
          COMPUTER READABLE FORM:
            MEDIUM TYPE: floppy disk
            COMPUTER: IBM PC compatible
            SOFTWARE: PC-DOS/MS-DOS
            OPERATING SYSTEM: PC-DOS/MS-DOS
            CURRENT APPLICATION DATA:
              FILING DATE: 07-JUN-1995
              CLASSIFICATION: 435
            PRIOR APPLICATION DATA:
              FILING DATE: 07-JUN-1995
              CLASSIFICATION: 435
          RESULT 15
          US-09-146-249A-25
          Sequence 25, Application US/09146249A
          Patent No. 6069240
          APPLICANT: Wiegler, Michael H.
          APPLICANT: Wiegler, Michael H.
          TITLE OF INVENTION: Cloning by Complementation and Related Processes
          NUMBER OF SEQUENCES: 85
          CORRESPONDENCE ADDRESS:
            ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borum
            STREET: 233 South Wacker Drive/6300 Sears Tower
            CITY: Chicago
            STATE: Illinois
            COUNTRY: United States of America
            ZIP: 60606-6402
          COMPUTER READABLE FORM:
            MEDIUM TYPE: floppy disk
            COMPUTER: IBM PC compatible
            SOFTWARE: PC-DOS/MS-DOS
            OPERATING SYSTEM: PC-DOS/MS-DOS
            CURRENT APPLICATION DATA:
              FILING DATE: 07-JUN-1995
              CLASSIFICATION: 435
            PRIOR APPLICATION DATA:
              FILING DATE: 07-JUN-1995
              CLASSIFICATION: 435
          PRIOR APPLICATION DATA:
            FILING DATE: 01-MAR-1994
            CLASSIFICATION: 435
            FILING DATE: 19-APR-1991
            CLASSIFICATION: 435
            FILING DATE: 19-APR-1991
            CLASSIFICATION: 435
            NAME: Clough, David W.
            ADDRESS: 27866/32771
            TELECOMMUNICATION INFORMATION:
              REFERENCE/DOCKET NUMBER: 27866/32771
              TELEPHONE: (312) 474-6300
              TELEFAX: (312) 474-6300
            INFORMATION FOR SEQ ID NO: 25:
              SEQUENCE CHARACTERISTICS:
                LENGTH: 1273 base pairs
                MOLECULE TYPE: cDNA
                STANDARDS: single
                TOPOLOGY: linear
              SEQUENCE DESCRIPTION: SEQ ID NO: 25:
                US-08-474-379C-25
                  Query Match
                  Best Local Similarity 57.1%; Pred. No. 3.7e-05;
                  Matches 93; Conservative 0; Mismatches 75; Indels 1; Gaps 1;
                  QY 93 GATCTCTCTGAGATTAAGATCATGTCTCTCTCTTAATCTACTGGGATGATCTATTAA 152
                  DB 922 GATCTCTCTGAGATTAAGATCATGTCTCTCTCTTAATCTACTGGGATGATCTATTAA 981
                  QY 153 ATTANTAGAGATTAAGATCATGTCTCTCTCTTAATCTACTGGGATGATCTATTAA 212
                  DB 982 ATTANTAGAGATTAAGATCATGTCTCTCTCTTAATCTACTGGGATGATCTATTAA 1040
                  QY 213 CACTCTGAGGATTAAGATCATGTCTCTCTCTTAATCTACTGGGATGATCTATTAA 265
                  DB 1041 TATTTGATCTGAGTCTACTCTCTCTCTTAATCTACTGGGATGATCTATTAA 1097
          RESULT 16
          US-09-146-249A-25
          Sequence 25, Application US/09146249A
          Patent No. 6069240
          APPLICANT: Wiegler, Michael H.
          APPLICANT: Wiegler, Michael H.
          TITLE OF INVENTION: Cloning by Complementation and Related Processes
          NUMBER OF SEQUENCES: 85
          CORRESPONDENCE ADDRESS:
            ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borum
            STREET: 233 South Wacker Drive/6300 Sears Tower
            CITY: Chicago
            STATE: Illinois
            COUNTRY: United States of America
            ZIP: 60606-6402
          COMPUTER READABLE FORM:
            MEDIUM TYPE: floppy disk
            COMPUTER: IBM PC compatible
            SOFTWARE: PC-DOS/MS-DOS
            OPERATING SYSTEM: PC-DOS/MS-DOS
            CURRENT APPLICATION DATA:
              FILING DATE: 07-JUN-1995
              CLASSIFICATION: 435
            PRIOR APPLICATION DATA:
              FILING DATE: 07-JUN-1995
              CLASSIFICATION: 435
          PRIOR APPLICATION DATA:
            FILING DATE: 01-MAR-1994
            CLASSIFICATION: 435
            FILING DATE: 19-APR-1991
            CLASSIFICATION: 435
            FILING DATE: 19-APR-1991
            CLASSIFICATION: 435
            NAME: Clough, David W.
            ADDRESS: 27866/32771
            TELECOMMUNICATION INFORMATION:
              REFERENCE/DOCKET NUMBER: 27866/32771
              TELEPHONE: (312) 474-6300
              TELEFAX: (312) 474-6300
            INFORMATION FOR SEQ ID NO: 25:
              SEQUENCE CHARACTERISTICS:
                LENGTH: 1273 base pairs
                MOLECULE TYPE: cDNA
                STANDARDS: single
                TOPOLOGY: linear
              SEQUENCE DESCRIPTION: SEQ ID NO: 25:
                US-08-474-379C-25

```

```

? REGISTRATION NUMBER: 36,107
? TELEPHONE: 312-474-6300
? TELEFAX: 312-474-0448
? TELEX: 25-3856
? INFORMATION: CDS ID NO. 25:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1273 base pairs
? TYPE: nucleic acid
? ORGANISM: single
? TOPLOC: 1
? MOLECULE TYPE: cDNA
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 1..1273
? US-09-146-245A-25

```

```

Query Match          9.0%: Score 45; DB 3; Length 1273;
Match Local Similarity 57.1%: Pred. No. 3.7e-05;
Matches 101; Conservative 0; Mismatches 75; Indels 1; Gaps 1;
QY 93 GATGACTCTGAGGATTAAAGTCGATGCTCTCTCTTAATTAAGTGGATGATCTC 152
DB 01111111111111111111111111111111111111111111111111111
QY 922 GATGAGCTGGAGAAATTAAGAGATCTCTCTCTTAATTAAGTGGATGATCTC 981
DB 01111111111111111111111111111111111111111111111111111
QY 153 ATTATAAGAGATTACTCCCTTTTAAACCAATGTGAGTGGGCCCAAGGCTACGG 212
DB 11111111111111111111111111111111111111111111111111111
QY 982 TTTAGAGAGAA-ATTCATCTGGCATTTTAACTGTGACGGCGGCGCTGAGATATC 1040
DB 11111111111111111111111111111111111111111111111111111
QY 213 CACTTTGACCCGAGTTTACCGAAGGCTGTGCCCACTCGATTGGCAAGTCCCT 269
DB 11111111111111111111111111111111111111111111111111111
QY 1041 TATTTTGATCCTGAGTTTACTGCAAAAGTCCCAAGAGATTACCTGGCATTCACCT 1097
DB 11111111111111111111111111111111111111111111111111111

```

Search completed: August 11, 2003, 15:00:58
Job time : 74 secs

source	1...2370	100.0%	Score	DB 6	Length	2370
BASE COUNT	636 a 517 c 513 g 704 t					
ORIGIN	/o-genism*-unknown*					
	Query Match	100.0%	100.0%	Score	2370	
	Best Local Similarity	100.0%	100.0%	Score	2370	
	Matches 2370	Conservative	0	Mismatches	0	Indels
						Gaps
OY	1 CAGGAGGAGGCTTAACGCTTTCTGCTCCGCCGCTGGTGTAGTGGGTGAAGAACTGAG	60				
DB	1 CAGGAGGAGGCTTAACGCTTTCTGCTCCGCCGCTGGTGTAGTGGGTGAAGAACTGAG	60				
OY	61 GCTGCTTAAGGCGACCTCTACTTACTCAGAGGATGGGCAATGGGCAATCTATCACTC	120				
DB	61 GCTGCTTAAGGCGACCTCTACTTACTCAGAGGATGGGCAATGGGCAATCTATCACTC	120				
OY	121 TCTGATGAGGCGACCTCTACTTACTCAGAGGATGGGCAATGGGCAATCTATCACTC	180				
DB	121 TCTGATGAGGCGACCTCTACTTACTCAGAGGATGGGCAATGGGCAATCTATCACTC	180				
OY	181 TATGATGATGAGGCGACCTCTACTTACTCAGAGGATGGGCAATGGGCAATCTATCACTC	240				
DB	181 TATGATGATGAGGCGACCTCTACTTACTCAGAGGATGGGCAATGGGCAATCTATCACTC	240				
OY	241 GAGCTTAATGATGAGGCGACCTCTACTTACTCAGAGGATGGGCAATGGGCAATCTATCACTC	300				
DB	241 GAGCTTAATGATGAGGCGACCTCTACTTACTCAGAGGATGGGCAATGGGCAATCTATCACTC	300				
OY	301 GCTGCTTAATGATGAGGCGACCTCTACTTACTCAGAGGATGGGCAATGGGCAATCTATCACTC	360				
DB	301 GCTGCTTAATGATGAGGCGACCTCTACTTACTCAGAGGATGGGCAATGGGCAATCTATCACTC	360				
OY	361 GCTGCTTAATGATGAGGCGACCTCTACTTACTCAGAGGATGGGCAATGGGCAATCTATCACTC	420				
DB	361 GCTGCTTAATGATGAGGCGACCTCTACTTACTCAGAGGATGGGCAATGGGCAATCTATCACTC	420				
OY	421 TATGATGATGAGGCGACCTCTACTTACTCAGAGGATGGGCAATGGGCAATCTATCACTC	480				
DB	421 TATGATGATGAGGCGACCTCTACTTACTCAGAGGATGGGCAATGGGCAATCTATCACTC	480				
OY	481 TATGATGATGAGGCGACCTCTACTTACTCAGAGGATGGGCAATGGGCAATCTATCACTC	540				
DB	481 TATGATGATGAGGCGACCTCTACTTACTCAGAGGATGGGCAATGGGCAATCTATCACTC	540				
OY	541 TATGATGATGAGGCGACCTCTACTTACTCAGAGGATGGGCAATGGGCAATCTATCACTC	600				
DB	541 TATGATGATGAGGCGACCTCTACTTACTCAGAGGATGGGCAATGGGCAATCTATCACTC	600				
OY	601 TATGATGATGAGGCGACCTCTACTTACTCAGAGGATGGGCAATGGGCAATCTATCACTC	660				
DB	601 TATGATGATGAGGCGACCTCTACTTACTCAGAGGATGGGCAATGGGCAATCTATCACTC	660				
OY	661 TATGATGATGAGGCGACCTCTACTTACTCAGAGGATGGGCAATGGGCAATCTATCACTC	720				
DB	661 TATGATGATGAGGCGACCTCTACTTACTCAGAGGATGGGCAATGGGCAATCTATCACTC	720				
OY	721 TATGATGATGAGGCGACCTCTACTTACTCAGAGGATGGGCAATGGGCAATCTATCACTC	780				
DB	721 TATGATGATGAGGCGACCTCTACTTACTCAGAGGATGGGCAATGGGCAATCTATCACTC	780				
OY	781 TATGATGATGAGGCGACCTCTACTTACTCAGAGGATGGGCAATGGGCAATCTATCACTC	840				
DB	781 TATGATGATGAGGCGACCTCTACTTACTCAGAGGATGGGCAATGGGCAATCTATCACTC	840				
OY	841 TATGATGATGAGGCGACCTCTACTTACTCAGAGGATGGGCAATGGGCAATCTATCACTC	900				
DB	841 TATGATGATGAGGCGACCTCTACTTACTCAGAGGATGGGCAATGGGCAATCTATCACTC	900				
OY	901 TATGATGATGAGGCGACCTCTACTTACTCAGAGGATGGGCAATGGGCAATCTATCACTC	960				
DB	901 TATGATGATGAGGCGACCTCTACTTACTCAGAGGATGGGCAATGGGCAATCTATCACTC	960				

61	CTCTTAAGGCGACCTCGACTACTACTGAGATGAGGGGGGATGGTGGCAATCTCATGGCT	120	1141	AGATTAATCTCCGCTTTTAACTTCAAATTTGAGTGGGGCGACGACGACTACGATCTTAC	1201
a					
b					
61	CTCTTAAGGCGACCTCGACTACTACTGAGATGAGGGGGGATGGTGGCAATCTCATGGCT	120	1141	AGATTAATCTCCGCTTTTAACTTCAAATTTGAGTGGGGCGACGACGACTACGATCTTAC	1201
a					
b					
121	TTCTATGAGCAGCAGAGGATGGGCTGACGACGACTTTATTCAGAGATATGCGAATACATCC	180	1201	CCGAGATCTCGAGAGATTTGATCCGCTTACTGACTGATGGCGACGATCCGCTGAC	1260
a					
b					
121	TTCTATGAGCAGCAGAGGATGGGCTGACGACGACTTTATTCAGAGATATGCGAATACATCC	180	1201	CCGAGATCTCGAGAGATTTGATCCGCTTACTGACTGATGGCGACGATCCGCTGAC	1260
a					
b					
181	TATGCGATCAAAACAGATGGATGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTG	240	1261	GTACAGCAGGCTGACGAGATGTGAGAGATCTTCTGAGCTTTGCTATGCTATGCTATG	1320
a					
b					
181	TATGCGATCAAAACAGATGGATGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTG	240	1261	GTACAGCAGGCTGACGAGATGTGAGAGATCTTCTGAGCTTTGCTATGCTATGCTATG	1320
a					
b					
241	GACCTATTGATGCAACACCTCTCTCTCCACAGCTCTCTCGCAATCAACCTATGGC	300	1321	AGTCACTCTTTCGCTGACGCTTGTGAGGCTTGTGAGGCTTGTGAGGCTTGTGAGGCT	1380
a					
b					
241	GACCTATTGATGCAACACCTCTCTCTCCACAGCTCTCTCGCAATCAACCTATGGC	300	1321	AGTCACTCTTTCGCTGACGCTTGTGAGGCTTGTGAGGCTTGTGAGGCTTGTGAGGCT	1380
a					
b					
301	GCTCTATTGATGCAACACCTCTCTCTCCACAGCTCTCTCGCAATCAACCTATGGC	360	1381	CGAATGTTTATGATGCTTGTGAGGCTTGTGAGGCTTGTGAGGCTTGTGAGGCTTGTG	1440
a					
b					
301	GCTCTATTGATGCAACACCTCTCTCTCCACAGCTCTCTCGCAATCAACCTATGGC	360	1381	CGAATGTTTATGATGCTTGTGAGGCTTGTGAGGCTTGTGAGGCTTGTGAGGCTTGTG	1440
a					
b					
361	GGGATGTTTGGAAAGGCTCTCTCTCCACAGCTCTCTCGCAATCAACCTATGGC	420	1441	TTGTCACATCTCTGAGGCTTGTGAGGCTTGTGAGGCTTGTGAGGCTTGTGAGGCTTGTG	1500
a					
b					
361	GGGATGTTTGGAAAGGCTCTCTCTCCACAGCTCTCTCGCAATCAACCTATGGC	420	1441	TTGTCACATCTCTGAGGCTTGTGAGGCTTGTGAGGCTTGTGAGGCTTGTGAGGCTTGTG	1500
a					
b					
421	AAAGTTTACGAGAGGCTCTCTCTCCACAGCTCTCTCGCAATCAACCTATGGC	480	1501	GGGATGTTTGGAAAGGCTCTCTCTCCACAGCTCTCTCGCAATCAACCTATGGC	1560
a					
b					
421	AAAGTTTACGAGAGGCTCTCTCTCCACAGCTCTCTCGCAATCAACCTATGGC	480	1501	GGGATGTTTGGAAAGGCTCTCTCTCCACAGCTCTCTCGCAATCAACCTATGGC	1560
a					
b					
481	CGGATGTTTGGAAAGGCTCTCTCTCCACAGCTCTCTCGCAATCAACCTATGGC	540	1561	GGGATGTTTGGAAAGGCTCTCTCTCCACAGCTCTCTCGCAATCAACCTATGGC	1620
a					
b					
481	CGGATGTTTGGAAAGGCTCTCTCTCCACAGCTCTCTCGCAATCAACCTATGGC	540	1561	GGGATGTTTGGAAAGGCTCTCTCTCCACAGCTCTCTCGCAATCAACCTATGGC	1620
a					
b					
541	CGGATGTTTGGAAAGGCTCTCTCTCCACAGCTCTCTCGCAATCAACCTATGGC	600	1621	GGGATGTTTGGAAAGGCTCTCTCTCCACAGCTCTCTCGCAATCAACCTATGGC	1680
a					
b					
541	CGGATGTTTGGAAAGGCTCTCTCTCCACAGCTCTCTCGCAATCAACCTATGGC	600	1621	GGGATGTTTGGAAAGGCTCTCTCTCCACAGCTCTCTCGCAATCAACCTATGGC	1680
a					
b					
601	CGGATGTTTGGAAAGGCTCTCTCTCCACAGCTCTCTCGCAATCAACCTATGGC	660	1681	GGGATGTTTGGAAAGGCTCTCTCTCCACAGCTCTCTCGCAATCAACCTATGGC	1740
a					
b					
601	CGGATGTTTGGAAAGGCTCTCTCTCCACAGCTCTCTCGCAATCAACCTATGGC	660	1681	GGGATGTTTGGAAAGGCTCTCTCTCCACAGCTCTCTCGCAATCAACCTATGGC	1740
a					
b					
661	CGGATGTTTGGAAAGGCTCTCTCTCCACAGCTCTCTCGCAATCAACCTATGGC	720	1741	GGGATGTTTGGAAAGGCTCTCTCTCCACAGCTCTCTCGCAATCAACCTATGGC	1800
a					
b					
661	CGGATGTTTGGAAAGGCTCTCTCTCCACAGCTCTCTCGCAATCAACCTATGGC	720	1741	GGGATGTTTGGAAAGGCTCTCTCTCCACAGCTCTCTCGCAATCAACCTATGGC	1800
a					
b					
721	AAATTTTGGAAAGGCTCTCTCTCCACAGCTCTCTCGCAATCAACCTATGGC	780	1801	GGGATGTTTGGAAAGGCTCTCTCTCCACAGCTCTCTCGCAATCAACCTATGGC	1860
a					
b					
721	AAATTTTGGAAAGGCTCTCTCTCCACAGCTCTCTCGCAATCAACCTATGGC	780	1801	GGGATGTTTGGAAAGGCTCTCTCTCCACAGCTCTCTCGCAATCAACCTATGGC	1860
a					
b					

188 CAAACACCCCTGAAGCTGAGTCACCACTCTTGAGAGTCTCCCAAGACCTCTGAGCTTA 247
 248 TGAAATCAACCCCTGAGCTGAGTCACCACTCTTGAGAGTCTCCCAAGACCTCTGAGCTTA 307
 248 TGAAATCAACCCCTGAGCTGAGTCACCACTCTTGAGAGTCTCCCAAGACCTCTGAGCTTA 307
 308 CAAATCTCTATGCTAAACACCTGAGCTGAGTCACCACTCTTGAGAGTCTCCCAAGACCT 367
 368 CAAATCTCTATGCTAAACACCTGAGCTGAGTCACCACTCTTGAGAGTCTCCCAAGACCT 367
 368 TCGAAGAGCTCTCTTACGACACACCTGAGCTGAGTCACCACTCTTGAGAGTCTCCCAAG 427
 428 TCGAAGAGCTCTCTTACGACACACCTGAGCTGAGTCACCACTCTTGAGAGTCTCCCAAG 427
 428 TCGAAGAGCTCTCTTACGACACACCTGAGCTGAGTCACCACTCTTGAGAGTCTCCCAAG 487
 488 TCGAAGAGCTCTCTTACGACACACCTGAGCTGAGTCACCACTCTTGAGAGTCTCCCAAG 547
 488 TCGAAGAGCTCTCTTACGACACACCTGAGCTGAGTCACCACTCTTGAGAGTCTCCCAAG 547
 548 CTAACAAATGCTACTTGTCTGACACACCTGAGCTGAGTCACCACTCTTGAGAGTCTCCCA 607
 548 CTAACAAATGCTACTTGTCTGACACACCTGAGCTGAGTCACCACTCTTGAGAGTCTCCCA 607
 608 AAGGAGACCTCTCTTACGACACACCTGAGCTGAGTCACCACTCTTGAGAGTCTCCCAAG 667
 608 AAGGAGACCTCTCTTACGACACACCTGAGCTGAGTCACCACTCTTGAGAGTCTCCCAAG 667
 668 CTTGGGCTACTGCTTACGACACACCTGAGCTGAGTCACCACTCTTGAGAGTCTCCCAAG 727
 668 CTTGGGCTACTGCTTACGACACACCTGAGCTGAGTCACCACTCTTGAGAGTCTCCCAAG 727
 728 TCTAGATTCAGAGGACACCTGAGCTGAGTCACCACTCTTGAGAGTCTCCCAAGACATTTG 787
 728 TCTAGATTCAGAGGACACCTGAGCTGAGTCACCACTCTTGAGAGTCTCCCAAGACATTTG 787
 788 AACACACACACACACCTGAGCTGAGTCACCACTCTTGAGAGTCTCCCAAGACATTTG 847
 788 AACACACACACACACCTGAGCTGAGTCACCACTCTTGAGAGTCTCCCAAGACATTTG 847
 848 TCTAGATTCAGAGGACACCTGAGCTGAGTCACCACTCTTGAGAGTCTCCCAAGACATTTG 907
 848 TCTAGATTCAGAGGACACCTGAGCTGAGTCACCACTCTTGAGAGTCTCCCAAGACATTTG 907
 908 AGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 967
 908 AGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 967
 968 TCTAGATTCAGAGGACACCTGAGCTGAGTCACCACTCTTGAGAGTCTCCCAAGACATTTG 1027
 968 TCTAGATTCAGAGGACACCTGAGCTGAGTCACCACTCTTGAGAGTCTCCCAAGACATTTG 1027
 1028 AGGCTCTCTCTGAGAGGACACCTGAGCTGAGTCACCACTCTTGAGAGTCTCCCAAGAC 1087
 1028 AGGCTCTCTCTGAGAGGACACCTGAGCTGAGTCACCACTCTTGAGAGTCTCCCAAGAC 1087
 1088 TTAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1147
 1088 TTAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1147
 1148 CTGCTCTCTCTTACGACACACCTGAGCTGAGTCACCACTCTTGAGAGTCTCCCAAGAC 1207
 1148 CTGCTCTCTCTTACGACACACCTGAGCTGAGTCACCACTCTTGAGAGTCTCCCAAGAC 1207
 1208 TTAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1267
 1208 TTAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1267
 1268 CAGCTCTCTGAGAGGACACCTGAGCTGAGTCACCACTCTTGAGAGTCTCCCAAGAC 1327

1268 CAGCTCTGAGAGGACCTGAGCTGAGTCACCACTCTTGAGAGTCTCCCAAGACCTCTGAG 1327
 1328 CTTCTCTCTGAGAGGACCTGAGCTGAGTCACCACTCTTGAGAGTCTCCCAAGACCTCTGAG 1387
 1328 CTTCTCTCTGAGAGGACCTGAGCTGAGTCACCACTCTTGAGAGTCTCCCAAGACCTCTGAG 1387
 1388 TTTAGTGAAGCTCTGAGCTGAGTCACCACTCTTGAGAGTCTCCCAAGACCTCTGAGAG 1447
 1388 TTTAGTGAAGCTCTGAGCTGAGTCACCACTCTTGAGAGTCTCCCAAGACCTCTGAGAG 1447
 1448 ATCTCTGAGAGCTCTGAGCTGAGTCACCACTCTTGAGAGTCTCCCAAGACCTCTGAGAG 1506
 1448 ATCTCTGAGAGCTCTGAGCTGAGTCACCACTCTTGAGAGTCTCCCAAGACCTCTGAGAG 1506
 1507 ATTCTCTCTGAGAGCTCTGAGCTGAGTCACCACTCTTGAGAGTCTCCCAAGACCTCTGAG 1566
 1507 ATTCTCTCTGAGAGCTCTGAGCTGAGTCACCACTCTTGAGAGTCTCCCAAGACCTCTGAG 1566
 1508 ATCTCTGAGAGCTCTGAGCTGAGTCACCACTCTTGAGAGTCTCCCAAGACCTCTGAGAG 1626
 1508 ATCTCTGAGAGCTCTGAGCTGAGTCACCACTCTTGAGAGTCTCCCAAGACCTCTGAGAG 1626
 1567 CTTCTGAGAGGACCTGAGCTGAGTCACCACTCTTGAGAGTCTCCCAAGACCTCTGAGAG 1685
 1567 CTTCTGAGAGGACCTGAGCTGAGTCACCACTCTTGAGAGTCTCCCAAGACCTCTGAGAG 1685
 1627 AC GTGCTCTGAGAGGACCTGAGCTGAGTCACCACTCTTGAGAGTCTCCCAAGACCTCT 1745
 1627 AC GTGCTCTGAGAGGACCTGAGCTGAGTCACCACTCTTGAGAGTCTCCCAAGACCTCT 1745
 1686 AATGCTCTCTGAGAGGACCTGAGCTGAGTCACCACTCTTGAGAGTCTCCCAAGACCTCT 1805
 1686 AATGCTCTCTGAGAGGACCTGAGCTGAGTCACCACTCTTGAGAGTCTCCCAAGACCTCT 1805
 1746 GTTCTCTGAGAGGACCTGAGCTGAGTCACCACTCTTGAGAGTCTCCCAAGACCTCTG 1867
 1746 GTTCTCTGAGAGGACCTGAGCTGAGTCACCACTCTTGAGAGTCTCCCAAGACCTCTG 1867
 1806 ATCTCTGAGAGGACCTGAGCTGAGTCACCACTCTTGAGAGTCTCCCAAGACCTCTGAG 1865
 1806 ATCTCTGAGAGGACCTGAGCTGAGTCACCACTCTTGAGAGTCTCCCAAGACCTCTGAG 1865
 1866 AATGCTCTCTGAGAGGACCTGAGCTGAGTCACCACTCTTGAGAGTCTCCCAAGACCTCT 1925
 1866 AATGCTCTCTGAGAGGACCTGAGCTGAGTCACCACTCTTGAGAGTCTCCCAAGACCTCT 1925
 1868 AATGCTCTCTGAGAGGACCTGAGCTGAGTCACCACTCTTGAGAGTCTCCCAAGACCTCT 1987
 1868 AATGCTCTCTGAGAGGACCTGAGCTGAGTCACCACTCTTGAGAGTCTCCCAAGACCTCT 1987
 1926 AAGCTTAACTAACTAACTAACTAACTAACTAACTAACTAACTAACTAACTAACTAACTAA 1985
 1926 AAGCTTAACTAACTAACTAACTAACTAACTAACTAACTAACTAACTAACTAACTAACTAA 1987
 1986 AAGAGCAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2045
 1986 AAGAGCAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2047
 2046 CAGCTCTGAGAGGACCTGAGCTGAGTCACCACTCTTGAGAGTCTCCCAAGACCTCTGAG 2105
 2046 CAGCTCTGAGAGGACCTGAGCTGAGTCACCACTCTTGAGAGTCTCCCAAGACCTCTGAG 2105
 2048 CAGCTCTGAGAGGACCTGAGCTGAGTCACCACTCTTGAGAGTCTCCCAAGACCTCTGAG 2107
 2048 CAGCTCTGAGAGGACCTGAGCTGAGTCACCACTCTTGAGAGTCTCCCAAGACCTCTGAG 2107
 2106 CAGCTCTGAGAGGACCTGAGCTGAGTCACCACTCTTGAGAGTCTCCCAAGACCTCTGAG 2165
 2106 CAGCTCTGAGAGGACCTGAGCTGAGTCACCACTCTTGAGAGTCTCCCAAGACCTCTGAG 2165
 2108 CAGCTCTGAGAGGACCTGAGCTGAGTCACCACTCTTGAGAGTCTCCCAAGACCTCTGAG 2167
 2108 CAGCTCTGAGAGGACCTGAGCTGAGTCACCACTCTTGAGAGTCTCCCAAGACCTCTGAG 2167
 2166 CTTGAGCTGAGAGGACCTGAGCTGAGTCACCACTCTTGAGAGTCTCCCAAGACCTCTGAG 2225
 2166 CTTGAGCTGAGAGGACCTGAGCTGAGTCACCACTCTTGAGAGTCTCCCAAGACCTCTGAG 2225
 2168 CTTGAGCTGAGAGGACCTGAGCTGAGTCACCACTCTTGAGAGTCTCCCAAGACCTCTGAG 2287
 2168 CTTGAGCTGAGAGGACCTGAGCTGAGTCACCACTCTTGAGAGTCTCCCAAGACCTCTGAG 2287
 2226 CAGCTCTCTGAGAGGACCTGAGCTGAGTCACCACTCTTGAGAGTCTCCCAAGACCTCTGAG 2345
 2226 CAGCTCTCTGAGAGGACCTGAGCTGAGTCACCACTCTTGAGAGTCTCCCAAGACCTCTGAG 2345
 2288 CAGCTCTCTGAGAGGACCTGAGCTGAGTCACCACTCTTGAGAGTCTCCCAAGACCTCTGAG 2347
 2288 CAGCTCTCTGAGAGGACCTGAGCTGAGTCACCACTCTTGAGAGTCTCCCAAGACCTCTGAG 2347
 2346 ATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAAT 2370
 2346 ATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAAT 2370
 2348 ATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAAT 2372

248 TGATGCCAACCCCTCTCTCCACCAAGTCCTCTCAGCAAACTCAACCTAGCGCCGCTGT 307
 249 TGATGCCAACCCCTCTCTCCACCAAGTCCTCTCAGCAAACTCAACCTAGCGCCGCTGT 308
 308 CCATCTCATCTTAATCAACATCTGACTTTTCACTGTGGAAGTGTGGAAGGCGATT 367
 309 CCATCTCATCTTAATCAACATCTGACTTTTCACTGTGGAAGTGTGGAAGGCGATT 368
 368 TTGAAGAGGCTTCTCTACAGACACAGCGAGAGAGTGTCTATGAGCTCAAGATT 427
 369 TTGAAGAGGCTTCTCTACAGACACAGCGAGAGAGTGTCTATGAGCTCAAGATT 428
 368 TTGAAGAGGCTTCTCTACAGACACAGCGAGAGAGTGTCTATGAGCTCAAGATT 427
 369 TTGAAGAGGCTTCTCTACAGACACAGCGAGAGAGTGTCTATGAGCTCAAGATT 428
 428 TACAGAGCAAGCAATCTCTGAAAGAAAGAGGAGGACATTAATGTCGGACGGATG 487
 429 TACAGAGCAAGCAATCTCTGAAAGAAAGAGGAGGACATTAATGTCGGACGGATG 488
 488 TTCTGTGTGAGAAATGTGAGACACCCCTTCTCTGTGGGCTCTGACTTCTCTCCAGACTG 547
 548 CTGCAAAATGTGACTTCTCTGACATCACTAATATGCTGGAGAGTGTCTACACATCC 607
 549 CTGCAAAATGTGACTTCTCTGACATCACTAATATGCTGGAGAGTGTCTACACATCC 608
 608 GAGGAGAACCTGCTTCTGGAACACACGCGCTGTTCTATCTGCTGAAATAGCACATG 667
 669 CTTTGGGCTACCTGCAATCACTGACATCTTATAGAGACTTAAGACACAGCAATTT 727
 668 CTTTGGGCTACCTGCAATCACTGACATCTTATAGAGACTTAAGACACAGCAATTT 728
 728 TCTAGATTCACAGGACACATATGCTTCTACTCTGGGACTCTGCAAGGACATG 787
 789 AACAGACAGCAAGCAAGTACGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 847
 788 AACAGACAGCAAGCAAGTACGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 848
 848 TTCAATAGGAGCTTATGACAGACATGAGACTGTGAGCTGTGGCTGGAGCTCTGTATG 907
 908 AGATGCTGTATGGCTCTCGCCTTTTATAGCGCAACACACTGAATGTACAGACACA 967
 909 AGATGCTGTATGGCTCTCGCCTTTTATAGCGCAACACACTGAATGTACAGACACA 968
 968 TTCTGACACAGCTCTCTGCTGACACCAACCAATTAATCAATTTCCGACAGACATCTCTGG 1027
 969 TTCTGACACAGCTCTCTGCTGACACCAACCAATTAATCAATTTCCGACAGACATCTCTGG 1028
 1028 AGGCTCTCTGAGAGGAGGACAGAGCGCTGGGGCCAGAGGACTTCTATGAGAGA 1087
 1029 AGGCTCTCTGAGAGGAGGACAGAGCGCTGGGGCCAGAGGACTTCTATGAGAGA 1088
 1088 TTAAAGATCATCTCTCTCTCTTAATTAACCTGGGATGATCATTAATAGAGAGATTA 1147
 1089 TTAAAGATCATCTCTCTCTCTTAATTAACCTGGGATGATCATTAATAGAGAGATTA 1148
 1148 CTCCCTCTTTTAAACCAATATGTGATGGGCGCCACAGGACTTACGACCTTTGACCGGAGT 1207
 1149 CTCCCTCTTTTAAACCAATATGTGATGGGCGCCACAGGACTTACGACCTTTGACCGGAGT 1208
 1208 TTACCAAGAGAGCTGTCCCACTCACTCCATTTGGCAAGTCCCTGACAGAGCTCTCTGTGACAG 1267
 1209 TTACCAAGAGAGCTGTCCCACTCACTCCATTTGGCAAGTCCCTGACAGAGCTCTCTGTGACAG 1268
 1268 CAGCCTCATAGAGCTGCCGAGGCTTCTAGCTTTTCTATGCTGCTCCCTGACAG 1327
 1269 CAGCCTCATAGAGCTGCCGAGGCTTCTAGCTTTTCTATGCTGCTCCCTGACAG 1328
 1328 CTTTCTCTGACACCTGTAGGCTGTGTTTAAAGGATTTATGTGTGTTCCCAATGT 1387

RESULT 9

1328 CTTTCTCTGACACCTGTAGGCTGTGTTTAAAGGATTTATGTGTGTTCCCAATGT 1387
 1389 CTTTCTCTGACACCTGTAGGCTGTGTTTAAAGGATTTATGTGTGTTCCCAATGT 1390
 1390 TTAATGATGATCTTCTGCTGACGCGCTGTGTAAGGACATCTATGTGTGTTCCCAATGT 1447
 1391 TTAATGATGATCTTCTGCTGACGCGCTGTGTAAGGACATCTATGTGTGTTCCCAATGT 1448
 1448 ATCCGAGAGAGCTTACAGATCTATATGACGATCTGTGCTGGAAAGCTTTTGTGAAGACAC 1506
 1449 ATCCGAGAGAGCTTACAGATCTATATGACGATCTGTGCTGGAAAGCTTTTGTGAAGACAC 1507
 1507 ATCTCTGGAAGCTTACGATCTATATGACGATCTGTGCTGGAAAGCTTTTGTGAAGACAC 1567
 1508 ATCTCTGGAAGCTTACGATCTATATGACGATCTGTGCTGGAAAGCTTTTGTGAAGACAC 1568
 1567 CTCTGAACACAGCTTATAGATGCGCCCTTACAGGAGGAGGAGAGTTCGTTAAGAGGCG 1627
 1568 CTCTGAACACAGCTTATAGATGCGCCCTTACAGGAGGAGGAGAGTTCGTTAAGAGGCG 1628
 1627 AC-CTGTCTTAAAGAGCTCTCTGCAAGCTGTGTGTGGCTGTGATGAGCAATATTGCA 1685
 1628 AC-CTGTCTTAAAGAGCTCTCTGCAAGCTGTGTGTGGCTGTGATGAGCAATATTGCA 1686
 1686 AATGTCCTTTCTGAGAGATGTGTAGTCCCAAGCTTTTCTATGAGCAATATTGCA 1745
 1687 AATGTCCTTTCTGAGAGATGTGTAGTCCCAAGCTTTTCTATGAGCAATATTGCA 1746
 1746 AATGTCCTTTCTGAGAGATGTGTAGTCCCAAGCTTTTCTATGAGCAATATTGCA 1747
 1747 AATGTCCTTTCTGAGAGATGTGTAGTCCCAAGCTTTTCTATGAGCAATATTGCA 1805
 1805 AATGTCCTTTCTGAGAGATGTGTAGTCCCAAGCTTTTCTATGAGCAATATTGCA 1806
 1806 ATCAGAGAGGATTTGTTGTTAAGCATCAATGTGACACTTTCGAGACACACTACAAATGCG 1865
 1807 ATCAGAGAGGATTTGTTGTTAAGCATCAATGTGACACTTTCGAGACACACTACAAATGCG 1866
 1866 ACATTTGTTGTTCTTCATATTTGGAAGATAAATTAATGCTGTAGACTTTTGTGTAGAT 1925
 1867 ACATTTGTTGTTCTTCATATTTGGAAGATAAATTAATGCTGTAGACTTTTGTGTAGAT 1926
 1926 AGGTTTAATTAATAAATTTTATGAAATGCTGTGCAACACTGTATTCAGATGTTAA 1985
 1987 AGGTTTAATTAATAAATTTTATGAAATGCTGTGCAACACTGTATTCAGATGTTAA 1988
 1988 AGAAGCAATCTGCTTACAAATTTCTATTTTAAAGAGGCTTTTATGAGCAATATGCC 2045
 1989 AGAAGCAATCTGCTTACAAATTTCTATTTTAAAGAGGCTTTTATGAGCAATATGCC 2046
 2046 CAGTGTGTGAGTCAAGGCGCTGTGTGTTTCTGATTAATAAGTCACTGTATAAGTGG 2105
 2107 CAGTGTGTGAGTCAAGGCGCTGTGTGTTTCTGATTAATAAGTCACTGTATAAGTGG 2108
 2108 GCATTAATTAATTTTTTTTTTTCGATTCCTGATTAATAAGTCACTGTATAAGTGG 2165
 2109 GCATTAATTAATTTTTTTTTTTCGATTCCTGATTAATAAGTCACTGTATAAGTGG 2166
 2166 CTGTACATCTGGTATTAACACTGTATTAACACTGTATTAACACTGTATTAACACTGT 2225
 2167 CTGTACATCTGGTATTAACACTGTATTAACACTGTATTAACACTGTATTAACACTGT 2226
 2226 CACATTTTAATGATCTGTATTAAGTCAAGTGTATTAAGTCAAGTGTATTAAGTCAAGT 2285
 2227 CACATTTTAATGATCTGTATTAAGTCAAGTGTATTAAGTCAAGTGTATTAAGTCAAGT 2286
 2286 ATCAGACACTTTTTTGTGTGTGATTAACACTGTATTTGGTTTGCATTAACACTGTGAAA 2345
 2287 ATCAGACACTTTTTTGTGTGTGATTAACACTGTATTTGGTTTGCATTAACACTGTGAAA 2346
 2346 ATCAGACACTTTTTTGTGTGTGATTAACACTGTATTTGGTTTGCATTAACACTGTGAAA 2347
 2347 ATCAGACACTTTTTTGTGTGTGATTAACACTGTATTTGGTTTGCATTAACACTGTGAAA 2348
 2348 ATCAGACACTTTTTTGTGTGTGATTAACACTGTATTTGGTTTGCATTAACACTGTGAAA 2349

2346 ATA 2348

2348 ATA 2350

874 GGGAGCTGGTGGGAGCTGCTCTGTATGAGATATGCTGATGGCTGGCCGCTTT 933
 Db 841 GTGAGAGCTGGTGGGAGCTGCTCTGTATGAGATATGCTGATGGCTGGCCGCTTT 900
 934 TATAGCGAAACAGAGCTGAATATGACGACACATCTGACAGAGCTCTCCAGCTGAA 993
 Qy 901 TATAGCGAAACAGAGCTGAATATGACGACACATCTGACAGAGCTCTCCAGCTGAA 960
 Qy 994 CCAATATTACAAATTCGACAGACAGCTCTGGAGGAGCTCTGACAGAGCAGAC 1053
 Db 961 CCAATATTACAAATTCGACAGACAGCTCTGGAGGAGCTCTGACAGAGCAGAC 1020
 Qy 1054 AAGCGGCTCGGGGCAAGAGCTCTGACAGAGCTCTGGAGGAGCTCTGACAGAGC 1113
 Db 1021 AAGCGGCTCGGGGCAAGAGCTCTGACAGAGCTCTGGAGGAGCTCTGACAGAGC 1080
 Qy 1114 ATTAAGCTGAGATCTCAATTAATAGAGATTAAGAGATTAAGAGATTAAGAG 1173
 Db 1081 ATTAAGCTGAGATCTCAATTAATAGAGATTAAGAGATTAAGAGATTAAGAG 1140
 Qy 1174 GGGCCGAGAGCTGAGGAGCTCTGACAGAGCTCTGGAGGAGCTCTGACAGAGC 1233
 Db 1141 GGGCCGAGAGCTGAGGAGCTCTGACAGAGCTCTGGAGGAGCTCTGACAGAGC 1200
 Qy 1234 ATTCGAGAGCTGAGGAGCTCTGACAGAGCTCTGGAGGAGCTCTGACAGAGC 1293
 Db 1201 ATTCGAGAGCTGAGGAGCTCTGACAGAGCTCTGGAGGAGCTCTGACAGAGC 1260
 Qy 1294 TTCTGAGGCTTTTCTGAGGAGCTCTGACAGAGCTCTGGAGGAGCTCTGACAG 1353
 Db 1261 TTCTGAGGCTTTTCTGAGGAGCTCTGACAGAGCTCTGGAGGAGCTCTGACAG 1320
 Qy 1354 GTTAAAGAGATTTATGCTGTTTCCGAGATTTAGTATGCTTTAGTATGCTTT 1413
 Db 1321 GTTAAAGAGATTTATGCTGTTTCCGAGATTTAGTATGCTTTAGTATGCTTT 1380
 Qy 1414 CAGCTGAGAGGACCTTACAGAGATTTCCAGATTTCCAGATTTCCAGATTT 1473
 Db 1381 CAGCTGAGAGGACCTTACAGAGATTTCCAGATTTCCAGATTTCCAGATTT 1440
 Qy 1474 GCAGAGCTGCTGGAGCTTATGCTGTTTCCGAGATTTAGTATGCTTTAGTATG 1532
 Db 1441 GCAGAGCTGCTGGAGCTTATGCTGTTTCCGAGATTTAGTATGCTTTAGTATG 1500
 Qy 1533 TTGATGCTGCTGGAGCTTATGCTGTTTCCGAGATTTAGTATGCTTTAGTATG 1592
 Db 1501 TTGATGCTGCTGGAGCTTATGCTGTTTCCGAGATTTAGTATGCTTTAGTATG 1560
 Qy 1593 GTTAAAGAGATTTATGCTGTTTCCGAGATTTAGTATGCTTTAGTATGCTTT 1651
 Db 1561 GTTAAAGAGATTTATGCTGTTTCCGAGATTTAGTATGCTTTAGTATGCTTT 1620
 Qy 1652 AGATGCTGCTGGAGCTTATGCTGTTTCCGAGATTTAGTATGCTTTAGTATGCT 1710
 Db 1621 AGATGCTGCTGGAGCTTATGCTGTTTCCGAGATTTAGTATGCTTTAGTATGCT 1680
 Qy 1711 GTTAAAGAGATTTATGCTGTTTCCGAGATTTAGTATGCTTTAGTATGCTTT 1770
 Db 1681 GTTAAAGAGATTTATGCTGTTTCCGAGATTTAGTATGCTTTAGTATGCTTT 1740
 Qy 1771 GTTAAAGAGATTTATGCTGTTTCCGAGATTTAGTATGCTTTAGTATGCTTT 1830
 Db 1741 GTTAAAGAGATTTATGCTGTTTCCGAGATTTAGTATGCTTTAGTATGCTTT 1800
 Qy 1831 ATCAATGCTGCTGGAGCTTATGCTGTTTCCGAGATTTAGTATGCTTTAGTATG 1890
 Db 1801 ATCAATGCTGCTGGAGCTTATGCTGTTTCCGAGATTTAGTATGCTTTAGTATG 1860
 Qy 1891 GAAGATTAATTTATGCTGCTTTTGTGAGATTTTGTGAGATTTTGTGAGATTT 1950
 Db 1861 GAAGATTAATTTATGCTGCTTTTGTGAGATTTTGTGAGATTTTGTGAGATTT 1920

1951 AATGGCTGCTGCAATGATCTGATTCAGATGCTGCTAAGAGAAAGCTGCTGCTAA 2010
 Db 1921 AATGGCTGCTGCAATGATCTGATTCAGATGCTGCTAAGAGAAAGCTGCTGCTAA 1980
 Qy 2011 TCTATTTTATGAGAAAGCTTTTATGAGCAATGCTGCTGCTGCTGCTGCTGCTG 2070
 Db 1981 TCTATTTTATGAGAAAGCTTTTATGAGCAATGCTGCTGCTGCTGCTGCTGCTG 2040
 Qy 2071 GTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2130
 Db 2041 GTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2100
 Qy 2131 ATTCCTGAGAGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2190
 Db 2101 ATTCCTGAGAGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2160
 Qy 2191 ATTCCTGAGAGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2250
 Db 2161 ATTCCTGAGAGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2220
 Qy 2251 GCTGCTGAGAGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2310
 Db 2221 GCTGCTGAGAGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2280
 Qy 2311 TTAACAGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2341
 Db 2281 TTAACAGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2311

RESULT 11
 AR270209
 LOCUS AR270209 772 bp DNA 1 linear PAT 10-APR-2003
 DEFINITION Sequence AR270209.1
 VERSION AR270209.1
 KEYWORDS AR270209.1 G1:29701443
 ORGANISM unknown.
 ORGANISM unknown.
 AUTHORS Au-Yang, J. and Sellhammer, J. J.
 TITLE Composition for the detection of signalling pathway gene expression
 PATENT US 6,599,123 31-DEC-2002;
 FEATURES
 source 1. 2311
 BASE COUNT 604 a 508 c 506 g 692 t 1 others
 ORIGIN
 Query Match 95.5% Score 2262.8; DB 6; Length 2311;
 Best Local Similarity 99.5%; Pred. No. 0;
 Matches 2300, Conservative 0; Mismatches 8; Indels 3; Gaps 3;
 Qy 34 GGCTGGTGTGATGACGCTGAAAGCTGAGGCTGTATAGGGCAACCTCAGCTTACTTCCAGATC 93
 Db 1 GGCTGGTGTGATGACGCTGAAAGCTGAGGCTGTATAGGGCAACCTCAGCTTACTTCCAGATC 60
 Qy 94 AGGGCTCATGTGGCAATCTCTGCTGCTTCTGATGAGAGAGAGGAGTGGGTCTGAGACAC 153
 Db 61 AGGGCTCATGTGGCAATCTCTGCTGCTTCTGATGAGAGAGAGGAGTGGGTCTGAGACAC 120
 Qy 154 TTTATCAGAGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 213
 Db 121 TTTATCAGAGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
 Qy 214 TTTAGAGATTTCCCAAGCTGAGGAGCTGAGCTGTATGATGCGACCGCTGCTGCTGCA 273
 Db 181 TTTAGAGATTTCCCAAGCTGAGGAGCTGAGCTGTATGATGCGACCGCTGCTGCTGCA 240
 Qy 274 AGTCTCTCGAGCAATTAAGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCG 333
 Db 241 AGTCTCTCGAGCAATTAAGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCG 300

[illegible]

QY	1771	CTGTGTGTAAGACGCTGCTGAGTGGCGATCGTCATGACACATGCATGCTATGTAAGCG	1830	QY	1171	GCTTTCATGAGCAGAGAGATGAGTGTGTAACACCTTATTCAGAGATTCGCAATAC	1237	
DB	1741	CTGTGTGTGTAACGCTGCTGTGAGTGTGCTGATGCTGATGATGATGATGATGATGATG	1800	DB	959	GTCTTCATGAGCAGAGAGATGAGTGTGTAACACCTTATTCAGAGATTCGCAATAC	1018	
QY	1831	ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1860	QY	178	TCCTATGATGAGCAGAGAGATGAGTGTGTAACACCTTATTCAGAGATTCGCAATAC	237	
DB	1801	ATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1850	DB	1019	TCCTATGATGAGCAGAGAGATGAGTGTGTAACACCTTATTCAGAGATTCGCAATAC	1078	
QY	1891	GAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1950	QY	238	CTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	297	
DB	1861	GAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1920	DB	1079	CTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1148	
QY	1951	ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	2010	QY	298	GCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	357	
DB	1921	ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1980	DB	1148	GCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1198	
QY	2011	TCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	2070	QY	358	AGAGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	417	
DB	1981	TCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	2040	DB	1199	AGAGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1258	
QY	2071	CTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	2130	QY	418	GTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	477	
DB	2041	CTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	2110	DB	1259	GTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1318	
QY	2131	ATGTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	2190	QY	478	GAGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	537	
DB	2101	ATGTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	2160	DB	1319	GAGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1378	
QY	2191	ATGTTTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	2250	QY	538	TGCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	597	
DB	2161	ATGTTTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	2220	DB	1379	TGCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1438	
QY	2251	CAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	2310	QY	598	TAGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	657	
DB	2221	GAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	2280	DB	1439	TAGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1498	
QY	2311	TAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	2341	QY	658	ATAGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	717	
DB	2281	TAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	2311	DB	1499	ATAGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1558	
RESULT 13								
LOCUS	AX713538	3196 bp	DNA	linear	PAT 15-APR-2003			
REFERENCE	AX713538	222	from Patent EP1293569.					
ACCESSION	AX713538	1	GI:29888396					
VERSION	AX713538.1	GI:29888396						
KEYWORDS	homo sapiens (human)							
SOURCE	homo sapiens (human)							
ORGANISM	homo sapiens (human)							
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;							
AUTHORS	Eukaryota; Euteleostomi; Chordata; Craniata; Vertebrata; Euteleostomi;							
REVIEWERS	Isogai, T., Sugiyama, T., Otsuki, T., Nakamatsu, A., Sato, H., Ishii, S.,							
JOURNAL	Yamamoto, J.I., Isono, Y., Hiro, Y., Otsuka, K., Nagai, K., Irie, R.,							
TITLE	Tamachi, I., Seki, N., Yoshikawa, T., Otsuka, M., Negahari, K. and							
Patent: EP 1293569-A	222 19-MAR-2003;							
Helix Research Institute (JP); Research Association for								
Biotechnology (JP)								
Accession/Qualifiers								
1. contig								
/organism="Homo sapiens"								
/mol_type="genomic DNA"								
817 a	723 c	889 t						
BASE COUNT								
ORIGIN								
Query Match	92.98;	Score 2201;	DB 6;	Length 3196;				
BLAST Similarity	99.78;	Prod. No. 0;						
Matches 2226;	Conservative	0;	Mismatches	5;	Indels	2;	Gaps	2;

298 GGCCTGCTGCAATCTCTATGCTTAAGCAATCTGACCTTCTACTTCTTGAAAGTATCGGA 357
 1139 GGCCTGCTGCAATCTCTATGCTTAAGCAATCTGACCTTCTACTTCTTGAAAGTATCGGA 1198
 358 AAGGCAAGCTTTGGGAAGGTTCTCTACAGAGCAAGCAAGCAAGAGAGCTTCTATGCA 417
 1139 AAGGCAAGCTTTGGGAAGGTTCTCTACAGAGCAAGCAAGCAAGAGAGCTTCTATGCA 1258
 418 CTCGAAGCTTTACAGAGCAAGCAATCTCTGAAGAGAGAGAGAGAGAGCAATATATGTC 477
 1259 CTCGAAGCTTTACAGAGCAAGCAATCTCTGAAGAGAGAGAGAGAGAGCAATATATGTC 1318
 478 GCGAGAGATCTGCTTGGAAGAGATCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1378
 1319 GCGAGAGATCTGCTTGGAAGAGATCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1378
 538 TTCGCAAGCTCTGCAAGCAATCTACTTGTCTAGCACTACTATGCTGGAGAGGTGTC 597
 1379 TTCGCAAGCTCTGCAAGCAATCTACTTGTCTAGCACTACTATGCTGGAGAGGTGTC 1438
 598 TACCAATCTCTGCAAGCAAGCAATCTACTTGTCTAGCACTACTATGCTGGAGAGGTGTC 657
 1439 TACCAATCTCTGCAAGCAAGCAATCTACTTGTCTAGCACTACTATGCTGGAGAGGTGTC 1498
 658 TACCAATCTCTGCAAGCAAGCAATCTACTTGTCTAGCACTACTATGCTGGAGAGGTGTC 717
 1499 TACCAATCTCTGCAAGCAAGCAATCTACTTGTCTAGCACTACTATGCTGGAGAGGTGTC 1558
 718 GAGAGATCTGCTGAGAGCAAGCAATCTACTTGTCTAGCACTACTATGCTGGAGAGGTGTC 777
 1559 GAGAGATCTGCTGAGAGCAAGCAATCTACTTGTCTAGCACTACTATGCTGGAGAGGTGTC 1618
 778 GAGAGATCTGCTGAGAGCAAGCAATCTACTTGTCTAGCACTACTATGCTGGAGAGGTGTC 837
 1619 GAGAGATCTGCTGAGAGCAAGCAATCTACTTGTCTAGCACTACTATGCTGGAGAGGTGTC 1678
 838 GAGAGATCTGCTGAGAGCAAGCAATCTACTTGTCTAGCACTACTATGCTGGAGAGGTGTC 897
 1679 GAGAGATCTGCTGAGAGCAAGCAATCTACTTGTCTAGCACTACTATGCTGGAGAGGTGTC 1738
 898 GAGAGATCTGCTGAGAGCAAGCAATCTACTTGTCTAGCACTACTATGCTGGAGAGGTGTC 957
 1739 GAGAGATCTGCTGAGAGCAAGCAATCTACTTGTCTAGCACTACTATGCTGGAGAGGTGTC 1798
 958 TACCAAGCTCTGCAAGCAAGCAATCTACTTGTCTAGCACTACTATGCTGGAGAGGTGTC 1017
 1799 TACCAAGCTCTGCAAGCAAGCAATCTACTTGTCTAGCACTACTATGCTGGAGAGGTGTC 1858
 1018 GAGAGATCTGCTGAGAGCAAGCAATCTACTTGTCTAGCACTACTATGCTGGAGAGGTGTC 1077
 1859 GAGAGATCTGCTGAGAGCAAGCAATCTACTTGTCTAGCACTACTATGCTGGAGAGGTGTC 1918
 1078 GAGAGATCTGCTGAGAGCAAGCAATCTACTTGTCTAGCACTACTATGCTGGAGAGGTGTC 1137
 1919 GAGAGATCTGCTGAGAGCAAGCAATCTACTTGTCTAGCACTACTATGCTGGAGAGGTGTC 1978
 1138 GAGAGATCTGCTGAGAGCAAGCAATCTACTTGTCTAGCACTACTATGCTGGAGAGGTGTC 1197
 1979 GAGAGATCTGCTGAGAGCAAGCAATCTACTTGTCTAGCACTACTATGCTGGAGAGGTGTC 2038
 1198 GAGAGATCTGCTGAGAGCAAGCAATCTACTTGTCTAGCACTACTATGCTGGAGAGGTGTC 1257
 2039 GAGAGATCTGCTGAGAGCAAGCAATCTACTTGTCTAGCACTACTATGCTGGAGAGGTGTC 2098
 1258 GAGAGATCTGCTGAGAGCAAGCAATCTACTTGTCTAGCACTACTATGCTGGAGAGGTGTC 1317
 2099 GAGAGATCTGCTGAGAGCAAGCAATCTACTTGTCTAGCACTACTATGCTGGAGAGGTGTC 2158
 1317 GAGAGATCTGCTGAGAGCAAGCAATCTACTTGTCTAGCACTACTATGCTGGAGAGGTGTC 1377
 2159 GAGAGATCTGCTGAGAGCAAGCAATCTACTTGTCTAGCACTACTATGCTGGAGAGGTGTC 2218
 1378 TTCGAAGCTTTTGGGAAGGTTCTCTACAGAGCAAGCAAGCAAGAGAGCTTCTATGCA 1437

2219 TTCGAAGCTTTTGGGAAGGTTCTCTACAGAGCAAGCAAGCAAGAGAGCTTCTATGCA 2278
 1438 GAGTTCACATCTGGAAGGTTCTCTACAGAGCAAGCAAGCAAGAGAGCTTCTATGCA 2497
 2279 GAGTTCACATCTGGAAGGTTCTCTACAGAGCAAGCAAGCAAGAGAGCTTCTATGCA 2338
 1497 TGAAGAGCAATCTGGAAGGTTCTCTACAGAGCAAGCAAGCAAGAGAGCTTCTATGCA 1556
 2339 TGAAGAGCAATCTGGAAGGTTCTCTACAGAGCAAGCAAGCAAGAGAGCTTCTATGCA 2398
 1557 GTGGTCTATCTGGAAGGTTCTCTACAGAGCAAGCAAGCAAGAGAGCTTCTATGCA 1616
 2399 GTGGTCTATCTGGAAGGTTCTCTACAGAGCAAGCAAGCAAGAGAGCTTCTATGCA 2458
 1617 TGAAGAGCAAGCTTCTGGAAGGTTCTCTACAGAGCAAGCAAGAGAGCTTCTATGCA 1675
 2459 TGAAGAGCAAGCTTCTGGAAGGTTCTCTACAGAGCAAGCAAGAGAGCTTCTATGCA 2518
 1676 ATATATGAATATGCGCTTTCTGGAAGGTTCTCTACAGAGCAAGCAAGAGAGCTTCTATGCA 1735
 2519 ATATATGAATATGCGCTTTCTGGAAGGTTCTCTACAGAGCAAGCAAGAGAGCTTCTATGCA 2578
 1735 GAGTTCACATCTGGAAGGTTCTCTACAGAGCAAGCAAGCAAGAGAGCTTCTATGCA 1795
 2579 GAGTTCACATCTGGAAGGTTCTCTACAGAGCAAGCAAGCAAGAGAGCTTCTATGCA 2638
 1796 GAGTTCACATCTGGAAGGTTCTCTACAGAGCAAGCAAGCAAGAGAGCTTCTATGCA 1855
 2639 GAGTTCACATCTGGAAGGTTCTCTACAGAGCAAGCAAGCAAGAGAGCTTCTATGCA 2698
 1856 GAGTTCACATCTGGAAGGTTCTCTACAGAGCAAGCAAGCAAGAGAGCTTCTATGCA 1915
 2699 GAGTTCACATCTGGAAGGTTCTCTACAGAGCAAGCAAGCAAGAGAGCTTCTATGCA 2758
 1916 TTTGTAAGATACGCTTAATACAAATTTTATGGAAGTGTCTGCAATGACTGATTC 1975
 2759 TTTGTAAGATACGCTTAATACAAATTTTATGGAAGTGTCTGCAATGACTGATTC 2818
 1976 AGATGCTTACGAAGAGCTTCTGCTACAAATTTTATGGAAGTGTCTGCAATGACTGATTC 2035
 2819 AGATGCTTACGAAGAGCTTCTGCTACAAATTTTATGGAAGTGTCTGCAATGACTGATTC 2878
 2036 GAGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2095
 2879 GAGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2938
 2096 TGTAAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2155
 2939 TGTAAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2998
 2156 TAAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2215
 2999 TAAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3058
 2216 TAAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2275
 3059 TAAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3118
 2276 GCT 2335
 3119 GCT 3178
 2336 ACCTGGAAGAATA 3348
 3179 ACCTGGAAGAATA 3191

RESULT 15
 AX017284
 LOCUS
 DDB/BLAST
 ACCESSION
 AX017284

2384 bp
 39 from Patent WO/94/16099

linear

PAT 07-SEP-2000


```

Oy 1993 ATGCGCTGCAAAATATTCATTTTCAGANGGCTTTATGCGAGCAATGCCGAGTGG 2052
Db 1895 ATTGCTGCTCAAAATATTTCTATTTTATAGAAAGGGTTTTATGGAGCCATATCCCCNCTGG 1954
Oy 2053 TCGAGCAGAGCGCTGGGCTTCTGATGCTGTAAAGTGTCACTGCGCSPANANRGGGCTAT 2112
Db 1955 TCAAGTCAGAGCGCTGGGCTTCTGATGCTGTAAAGTGTCACTGCGCSPANANRGGGCTAT 2014
Oy 2113 TTATGCTTTTCTTCTGATGCTGTAAAGTGTCACTGCGCSPANANRGGGCTAT 2172
Db 2015 TTATGCTTTTCTTCTGATGCTGTAAAGTGTCACTGCGCSPANANRGGGCTAT 2074
Oy 2173 TTGCGCTTAAAGCTGTAAAGTGTCACTGCGCSPANANRGGGCTAT 2232
Db 2075 TTGCGCTTAAAGCTGTAAAGTGTCACTGCGCSPANANRGGGCTAT 2134
Oy 2233 TTATGCTTAAAGCTGTAAAGTGTCACTGCGCSPANANRGGGCTAT 2292
Db 2135 TTATGCTTAAAGCTGTAAAGTGTCACTGCGCSPANANRGGGCTAT 2194
Oy 2293 AATGCTTTTCTGCTGCTGATAAAGTGTCACTGCGCSPANANRGGGCTAT 2352
Db 2195 AATGCTTTTCTGCTGCTGATAAAGTGTCACTGCGCSPANANRGGGCTAT 2254
Oy 2353 AAAAAAAAAAAAAA 2368
Db 2255 AAAAAAAAAAAAAA 2270

```

Search completed: August 11, 2003, 04:53:03
 Job time : 8496 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 11, 2003, 01:25:43 ; Search time 616 Seconds
(without alignments)
10985:925 Million cell updates/sec

Title: US-10-000-039a-1
Perfect score: 2370
Sequence: 1 CACGAGGAGCCTTACCTC.....AAAAAAAAAAAAAAAAAAAAA 2370
Scoring table: IDENTITY_NUC
Gap10 10.0, Gapext 1.0
Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 510512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Minimum Match 100%

Listing first 45 summaries

Database :
1: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1980.DAT.*
2: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1981.DAT.*
3: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1982.DAT.*
4: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1983.DAT.*
5: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1984.DAT.*
6: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1985.DAT.*
7: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1986.DAT.*
8: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1987.DAT.*
9: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1988.DAT.*
10: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1989.DAT.*
11: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1990.DAT.*
12: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1991.DAT.*
13: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1992.DAT.*
14: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1993.DAT.*
15: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1994.DAT.*
16: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1995.DAT.*
17: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1996.DAT.*
18: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1997.DAT.*
19: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1998.DAT.*
20: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1999.DAT.*
21: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2000.DAT.*
22: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.*
23: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
24: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*
25: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query	Length	DB	ID	Description
1	2370	100.0	2370	19	AAV48311	Human cell-volume
2	2370	100.0	2370	24	AKN34719	Human CDNA differ
3	2370	100.0	2370	24	AKL70006	Human CDNA differ
4	2370	100.0	2370	24	ABX74395	Pancreas cancer te
5	2312.6	97.6	2343	25	ABX74395	Human CDNA sequenc
6	2301.6	97.1	2346	20	AAV74190	Human agk DNA. Ho
7	2262.8	95.5	2311	19	AAV23513	Human protein kina
8	2262.8	95.5	2311	23	AKN69174	Human Signalling p

Human breast tumor
DNA encoding a rat
Novel protein kina
Novel protein kina
Novel protein kina
Human serum and g
Human serum and g
Human serum and g
Human serum and g
Human serum glucoc
DNA encoding novel
Human polyprotein
Human polyprotein
Human serine threo
Human serine threo
Human serine threo
Human prostate can
Nucleotide sequenc
Human polyprotein
DNA encoding novel
Human full-length
Human que signalin
Human protein kina
Human protein kina
Sovine ESH associa
Human colon specif
Novel protein kina
Novel protein kina
Broscahilia melano
Androgen receptor
Human Akt-3 coding
Human Akt-3 coding
Human Akt-3 nucleo
DNA encoding a hum
Human Akt3 encodin

ALIGNMENTS

RESULT 1
AAV48311
ID AAV48311 standard; CINA; 2370 bp.
XX AAV48311;
XX AAV48311;
DT 16-NOV-1998 (first entry)
XX Human cell-volume regulating kinase h-agk.
XX Human cell-volume; kinase: h-agk; diabetes mellitus;
XX ss: human; cell-volume; kinase: h-agk; diabetes mellitus;
KW renal insufficiency; Inflammation; Alzheimer's disease.
XX Homo sapiens.
XX Key
XX Location/Qualifiers
XX 424338
XX /product: "Kinase h-agk"

XX EP86189c-A2.
XX 02-SEP-1998.
XX 27-JAN-1998; 98EP-0101338.
XX 28-FEB-1997; 97US-1008171.
XX (DADE-) DADE BEHRING MARBURG OHNH.
XX Lang F. Waldegger S.
XX

Db 241. GAGCTATGATGCGAACCCCTCTGCTCCACCAAGTCCTCTCGCAAAATCAACCTTTGGC 300
 Oy 301. CGGTGCTCGAATCTGATGCTTAACACATGCTGACTTTTCATCTCTGTAAGTGCAGGAAG 360
 Db 301. CGTCTCGAATCTGATGCTTAACACATGCTGACTTTTCATCTCTGTAAGTGCAGGAAG 360
 Oy 361. GCGAGTTTGGAAAGTCTCTCTACGACAGACAGACAGGCAAGAGAGTGTCTATCGACATC 420
 Db 361. GCGAGTTTGGAAAGTCTCTCTACGACAGACAGACAGGCAAGAGAGTGTCTATCGACATC 420
 Oy 421. AAGGTTTACAGAGAGAGTCTCTGTAAGAAAGAGAGAGAGAGTGTCTATCGACATC 480
 Db 421. AAGGTTTACAGAGAGAGTCTCTGTAAGAAAGAGAGAGAGAGTGTCTATCGACATC 480
 Oy 481. CGAAGTCTCTGTAAGAGTGTGAAGACACCTCTCTGCTGGTGGCTCTCACTCTCTCTTC 540
 Db 481. CGAAGTCTCTGTAAGAGTGTGAAGACACCTCTCTGCTGGTGGCTCTCACTCTCTCTTC 540
 Oy 541. CAGAGTCTCTGTAAGAGTGTGAAGACACCTCTCTGCTGGTGGCTCTCACTCTCTCTTC 540
 Db 541. CAGAGTCTCTGTAAGAGTGTGAAGACACCTCTCTGCTGGTGGCTCTCACTCTCTCTTC 540
 Oy 601. CATCTCGAGAGAGACCTGCTCTCTCGACACAGGGCTCGTTTCTATGCTCTGAAATA 660
 Db 601. CATCTCGAGAGAGACCTGCTCTCTCGACACAGGGCTCGTTTCTATGCTCTGAAATA 660
 Oy 661. GCGAGTCTCTGGGCTCTGCTGATCTCACTGACATGCTTTATAGAGACTTAACACAGAG 720
 Db 661. GCGAGTCTCTGGGCTCTGCTGATCTCACTGACATGCTTTATAGAGACTTAACACAGAG 720
 Oy 721. AATATTTTGTAGATTCAGAGAGACATGCTCTACTGATTTTGGAGCTCTCGACAGAG 780
 Db 721. AATATTTTGTAGATTCAGAGAGACATGCTCTACTGATTTTGGAGCTCTCGACAGAG 780
 Oy 781. AACATTGAACACACACACACATCCACCTCTCTGCGACCGCGAGATCTCCACACT 840
 Db 781. AACATTGAACACACACACATCCACCTCTCTGCGACCGCGAGATCTCCACACT 840
 Oy 841. GAGGTCTCTATAGACAGCTTATGACAGAGCTGTGAGCTGTGCTGCGGAGCTCTC 900
 Db 841. GAGGTCTCTATAGACAGCTTATGACAGAGCTGTGAGCTGTGCTGCGGAGCTCTC 900
 Oy 901. TTGATGTAGATCTGTATGGCTGCGCGCTTTTATAGCCGAACACAGACTGAAGATAC 960
 Db 901. TTGATGTAGATCTGTATGGCTGCGCGCTTTTATAGCCGAACACAGACTGAAGATAC 960
 Oy 961. GACACATCTGACAGAGCTCTCCAGCTGACACCAATATACAAATTCGGACAGAC 1020
 Db 961. GACACATCTGACAGAGCTCTCCAGCTGACACCAATATACAAATTCGGACAGAC 1020
 Oy 1021. CTCCTGGAGGGCTCTCTGCAAGAGACAGCAAGCGCTGCGGCGCAAGATCATCTC 1080
 Db 1021. CTCCTGGAGGGCTCTCTGCAAGAGACAGCAAGCGCTGCGGCGCAAGATCATCTC 1080
 Oy 1081. ATGAGATTAAGATGATCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1140
 Db 1081. ATGAGATTAAGATGATCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1140
 Oy 1141. ATGAGATTAAGATGATCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1200
 Db 1141. ATGAGATTAAGATGATCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1200
 Oy 1201. CCGAGTTTACAGAGAGCTGTCTCCACCAATGTGAGTGGGCGCACAGAGCTACGACATCT 1260
 Db 1201. CCGAGTTTACAGAGAGCTGTCTCCACCAATGTGAGTGGGCGCACAGAGCTACGACATCT 1260
 Oy 1261. GTACAGCAGCGCTGTACAGACAGCTGTGAGAGGCTTCTAGGCTTTCTATGCGGCTCTCC 1320
 Db 1261. GTACAGCAGCGCTGTACAGACAGCTGTGAGAGGCTTCTAGGCTTTCTATGCGGCTCTCC 1320
 Oy 1321. AGGAGCTCTCTCTGACACCTGTATAGGCTCTGTGTTTATAGAGATTTATGTGTGTTTC 1380
 Db 1321. AGGAGCTCTCTCTGACACCTGTATAGGCTCTGTGTTTATAGAGATTTATGTGTGTTTC 1380

RESULT 3
 ABN97360
 ID ABN97360 standard; DNA: 2370 BP.

Oy 1381. CGAATGTTTANGTTAGCTTTAGCTTTTGTGTGAGCGCCGACCTGACAGACATCTTAAGACAGAA 1440
 Db 1381. CGAATGTTTANGTTAGCTTTAGCTTTTGTGTGAGCGCCGACCTGACAGACATCTTAAGACAGAA 1440
 Oy 1441. TTGTCACATCTCTGAGAGTGTAGACATGTTATGTTATGACACATCTGCTCGGAATTTTGA 1500
 Db 1441. TTGTCACATCTCTGAGAGTGTAGACATCTTATGACACATCTGCTCGGAATTTTGA 1500
 Oy 1501. GAGCAGATCTCTCACTGAGCTCTGACAGTGTTCATTTTATCTCTCTCCCAAGCTG 1560
 Db 1501. GAGCAGATCTCTCACTGAGCTCTGACAGTGTTCATTTTATCTCTCTCCCAAGCTG 1560
 Oy 1561. TACTATCTCTGAAAGAGCTGTAGAGCTGCGGCTTATAGAGCGAGGAGAGTTTGTATGA 1620
 Db 1561. TACTATCTCTGAAAGAGCTGTAGAGCTGCGGCTTATAGAGCGAGGAGAGTTTGTATGA 1620
 Oy 1621. AAGGAGACCTCTCTTAAAGAGCTCTCTGAGAGATGCTCTGAGCTGTGATGAGATAT 1680
 Db 1621. AAGGAGACCTCTCTTAAAGAGCTCTCTGAGAGATGCTCTGAGCTGTGATGAGATAT 1680
 Oy 1681. TATGAAATGCGCTTTCTGAGAGAGATGCTGTAGCTCTCAAGCTTTCTCTATGACATG 1740
 Db 1681. TATGAAATGCGCTTTCTGAGAGAGATGCTGTAGCTCTCAAGCTTTCTCTATGACATG 1740
 Oy 1741. TTTCACTGCTCTTATTTCCCTCTGATATGCTGTCTGACGCTGCTGTATGATAT 1800
 Db 1741. TTTCACTGCTCTTATTTCCCTCTGATATGCTGTCTGACGCTGCTGTATGATAT 1800
 Oy 1801. GCTGTGACAGAGCTGATTTGTATGAGAGATGCTGTGAGCTGTGATGATGATAT 1860
 Db 1801. GCTGTGACAGAGCTGATTTGTATGAGAGATGCTGTGAGCTGTGATGATGATAT 1860
 Oy 1861. GTGGGAGATGCTGCT 1920
 Db 1861. GTGGGAGATGCTGCT 1920
 Oy 1921. AAGTATGCTGTATGATGATATTTATGAAATGCTGTGCAATGACTCTGATATGATG 1980
 Db 1921. AAGTATGCTGTATGATGATATTTATGAAATGCTGTGCAATGACTCTGATATGATG 1980
 Oy 1981. CTTAAGAGAGATGCT 2040
 Db 1981. CTTAAGAGAGATGCT 2040
 Oy 2041. ATGCGCCAGTGTCTAGTGTAGAGCTGTGCTGTTCTATGTTTAAATGTCACTGATTA 2100
 Db 2041. ATGCGCCAGTGTCTAGTGTAGAGCTGTGCTGTTCTATGTTTAAATGTCACTGATTA 2100
 Oy 2101. AATGCGCATTTATTTTCTTT 2160
 Db 2101. AATGCGCATTTATTTTCTTT 2160
 Oy 2161. AAGCTCTGACATGGGTATTAACACTAGTATTTTAACTTACAGCTTATTTGATG 2220
 Db 2161. AAGCTCTGACATGGGTATTAACACTAGTATTTTAACTTACAGCTTATTTGATG 2220
 Oy 2221. TAAACACACATTTAATGCTACTGTCTATACATGCTGTATTAATCTAGATCTCTCTCTCT 2280
 Db 2221. TAAACACACATTTAATGCTACTGTCTATACATGCTGTATTAATCTAGATCTCTCTCTCT 2280
 Oy 2281. ATCCCACTCACACACTTTTTTGTGTGTGAAGAACTGATTTGTTTGTGCAATAAATCT 2340
 Db 2281. ATCCCACTCACACACTTTTTTGTGTGTGAAGAACTGATTTGTTTGTGCAATAAATCT 2340
 Oy 2341. GAAATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 2370
 Db 2341. GAAATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 2370

1372	1373	1374	1375	1376	1377	1378	1379	1380	1381	1382	1383	1384	1385	1386	1387	1388	1389	1390	1391	1392	1393	1394	1395	1396	1397	1398	1399	1400	1401	1402	1403	1404	1405	1406	1407	1408	1409	1410	1411	1412	1413	1414	1415	1416	1417	1418	1419	1420	1421	1422	1423	1424	1425	1426	1427	1428	1429	1430	1431	1432	1433	1434	1435	1436	1437	1438	1439	1440	1441	1442	1443	1444	1445	1446	1447	1448	1449	1450	1451	1452	1453	1454	1455	1456	1457	1458	1459	1460	1461	1462	1463	1464	1465	1466	1467	1468	1469	1470	1471	1472	1473	1474	1475	1476	1477	1478	1479	1480	1481	1482	1483	1484	1485	1486	1487	1488	1489	1490	1491	1492	1493	1494	1495	1496	1497	1498	1499	1500	1501	1502	1503	1504	1505	1506	1507	1508	1509	1510	1511	1512	1513	1514	1515	1516	1517	1518	1519	1520	1521	1522	1523	1524	1525	1526	1527	1528	1529	1530	1531	1532	1533	1534	1535	1536	1537	1538	1539	1540	1541	1542	1543	1544	1545	1546	1547	1548	1549	1550	1551	1552	1553	1554	1555	1556	1557	1558	1559	1560	1561	1562	1563	1564	1565	1566	1567	1568	1569	1570	1571	1572	1573	1574	1575	1576	1577	1578	1579	1580	1581	1582	1583	1584	1585	1586	1587	1588	1589	1590	1591	1592	1593	1594	1595	1596	1597	1598	1599	1600	1601	1602	1603	1604	1605	1606	1607	1608	1609	1610	1611	1612	1613	1614	1615	1616	1617	1618	1619	1620	1621	1622	1623	1624	1625	1626	1627	1628	1629	1630	1631	1632	1633	1634	1635	1636	1637	1638	1639	1640	1641	1642	1643	1644	1645	1646	1647	1648	1649	1650	1651	1652	1653	1654	1655	1656	1657	1658	1659	1660	1661	1662	1663	1664	1665	1666	1667	1668	1669	1670	1671	1672	1673	1674	1675	1676	1677	1678	1679	1680	1681	1682	1683	1684	1685	1686	1687	1688	1689	1690	1691	1692	1693	1694	1695	1696	1697	1698	1699	1700	1701	1702	1703	1704	1705	1706	1707	1708	1709	1710	1711	1712	1713	1714	1715	1716	1717	1718	1719	1720	1721	1722	1723	1724	1725	1726	1727	1728	1729	1730	1731	1732	1733	1734	1735	1736	1737	1738	1739	1740	1741	1742	1743	1744	1745	1746	1747	1748	1749	1750	1751	1752	1753	1754	1755	1756	1757	1758	1759	1760	1761	1762	1763	1764	1765	1766	1767	1768	1769	1770	1771	1772	1773	1774	1775	1776	1777	1778	1779	1780	1781	1782	1783	1784	1785	1786	1787	1788	1789	1790	1791	1792	1793	1794	1795	1796	1797	1798	1799	1800	1801	1802	1803	1804	1805	1806	1807	1808	1809	1810	1811	1812	1813	1814	1815	1816	1817	1818	1819	1820	1821	1822	1823	1824	1825
------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------

ABL7/0006;		ABL7/0006; standard; DNA; 2370
15-MAY-2002	(first entry)	
Pancreas cancer related gene		
Human; cancer; colon; breast;		
stomach; lung; prostate; pancreatic		
cystic fibrosis; gene therapy; anti-		
gene; ds.		
Homo sapiens.		
WOM200194629-A2,		
13-DEC-2001;		
30-MAY-2001; 2001WO-US10838.		
05-JUN-2000; 2000US-209473P.		
05-JUN-2000; 2000US-209531P.		
05-JUN-2000; 2000US-209541P.		
05-JUN-2000; 2000US-209542P.		
25-SEP-2000; 2000US-235028P.		
25-SEP-2000; 2000US-235134P.		
25-SEP-2000; 2000US-235261P.		
25-SEP-2000; 2000US-235262P.		
25-SEP-2000; 2000US-235368P.		
25-SEP-2000; 2000US-235371P.		
27-SEP-2000; 2000US-235620P.		
27-SEP-2000; 2000US-235833P.		
27-SEP-2000; 2000US-235834P.		
28-SEP-2000; 2000US-236028P.		
28-SEP-2000; 2000US-236032P.		
28-SEP-2000; 2000US-236103P.		
28-SEP-2000; 2000US-236104P.		
28-SEP-2000; 2000US-236111P.		
28-SEP-2000; 2000US-236911P.		
03-OCT-2000; 2000US-237172P.		
03-OCT-2000; 2000US-237173P.		
03-OCT-2000; 2000US-237294P.		
03-OCT-2000; 2000US-237295P.		
03-OCT-2000; 2000US-237316P.		
03-OCT-2000; 2000US-237358P.		
03-OCT-2000; 2000US-237568P.		
03-OCT-2000; 2000US-237604P.		
03-OCT-2000; 2000US-237606P.		
03-OCT-2000; 2000US-237608P.		
03-OCT-2000; 2000US-237609P.		
01-NOV-2000; 2000US-245984P.		

RESULT 4
ABI-70006

PT XX 30 Query Match 2370; 636 A; 517 G; 704 T; 0 other;

XX Best Local Similarity 100.0%; Prod. No. 0;

XX Machines 2370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Claim 1: SEQ ID 8343; 44pp; English.

The present invention describes a method (M1) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical agent (A) and determining whether the cells exhibit a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 847 sequences (given in ABLE1664 to ABU70101), or is at least partially identical to (S). Where the change in expression of (I) is indicative of a change in the activity and/or an anti-neoplastic agent, and can be used for producing a product which is the data collected that is specific to the anti-neoplastic agent as a structure and/or properties of the agent. M1 can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, esophageal, ovarian, kidney, prostate or pancreatic cancer, melanoma, leukemia, lymphoma, multiple myeloma, glioma, sarcoma, ductal cancer, infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Kilm's tumour.

XX 30 Sequence 2370 BP; 636 A; 517 G; 704 T; 0 other;

Query Match 2370; 636 A; 517 G; 704 T; Length 2370;

Best Local Similarity 100.0%; Prod. No. 0;

Machines 2370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACGAGGAGGCTAACGCTCTCTCTCCGCGGGGTGATGACGGTGAACACTG 60

DB 1 CACGAGGAGGCTAACGCTCTCTCTCCGCGGGGTGATGACGGTGAACACTG 60

QY 61 GTGCTGAAGGCAACCTCAGCTTACTCCAGATGGGCGATGGTGCATCTCATCGCT 120

DB 61 GTGCTGAAGGCAACCTCAGCTTACTCCAGATGGGCGATGGTGCATCTCATCGCT 120

QY 62 GCTCTTGGGCGACCTCCTCTCTCCGAGATGGGCGATGGTGCATCTCATCGCT 120

DB 62 GCTCTTGGGCGACCTCCTCTCTCCGAGATGGGCGATGGTGCATCTCATCGCT 120

QY 121 TTATGATGACGAGGAGGATGGTGTGACGACTTATTCAGAGATTGCCAATACCTC 180

DB 121 TTATGATGACGAGGAGGATGGTGTGACGACTTATTCAGAGATTGCCAATACCTC 180

QY 181 TATGCTGCAACACCTCGAAGTTCAGTCTGATGACTTATTCAGAGATTGCCAATACCTC 240

DB 181 TATGCTGCAACACCTCGAAGTTCAGTCTGATGACTTATTCAGAGATTGCCAATACCTC 240

QY 191 TATGCTGCAACACCTCGAAGTTCAGTCTGATGACTTATTCAGAGATTGCCAATACCTC 240

DB 191 TATGCTGCAACACCTCGAAGTTCAGTCTGATGACTTATTCAGAGATTGCCAATACCTC 240

QY 241 GAGCTTATGATGACCAACCTCTCTCCAGCAACCTCTCTCAGAAATCAACCTTGGC 300

DB 241 GAGCTTATGATGACCAACCTCTCTCCAGCAACCTCTCTCAGAAATCAACCTTGGC 300

QY 301 CGGTGCTCAATCTCATGCTAAACATCATGACTTCACTCTTGAAGTGTGCGAAG 360

DB 301 CGGTGCTCAATCTCATGCTAAACATCATGACTTCACTCTTGAAGTGTGCGAAG 360

QY 361 GCGAGTGTGGAAGGCTCTCTGACGACACAGGACGAGAGTGTCTATCGACT 420

DB 361 GCGAGTGTGGAAGGCTCTCTGACGACACAGGACGAGAGTGTCTATCGACT 420

QY 421 AAGTGTTCAGAGAGCAATCCTGTAAGAGAGAGAGAGAGCAATATGCTCGAG 480

DB 421 AAGTGTTCAGAGAGCAATCCTGTAAGAGAGAGAGAGAGCAATATGCTCGAG 480

QY 481 CGGATGCTCTGTGAGATGTCAGACACCTCTCTCTCTCTCTCTCTCTCTCTCTCT 540

DB 481 CGGATGCTCTGTGAGATGTCAGACACCTCTCTCTCTCTCTCTCTCTCTCTCTCT 540

QY 541 CAGACTCTGCAAAATATGTTCTTCTGAGTCAATATGATGGAGAGTGTCTTAC 600

DB 541 CAGACTCTGCAAAATATGTTCTTCTGAGTCAATATGATGGAGAGTGTCTTAC 600

QY 601 CATCTCAGAGGAGAGAGTCTCTGAGACACGGGCTGTTTCTATGCTGTGAATA 660

DB 601 CATCTCAGAGGAGAGAGTCTCTGAGACACGGGCTGTTTCTATGCTGTGAATA 660

QY 661 GCGAGGCTCTGGCTTACCTGACATCTCTATAGAGACTTAAACACGAG 720

DB 661 GCGAGGCTCTGGCTTACCTGACATCTCTATAGAGACTTAAACACGAG 720

QY 721 AATATTTTCTAGATTCACAGGACACATGCTCTTACTGATTTGGGCTCTGACGAG 780

DB 721 AATATTTTCTAGATTCACAGGACACATGCTCTTACTGATTTGGGCTCTGACGAG 780

QY 781 AATATTTTCTAGATTCACAGGACACATGCTCTTACTGATTTGGGCTCTGACGAG 840

DB 781 AATATTTTCTAGATTCACAGGACACATGCTCTTACTGATTTGGGCTCTGACGAG 840

QY 841 AATATTTTCTAGATTCACAGGACACATGCTCTTACTGATTTGGGCTCTGACGAG 900

DB 841 AATATTTTCTAGATTCACAGGACACATGCTCTTACTGATTTGGGCTCTGACGAG 900

QY 901 TGTATGATGCTGTATGCTGCTGCTCTTATATGCGAAGCAAGCACTGAAATGAT 960

DB 901 TGTATGATGCTGTATGCTGCTGCTCTTATATGCGAAGCAAGCACTGAAATGAT 960

QY 961 GACAACTTCTGACACAGCTCTCTGCTAGTCAAGCAAAATATTAATTTCCGCAAGAC 1020

DB 961 GACAACTTCTGACACAGCTCTCTGCTAGTCAAGCAAAATATTAATTTCCGCAAGAC 1020

QY 1021 GACAACTTCTGACACAGCTCTCTGCTAGTCAAGCAAAATATTAATTTCCGCAAGAC 1080

DB 1021 GACAACTTCTGACACAGCTCTCTGCTAGTCAAGCAAAATATTAATTTCCGCAAGAC 1080

QY 1081 ATGAGATTAAGATGATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1140

DB 1081 ATGAGATTAAGATGATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1140

QY 1141 ATGAGATTAAGATGATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1200

DB 1141 ATGAGATTAAGATGATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1200

QY 1201 CCGAGGCTTACGAGAGGCTTGCCCAACTCTGATGCAATCTGCAAGTCCGCTGCTTC 1260

DB 1201 CCGAGGCTTACGAGAGGCTTGCCCAACTCTGATGCAATCTGCAAGTCCGCTGCTTC 1260

QY 1261 CCGAGGCTTACGAGAGGCTTGCCCAACTCTGATGCAATCTGCAAGTCCGCTGCTTC 1320

DB 1261 CCGAGGCTTACGAGAGGCTTGCCCAACTCTGATGCAATCTGCAAGTCCGCTGCTTC 1320

QY 1321 AGGACTCTCTCTCTGACACCTCTGATGAGCTCTGCTAGGCTTGTATATGATGCTTC 1380

DB 1321 AGGACTCTCTCTCTGACACCTCTGATGAGCTCTGCTAGGCTTGTATATGATGCTTC 1380

QY 1381 AGGACTCTCTCTCTGACACCTCTGATGAGCTCTGCTAGGCTTGTATATGATGCTTC 1440

DB 1381 AGGACTCTCTCTCTGACACCTCTGATGAGCTCTGCTAGGCTTGTATATGATGCTTC 1440

QY 1441 TTTGCACTCTGGAAGCTTACGATCTTATGACACCTCTGACACCTCTGACACCTCTG 1500

DB 1441 TTTGCACTCTGGAAGCTTACGATCTTATGACACCTCTGACACCTCTGACACCTCTG 1500

QY 1501 GAGCACTCTCTGACACCTCTGACACCTCTGACACCTCTGACACCTCTGACACCTCTG 1560

DB 1501 GAGCACTCTCTGACACCTCTGACACCTCTGACACCTCTGACACCTCTGACACCTCTG 1560

QY 1561 TGTATCTCTGGAAGCTTACGATCTTATGACACCTCTGACACCTCTGACACCTCTG 1620

DB 1561 TGTATCTCTGGAAGCTTACGATCTTATGACACCTCTGACACCTCTGACACCTCTG 1620

QY 1621 AAGGAGGCTCTCTGGAAGCTTACGATCTTATGACACCTCTGACACCTCTGACACCTCTG 1680

DB 1621 AAGGAGGCTCTCTGGAAGCTTACGATCTTATGACACCTCTGACACCTCTGACACCTCTG 1680

QY 1681 TATGAGAGGCTCTCTGGAAGCTTACGATCTTATGACACCTCTGACACCTCTGACACCTCTG 1740

DB 1681 TATGAGAGGCTCTCTGGAAGCTTACGATCTTATGACACCTCTGACACCTCTGACACCTCTG 1740

QY 1741 TATGAGAGGCTCTCTGGAAGCTTACGATCTTATGACACCTCTGACACCTCTGACACCTCTG 1800

DB 1741 TATGAGAGGCTCTCTGGAAGCTTACGATCTTATGACACCTCTGACACCTCTGACACCTCTG 1800

XX (SMK) SMITIKLINE BEZIAN CORP.
 PA KUMAR JN;
 PT NPT: 1999-047627/05.
 XX P-FSD: AM90139.
 XX Treating chronic renal failure, diabetic nephropathy and Alzheimer's
 PT disease - by administration of nucleic acids and antagonists which
 XX inhibit the expression of the gene for the protein kinase C
 PT regulated kinase (sgk), a serine/threonine protein kinase
 XX Disclosure: Page 14-15; 17pp; English.
 XX This sequence encodes a novel human serum glucocorticoid regulated kinase
 CC (sgk) protein which is a member of the serine/threonine protein kinase
 CC family. This protein is used for the treatment of a subject having need
 CC for a protein kinase C regulated kinase, e.g., for the treatment of chronic renal failure, diabetic nephropathy,
 CC inflammation, Alzheimer's disease and wounds.
 XX Sequence 2346 BP: 608 A; 520 C; 518 G; 700 T; 0 other;
 XX

Query Match 97.1%; Score 2301.6; DB 20; Length 2346;
 Best Local Similarity 99.74; Pred. No. 0; 4; Indels 3; Gaps 3;
 Matches 2337; Conservative

1 CACGAGGAGGCGCTTAAGCTCTTCTGCTCCGCGGGTGATACAGGTGAAACATGAG 60
 3 CAGGAGGAGGCGCTTAAGCTCTTCTGCTCCGCGGGTGATACAGGTGAAACATGAG 62
 61 GCTGCTTAAGGCGACCTTACTTACTTCTAGGATGAGGCGATGTCGCAATCTCATGCT 120
 63 GCTGCTTAAGGCGACCTTACTTACTTCTAGGATGAGGCGATGTCGCAATCTCATGCT 122
 121 TCTATGAGGAGGAGGAGTGGTCTGAAGACTTTATTCAGAGATTGCCAATACCTC 180
 123 TCTATGAGGAGGAGGAGTGGTCTGAAGACTTTATTCAGAGATTGCCAATACCTC 182
 181 TATGATATCCAAAGACCTCGAAGTCTAGTCCATCTGAAGATCTCCCACTCAGGAGCT 240
 183 TATGATATCCAAAGACCTCGAAGTCTAGTCCATCTGAAGATCTCCCACTCAGGAGCT 242
 241 GAGCTATGATATCCAAAGACCTCGAAGTCTAGTCCATCTGAAGATCTCCCACTCAGGAGCT 300
 243 GAGCTATGATATCCAAAGACCTCGAAGTCTAGTCCATCTGAAGATCTCCCACTCAGGAGCT 302
 301 CGGTGCTCCATCTCTCATCTTAACATCTGACTTTCATCTCTGAAGATGAGGAGAG 360
 303 CGGTGCTCCATCTCTCATCTTAACATCTGACTTTCATCTCTGAAGATGAGGAGAG 362
 361 GCGAGTGTGGAAGGCTCTCTAGACAGACAGACGAGGAAGGTCTCTATGACCT 420
 363 GCGAGTGTGGAAGGCTCTCTAGACAGACAGACGAGGAAGGTCTCTATGACCT 422
 421 AAGGTGTTCAGAGAGAGCAATCTGAAAGAGAGAGAGAGAGCAATATATGTCGAG 480
 423 AAGGTGTTCAGAGAGAGCAATCTGAAAGAGAGAGAGAGAGCAATATATGTCGAG 482
 481 CGGAATGTGTTGAGAGATGTGAGACACCTTCTCTGCGGCGCTCATCTCTCTC 540
 483 CGGAATGTGTTGAGAGATGTGAGACACCTTCTCTGCGGCGCTCATCTCTCTC 542
 541 CAGACTGCTCAAAATGTACTTGTCTCTAGACTACATATATGTCGAGAGATGTTCTAC 600
 543 CAGACTGCTCAAAATGTACTTGTCTCTAGACTACATATATGTCGAGAGATGTTCTAC 602
 601 CATCTCCAGAGAGAGGCTGCTCTGCAACACAGGCGCTGTTCTATGCTCTGCAATTA 660
 603 CATCTCCAGAGAGAGGCTGCTCTGCAACACAGGCGCTGTTCTATGCTCTGCAATTA 662
 661 GCGACTGCTCTGCGCTACCTGCACTCACTGCACTCTTATAGAGACTTAAACACAG 720

663 GCGACTGCTCTGCGCTACCTGCACTCACTGCACTCTTATAGAGACTTAAACACAG 722
 721 AATATTTTCTAGATTTACAGAGAGACATGCTCTACTGATTTGGAGCTCTGAAAG 780
 723 AATATTTTCTAGATTTACAGAGAGACATGCTCTACTGATTTGGAGCTCTGAAAG 782
 781 AATATTTTCTAGATTTACAGAGAGACATGCTCTACTGATTTGGAGCTCTGAAAG 840
 783 AATATTTTCTAGATTTACAGAGAGACATGCTCTACTGATTTGGAGCTCTGAAAG 842
 841 GAGGTGCTCTTATAGAGAGCTTTATAGAGAGCTTGAGACTTGCTGCTGAGATTTGTC 900
 843 GAGGTGCTCTTATAGAGAGCTTTATAGAGAGCTTGAGACTTGCTGCTGAGATTTGTC 902
 901 TGTATTTAGATCTGTATGCTGCTGCGCTCTTTATACCGCAAAACACTGAATATAC 960
 903 TGTATTTAGATCTGTATGCTGCTGCGCTCTTTATACCGCAAAACACTGAATATAC 962
 961 GACAAACATCTGCAAGAGAGCTCTGACAGCAAAACATATACAAATCTGCGAANAC 1020
 963 GACAAACATCTGCAAGAGAGCTCTGACAGCAAAACATATACAAATCTGCGAANAC 1022
 1021 GCGAGGAGGCTCTGCGAGAGAGAGCAAAACAGGCTGAGGAGCAAGAGATTTTC 1080
 1023 GCGAGGAGGCTCTGCGAGAGAGAGCAAAACAGGCTGAGGAGCAAGAGATTTTC 1082
 1141 ATGAGAGATTAAGAGTCACTGCTCTCTCTTAACTACTGGATGATCTCATTAATAG 1140
 1143 ATGAGAGATTAAGAGTCACTGCTCTCTCTTAACTACTGGATGATCTCATTAATAG 1142
 1141 AGATATTACTCCCTCTTACCCCAATGTGAGTGGCCACAGCACTACGCACTTTAG 1200
 1143 AGATATTACTCCCTCTTACCCCAATGTGAGTGGCCACAGCACTACGCACTTTAG 1202
 1201 CCGAGGATTAACAGAGAGCTCTCCCACTGCACTGAGCACTGCGCTGAGAGATTTTC 1260
 1203 CCGAGGATTAACAGAGAGCTCTCCCACTGCACTGAGCACTGCGCTGAGAGATTTTC 1262
 1261 GTACACAGAGCTGCAAGAGCTGCGAGAGCTTCTCTAGCTTTTCTCTGAGCTCTTC 1320
 1263 GTACACAGAGCTGCAAGAGCTGCGAGAGCTTCTCTAGCTTTTCTCTGAGCTCTTC 1322
 1321 ACAGACTCTTCTCTGACCTGTAGGCTGTGGTGTAAAGATTTATGTGTGTTTC 1380
 1323 ACAGACTCTTCTCTGACCTGTAGGCTGTGGTGTAAAGATTTATGTGTGTTTC 1382
 1381 CGAATGTATTGATGCTTTGAGTGGCCAGCTGCTTAAAGAGATTTATGTGTGTTTC 1440
 1383 CGAATGTATTGATGCTTTGAGTGGCCAGCTGCTTAAAGAGATTTATGTGTGTTTC 1442
 1441 TTTCACATCTCTGGAAGCTAGCACTATTTATGCACTGCTGCGAGTCTGAGAA 1499
 1443 TTTCACATCTCTGGAAGCTAGCACTATTTATGCACTGCTGCGAGTCTGAGAA 1502
 1500 AGAGAGACTCTCTCAGTCACTGAGGCTTCTGATTTTCTGATTTTCTCTCTCAAGT 1558
 1503 AGAGAGACTCTCTCAGTCACTGAGGCTTCTGATTTTCTGATTTTCTCTCTCAAGT 1562
 1559 GTTCATCTCTGGAAGAGAGCTTAGAGAGGCGCTTCTAGAGAGAGAGAGATTTGCTTA 1618
 1561 GTTCATCTCTGGAAGAGAGCTTAGAGAGGCGCTTCTAGAGAGAGAGAGATTTGCTTA 1622
 1619 GAAAGCGAGCCTCTCTTCTTAAAGAGCTGCGCACTGAGCTGTGGCGCTGATACAGA 1677
 1621 GAAAGCGAGCCTCTCTTCTTAAAGAGCTGCGCACTGAGCTGTGGCGCTGATACAGA 1682
 1679 TATATGAGAGAGAGCTTCTCTGAGAGAGAGAGCTGTGAGAGAGAGAGATTTGCTTA 1737
 1681 TATATGAGAGAGAGCTTCTCTGAGAGAGAGAGCTGTGAGAGAGAGAGATTTGCTTA 1742
 1739 GTTGTCTGAGTCTCTTCTTCTGAGAGAGAGAGCTGTGAGAGAGAGAGATTTGCTTA 1797

[illegible]

Db	1741	CTGTGTGACACCTCGTGTGAATGTGTGTATGCTGTATCAGAGAGGATTTGTGTATACG	
Qy	1831	ATCAATGCGACGCTGTGAGAGACATCAACGTCGATGCTGTCTGTCTCATATTTG	1890
Db	1801	ATCAATGCGACGCTGTGAGAGACATCAACGTCGATGCTGTCTGTCTCATATTTG	1860
Qy	1881	GAGATTAATTTATTTGTGTAGACTTTTGTAGATAGAGGTTATACTAAATTTATGA	1950
Db	1861	GAGATTAATTTATTTGTGTAGACTTTTGTAGATAGAGGTTATACTAAATTTATGA	1920
Qy	1951	ATATGCTGTGCATGACTGTATGATAGATGCTTAAGAAGCACTGCTGTACAAATTT	2010
Db	1921	ATATGCTGTGCATGACTGTATGATAGATGCTTAAGAAGCACTGCTGTACAAATTT	1980
Qy	2011	TCATATTTTAGAAGGGTTTTATGAGCAATGCCCACTGTCACTACAGCGTGTCT	2070
Db	1981	TCATATTTTAGAAGGGTTTTATGAGCAATGCCCACTGTCACTACAGCGTGTCT	2040
Qy	2071	GTITTTTCATCTTTAAATGACACTGTAAATGGCAATGCTCTTATTTTCTTTTCTG	2130
Db	2041	GTITTTTCATCTTTAAATGACACTGTAAATGGCAATGCTCTTATTTTCTTTTCTG	2100
Qy	2131	ATTCCTGTATATGTATGTATGATATAAAGACGCTGTACATGGGTATTAACATCT	2190
Db	2101	ATTCCTGTATATGTATGTATGATATAAAGACGCTGTACATGGGTATTAACATCT	2160
Qy	2191	ATTTTAAACTCTAGAGCCTATTTCTTAATGTAAACACCTATTAATGCTATTAATAA	2250
Db	2161	ATTTTAAACTCTAGAGCCTATTTCTTAATGTAAACACCTATTAATGCTATTAATAA	2220
Qy	2251	CATGSGTTATTAATAGCTCAATCTCTCCCTCATCCATCACACACTTTTGTGTGGA	2310
Db	2221	CATGSGTTATTAATAGCTCAATCTCTCCCTCATCCATCACACACTTTTGTGTGGA	2280
Qy	2311	TAACCTGATTTTGGCTTTTGCAATAAACCTGT 2341	
Db	2281	TAACCTGATTTTGGCTTTTGCAATAAACCTGT 2311	
RESULT 8			
Db	1741	ACA56174 standard; cDNA; 2311 bp.	
Qy	1831	ACA56174;	
Db	1801	ACA56174;	
Qy	1881	06-JUN-2003 (first entry)	
Db	1861	Human signalling pathway polynucleotide probe SEQ ID NO 772.	
Qy	1951	Human; probe; ss; array element; Parkinson's disease;	
Db	1921	Human; probe; ss; array element; Parkinson's disease;	
Qy	2011	signalling pathway population; cancer; adenocarcinoma; leukemias;	
Db	1981	immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; microarray.	
Qy	2101	Homo sapiens.	
Db	2071	US5050938-B1.	
Qy	2161	31-DEC-2002.	
Db	2131	30-JAN-1998; 98US-0016434.	
Qy	2221	30-JAN-1998; 98US-0016434.	
Db	2191	(INCY) INCYTE GENOMICS INC.	
Qy	2281	Am-Young J, Seilheimer JJ;	
Db	2251	WPI; 2003-352189/33.	
Combination of polynucleotide probes, useful as array elements in a microarray or monitoring the expression of a number of target			

xx

p8 Claim 1; SEQ ID NO 772: 65pp: English.

xx The invention relates to a combination which, comprises a number of
 cc polynucleotide probes comprising a sequence selected from one of the 1490
 cc sequences mentioned in the specification. The combination is useful as an
 cc array element in a microarray for monitoring the expression of a number
 cc of genes, for example, in the diagnosis and prognosis of a disease, for
 cc diagnosis and treatment of cancer and immunopathology and neuropathology.
 cc The microarray is useful in diagnostics and treatment regimens, drug
 cc discovery and development, toxicological and carcinogenicity studies,
 cc forensic and pharmaceutical research and for developing new tests and
 cc profiles for the effects of currently available therapeutic drugs. The
 cc combination is also useful for purifying a subpopulation of mRNAs, cDNAs
 cc and genomic fragments and in research and diagnostic applications. The
 cc combination is also useful for identifying and characterizing genes and
 cc for different signaling pathway populations which can be used to diagnose
 cc various diseases including cancer e.g. adenocarcinoma and leukemia,
 cc immunopathies e.g. AIDS and asthma, neuropathies e.g. Alzheimer's disease
 cc and other diseases. The present sequence represents a polynucleotide
 cc probe of the invention.
 cc Note: The sequence data for this patent did not form part of the printed
 cc specification but was obtained in electronic format directly from USPTO
 cc at seqdata.uspto.gov/sequence.html?docid=0650093881.

xx Sequence 2311 BP; 604 A; 508 G; 506 G; 692 T; 1 other;

Query Match 95.5%; Score 2262.0; DB 25; Length 2311;
 Query Similarity 99.5%; 7 mismatches; 8; Indels 3; Gaps 3;
 Matches 2300; Conservative 0; Mismatches

Qy 34 GGGTGGTGTATGAGCGTGAACCTCAGGCTGCTTAGGGGCAACCTCAGCTTACTCCGAGATG 93
 Db 1 GGGTGGTGTATGAGCGTGAACCTCAGGCTGCTTAGGGGCAACCTCAGCTTACTCCGAGATG 93
 Qy 94 AGGGCATGCTGGCAATTCATCTCCTTTTCATGAAGCAGAGAGAGATGGCTCTGAAGAC 153
 Db 1 AGGGCATGCTGGCAATTCATCTCCTTTTCATGAAGCAGAGAGAGATGGCTCTGAAGAC 153
 Qy 61 AGGGCGCTGCTGGCAATTCATCTCCTTTTCATGAAGCAGAGAGATGGCTCTGAAGAC 120
 Db 1 AGGGCGCTGCTGGCAATTCATCTCCTTTTCATGAAGCAGAGAGATGGCTCTGAAGAC 120
 Qy 134 TTTTATTTCAGAAATTGCCAATTAAGCTCTATGATGCAGCAACCTGAACTTCAGTCCATC 213
 Db 1 TTTTATTTCAGAAATTGCCAATTAAGCTCTATGATGCAGCAACCTGAACTTCAGTCCATC 213
 Qy 121 TTATGAGATATGAGATATGAGATATGAGATATGAGATATGAGATATGAGATATGAGAT 180
 Db 1 TTATGAGATATGAGATATGAGATATGAGATATGAGATATGAGATATGAGATATGAGAT 180
 Qy 214 TTGAAGATCTCCCAAGCTCAGAGAGCTGAGCTTATGATGATCAACACCTCTCTCCACCA 273
 Db 1 TTGAAGATCTCCCAAGCTCAGAGAGCTGAGCTTATGATGATCAACACCTCTCTCCACCA 273
 Qy 181 TGAAGATCTCCCAAGCTCAGAGAGCTGAGCTTATGATGATCAACACCTCTCTCCACCA 240
 Db 1 TGAAGATCTCCCAAGCTCAGAGAGCTGAGCTTATGATGATCAACACCTCTCTCCACCA 240
 Qy 274 AGTCTCTCTAGCAAACTCAGCTTGGCGCTGGCTGCAATCTCTATGCTTAACATCTGAC 333
 Db 241 AGTCTCTCTAGCAAACTCAGCTTGGCGCTGGCTGCAATCTCTATGCTTAACATCTGAC 333
 Qy 241 AGTCTCTCTAGCAAACTCAGCTTGGCGCTGGCTGCAATCTCTATGCTTAACATCTGAC 300
 Db 334 TTTCCATCTTGAAGATGATCGGAAGGGCAGTTTTGAAGAGTCTCTAGCAAGAC 393
 Qy 301 TTTCCATCTTGAAGATGATCGGAAGGGCAGTTTTGAAGAGTCTCTAGCAAGAC 360
 Db 394 AGGCAAGAAAGATGTTCTATGACGCTCAAGTGTTCAGCAAGAAAGCAATCTCGAAAG 453
 Qy 361 AGGCAAGAAAGATGTTCTATGACGCTCAAGTGTTCAGCAAGAAAGCAATCTCGAAAG 420
 Qy 451 AGGCAAGAAAGATGTTCTATGACGCTCAAGTGTTCAGCAAGAAAGCAATCTCGAAAG 420
 Db 421 AAGGAGAGAGCAATATATGCGAGCGGATGTTCTGTAAGATATGAAGCAACCT 513
 Qy 514 TTTCTGTGGGGCTCTACTCTCTTCCAGCTCTGACAAATTTGACTTTGTCTGAC 573
 Db 471 TTTCTGTGGGGCTCTACTCTCTTCCAGCTCTGACAAATTTGACTTTGTCTGAC 540
 Qy 484 TACATTAATGCGAGAGTGTCTACCATCTCCAGCAAGAGGCTCTCTCTGACCA 633
 Db 541 TACATTAATGCGAGAGTGTCTACCATCTCCAGCAAGAGGCTCTCTCTGACCA 600
 Qy 634 CGGGCTGCTTCTATGCTCTGAAATACCAAGTCCCTTGGGCTACCTGATCTGAC 693

Db 601 CGGGCTGCTTCTATGCTCTGAAATACGCAATTCGCTTGGGCTACCTGATCTATGAC 660
 Qy 694 ATCGCTTTATGAGAGCTTAAACGAGCAATTCGCTTGGGCTACCTGATCTATGAC 753
 Db 661 ATCGCTTTATGAGAGCTTAAACGAGCAATTCGCTTGGGCTACCTGATCTATGAC 720
 Qy 754 ATCGCTTTATGAGAGCTTAAACGAGCAATTCGCTTGGGCTACCTGATCTATGAC 813
 Db 721 ATCGCTTTATGAGAGCTTAAACGAGCAATTCGCTTGGGCTACCTGATCTATGAC 780
 Qy 813 ATCGCTTTATGAGAGCTTAAACGAGCAATTCGCTTGGGCTACCTGATCTATGAC 870
 Db 781 ATCGCTTTATGAGAGCTTAAACGAGCAATTCGCTTGGGCTACCTGATCTATGAC 840
 Qy 874 GTGGAGCTGTGGTGGGAGCTGCTTGTATGAGATGCTGTATGAGCTGGGCTTTT 933
 Db 841 GTGGAGCTGTGGTGGGAGCTGCTTGTATGAGATGCTGTATGAGCTGGGCTTTT 900
 Qy 934 TATAGCCAGAACAGAGCTGGAATGTAGACACACATCTGACAGAGCTCTCCAGTGAA 993
 Db 901 TATAGCCAGAACAGAGCTGGAATGTAGACACACATCTGACAGAGCTCTCCAGTGAA 960
 Qy 994 CTAATAATACAAATTCGCAAGAGAGCTCTGAGAGGCTCTGCAAGAGACAGACA 1053
 Db 961 CTAATAATACAAATTCGCAAGAGAGCTCTGAGAGGCTCTGCAAGAGACAGACA 1020
 Qy 1054 AAGGGCTCGGGGCAAGAGTACTCATGAGAGTAAGAGTCAATGCTCTCTCTCTT 1113
 Db 1021 AAGGGCTCGGGGCAAGAGTACTCATGAGAGTAAGAGTCAATGCTCTCTCTCTT 1080
 Qy 1114 ATTAAGTCTGGAGTCACTCAATTAATAGAGATTAAGTCAATGCTCTCTCTCTT 1173
 Db 1081 ATTAAGTCTGGAGTCACTCAATTAATAGAGTAACTTCCCTCTTTAACCCAAATGAGT 1140
 Qy 1174 GGGCCCAAGAGCTACGGCACTTTCAGCCCGAGTTTACGAGAGGCTCTCTCTCTCT 1233
 Db 1141 GGGCCCAAGAGCTACGGCACTTTCAGCCCGAGTTTACGAGAGGCTCTCTCTCTCT 1200
 Qy 1234 ATTGCCCAAGTCCCTGACAGCTCTGCTGACAGGAGCTCAAGAGCTCTCTCTCTCT 1293
 Db 1201 ATTGCCCAAGTCCCTGACAGCTCTGCTGACAGGAGCTCAAGAGCTCTCTCTCTCT 1260
 Qy 1294 TTTCTAGGCTTTTCTCTATGCGCTTCGACAGAGCTCTTCTCTCTCTCTCTCTCT 1353
 Db 1261 TTTCTAGGCTTTTCTCTATGCGCTTCGACAGAGCTCTTCTCTCTCTCTCTCTCT 1320
 Qy 1354 GTTCTTAAGAGATTTAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1413
 Db 1321 GTTCTTAAGAGATTTAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1380
 Qy 1414 CAGCTGACAGAGCTTACAGAGATTTTTCAGACCTCTGAGAGCTCTGAGAGCTCTCT 1473
 Db 1381 CAGCTGACAGAGCTTACAGAGATTTTTCAGACATTTGACAGCTCTGAGAGCTCTCT 1440
 Qy 1474 GAGAGAGAGCTCTGAGAGCTCTGAGAGCTCTGAGAGCTCTGAGAGCTCTGAGAGCT 1532
 Db 1441 GAGAGAGAGCTCTGAGAGCTCTGAGAGCTCTGAGAGCTCTGAGAGCTCTGAGAGCT 1500
 Qy 1533 TTTCTTTATTTCT 1592
 Db 1501 TTTCTTTATTTCT 1560
 Qy 1593 CTTAGAGAGAGAGAGAGTTCCTTGAAGAGGAGCCTGTCTCTCTCTCTCTCTCTCTCT 1651
 Db 1561 CTTAGAGAGAGAGAGAGTTCCTTGAAGAGGAGCCTGTCTCTCTCTCTCTCTCTCTCT 1620
 Qy 1652 AGATCTCTCTGGGCTGTGATGAGATATATGAAATGAGTCTCTCTCTCTCTCTCTCTCT 1710
 Db 1621 AGATCTCTCTGGGCTGTGATGAGATATATGAAATGAGTCTCTCTCTCTCTCTCTCTCT 1680
 Qy 1711 GTTAGCT 1770

Db 1681 GTTACGTCGAAGCTTTTCCTATGCGAGTGTTTCAGTCTTTATTTTCCTCTGGATAT 1740
 Qy 1771 GCTGTGTGACCTCGTGTGATGCTGTATGCTGATGACAGAGGATTTCTTTATTAAC 1830
 Db 1741 GCTGTGTGACCTCGTGTGATGCTGTATGCTGATGACAGAGGATTTCTTTATTAAC 1800
 Qy 1831 ATCATGATGACCTTTGACAGACATACAGCTGGACATGTTGCTTCTTCATATTTG 1890
 Db 1801 ATCATGATGACCTTTGACAGACATACAGCTGGACATGTTGCTTCTTCATATTTG 1860
 Qy 1891 GAAGTAAATATATGCTGACCTTTTGTGAAGATAGCTTAAATACAAATATATGA 1950
 Db 1861 GAAGTAAATATATGCTGACCTTTTGTGAAGATAGCTTAAATACAAATATATGA 1920
 Qy 1951 ATGGTCTTGCATGACTGATTCAGATGCTTAAAGAGCTTCTGCTACAAATAT 2010
 Db 1921 ATGGTCTTGCATGACTGATTCAGATGCTTAAAGAGCTTCTGCTACAAATAT 1980
 Qy 2011 TCAATTTTAAAGAGCTTTTATGAGCAATCCCTGCTTATGAGAGAGCTGTGT 2070
 Db 2071 TCAATTTTAAAGAGCTTTTATGAGCAATCCCTGCTTATGAGAGAGCTGTGT 2040
 Qy 2071 GTTCTTCAATGTTTAAATGCTGACCTGTTAAATGGGCAATATTTATGTTTCTTTC 2130
 Db 2131 GTTCTTCAATGTTTAAATGCTGACCTGTTAAATGGGCAATATTTATGTTTCTTTC 2100
 Qy 2131 ATTCCTTAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2190
 Db 2191 ATTCCTTAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2160
 Qy 2191 ATATTTAAATCTTACAGCTTATTTGATGATGATGATGATGATGATGATGATGAT 2250
 Db 2251 ATATTTAAATCTTACAGCTTATTTGATGATGATGATGATGATGATGATGATGAT 2220
 Qy 2251 CATGCTTAATACAGACATCTTCCCTGCTTCCCTGCTTCCCTGCTTCCCTGCT 2310
 Db 2311 CATGCTTAATACAGACATCTTCCCTGCTTCCCTGCTTCCCTGCTTCCCTGCT 2280
 Qy 2311 TAACTGATTTTGTGTCATTAACCTTG 2341
 Db 2341 TAACTGATTTTGTGTCATTAACCTTG 2311

RESULT 9

AM33647 standard; cDNA, 2281 BP.
 AC AM33647
 XX 08-DEC-1999 (first entry)
 XX Human breast tumour-associated BST 37.
 DE Suppressed sequence tag, EST; human; breast; cancer; gene therapy;
 SW treatment; tumour; cytosolic; medication; ss.
 OS Homo sapiens.
 PN DE19813839-AL.
 PD 23-SEP-1999.
 PF 20-MAR-1998; 98DE-1013839.
 PR 20-MAR-1998; 98DE-1013839.
 PA (HEPA-) METAGEN GES GENOWORKSHU MBH.

PI Specht T, Hinzmann B, Schwallt A, Pilarsky C, Dahl E, Rosenthal A;
 NP1; 1999-528981/45.
 DR P-PSDB; MN458573.

Human nucleic acid sequences and protein products from tumor breast tissue, useful for breast cancer therapy.

Claim 1a; 116-117; 188pp: German.

This invention describes novel human nucleic acid sequences from tumor breast tissue which have cytosolic activity. The nucleic acid sequences can be used to produce and isolate full-length gene sequences. They can be used to express proteins, which can be used as tools to find an antisense form. They are especially useful for medicaments for gene therapy to treat breast cancer. AM33611-248617 represents expressed sequence tags described in the method of the invention.

Sequence 2281 BP: 601 A; 498 G; 494 G; 688 T; 0 other;

Query Match: 90.3%; Score 2140.8; DB 20; Length 2281;
 Occurrence: 100%; Positives: 1; Mismatches: 0;
 Matches: 21; Conservative: 0; Mismatches: 0; Indels: 2; Gaps: 2;
 Db 195 CCTGAAGTTCAGCTCATCTTGAAGATCTCCCAACCTCAGAGCTCAGCTTATGATGC 254
 Qy 95 CCTGAAGTTCAGCTCATCTTGAAGATCTCCCAACCTCAGAGCTCAGCTTATGATGC 194
 Db 255 CAACCTCTCTCTCCACAGCTGCTTCTGACAAATCAACCTTGGCCCTGTGTATTC 114
 Qy 155 CAACCTCTCTCTCCACAGCTGCTTCTGACAAATCAACCTTGGCCCTGTGTATTC 214
 Db 315 TGTGCTTAACCTTCACTTCTTGAAGATGTCGGAAGGCGACCTTTTGAAGA 374
 Qy 215 TGTGCTTAACCTTCACTTCTTGAAGATGTCGGAAGGCGACCTTTTGAAGA 274
 Db 375 GGTCTTCTGACAGACACAGGACAGAGAGTGTCTATGAGTCAAAATTTTAAAGA 434
 Qy 275 GGTCTTCTGACAGACACAGGACAGAGAGTGTCTATGAGTCAAAATTTTAAAGA 334
 Db 335 GAAGCAATCTGTAAGAAAGAGAGAGAGATATATGTCGACGAGATTTCTGT 394
 Qy 495 GAGATATGTGAGACACCTTCTCTGTGTGTCTCTCTCTCTCTCTCTCTCTCTCTCT 454
 Db 395 GAGATATGTGAGACACCTTCTCTGTGTGTCTCTCTCTCTCTCTCTCTCTCTCTCT 454
 Qy 555 ATGTGACTTGTCTAGATTAATTAATGTCGAGAGAGTGTCTCTCTCTCTCTCTCTCT 614
 Db 455 ATGTGACTTGTCTAGATTAATTAATGTCGAGAGAGTGTCTCTCTCTCTCTCTCTCT 514
 Qy 615 AGCT 674
 Db 515 AGCT 574
 Qy 675 CTACCTGATCCTCAATCACTGTTATGAGAGCTTAAACCTAGAGAAATTTTCTTGA 734
 Db 575 CTACCTGATCCTCAATCACTGTTATGAGAGCTTAAACCTAGAGAAATTTTCTTGA 634
 Qy 735 TTTCAAGAGGACACATCTCTTCTTACTGATCTCTGAGAGAGAGATTTTCTTGA 794
 Db 635 TTTCAAGAGGACACATCTCTTCTTACTGATCTCTGAGAGAGAGATTTTCTTGA 694
 Qy 795 CAGCAGACACATCTCTCTTCTGAGAGAGAGAGTCTGAGCTGTCTTCTTGA 854
 Db 695 CAGCAGACACATCTCTTCTTCTGAGAGAGAGAGTCTGAGCTGTCTTCTTGA 754
 Qy 855 GAGGCTTATGAGAGAGAGTCTGAGCTGTCTGAGAGAGAGTCTCTTCTTGA 914
 Db 755 GAGGCTTATGAGAGAGAGTCTGAGCTGTCTGAGAGAGAGTCTCTTCTTGA 814
 Qy 915 GTATGAGCTGCTGCTTTTATGAGAGAGAGAGTCTGAGCTGTCTTCTTGA 974
 Db 815 GTATGAGCTGCTGCTTTTATGAGAGAGAGAGTCTGAGCTGTCTTCTTGA 874
 Qy 975 CAAAGCTCTCTCAGCTGAACCAATATTTAGAAATTTCCGACAGACCTCTCTGAGAGCT 1034

875 CAGGCTCTCAGCTCGAGCAGCAATATACAAATTCGCAAGACCTCTCGAGGCT 934
 1035 CTGCGAAGCAGGAGCAAGAGCGCTCGGGCGACAGGAGACTCTATGGAGTAAG 1094
 935 CTCGAGAGGAGGAGCAAGCGCTCGGGCGACAGGAGACTCTATGGAGTAAG 994
 1095 TCATGCT 1154
 995 TCATGCT 1054
 1155 TTTTAAACCAATATGAGTGGGCGGCGACAGGCTTTCAGCCAGGCTTTCAG 1214
 1055 TTTTAAACCAATATGAGTGGGCGGCGACAGGCTTTCAGCCAGGCTTTCAG 1114
 1215 AGAGCTCTCGCAACTCTGATTCGCAAGCTCTGCGCAGGCTCTGCGCAGG 1274
 1115 AGAGCTCTCGCAACTCTGATTCGCAAGCTCTGCGCAGGCTCTGCGCAGG 1174
 1275 CAGGAGGCTCTGAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1334
 1175 CAGGAGGCTCTGAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1234
 1335 CTGACGCTCTGAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1394
 1235 CTGACGCTCTGAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1294
 1395 AGCCTCTCTGAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1454
 1295 AGCCTCTCTGAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1354
 1455 GAGCTCTGAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1513
 1355 GAGCTCTGAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1414
 1515 TCAGTCTGAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1573
 1415 TCAGTCTGAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1474
 1575 AGGAGCTCTGAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1632
 1475 AGGAGCTCTGAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1534
 1635 TCTAAAGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1692
 1535 TCTAAAGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1594
 1695 CTCTTCTGAGGAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1752
 1595 CTCTTCTGAGGAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1654
 1755 ATTTCT 1812
 1655 ATTTCT 1714
 1815 ATGAGTCT 1872
 1715 ATGAGTCT 1774
 1875 TGTCT 1932
 1775 TGTCT 1834
 1935 ATAAATTAATTTAGATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1992
 1835 ATAAATTAATTTAGATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1894
 1995 ATGCT 2052
 1895 ATGCT 1954
 2055 TCAGTCT 2112

1955 TGTCT 2014
 2113 TTTATGTTTTTTTTTTCGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2172
 2015 TTTATGTTTTTTTTTTCGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2074
 2173 TTTGTTTATACACTACTATTTTAACTCTACAGGCTTATTTGATGTAAAT 2232
 2075 TTTGTTTATACACTACTATTTTAACTCTACAGGCTTATTTGATGTAAAT 2134
 2233 TTTATGTTTTTTTTTTCGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2292
 2135 TTTATGTTTTTTTTTTCGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2194
 2293 AACTTTTTTGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2352
 2195 AACTTTTTTGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2254
 2353 AAAAAAATTTTTTTTTT 2368
 2355 AAAAAAATTTTTTTTTT 2370

RESULT 10
 AAF4640 standard; CDNA: 2412 BP.
 AC AAF4640;
 XX 27-MAY-2001 (first entry)
 XX
 DE Novel protein kinase cDNA, SKG ID NO: 19.
 XX human; mouse; protein kinase; antihypertensive; antidiabetic; antineoplastic; immunosuppressive; cardiac; renal; antineoplastic; antineoplastic; dermatological; antidiabetic; antineoplastic; gene therapy; vaccine; immune disorder; cardiovascular disease; inflammatory bowel disease; inflammatory pelvic disease; multiple sclerosis; psoriasis; ss.
 XX
 XX Mus musculus.
 OS
 FN M0200073469-A2.
 XX
 XX 07-DEC-2000.
 XX 26-MAY-2000; 2000NO-0151842.
 XX 28-MAY-1999; 9905-0134503.
 XX
 XX (GUGS-) SUGEN INC.
 FA
 Ploman GD, Martinez R, Whyte D, Sudersanam S;
 WP1: 2001-032161/04.
 DR P-PDB; AAB65614.
 XX
 XX Nucleic acid encoding kinase polypeptides, useful for diagnosing and treating immune-related diseases and disorders, cardiovascular disease, neurodegenerative diseases and/or cancers -
 XX
 XX Disclosure; Fig 2; 310pp; English.
 XX
 XX The present sequence encodes a novel protein kinase. The nucleic acids and the protein kinases they encode may be used in the treatment and diagnosis of immune-related diseases and disorders, cardiovascular disease, neurodegenerative diseases and/or cancers. The nucleic acids and complementary sequences may also be used as RNA probes in diagnostic assays, as well as polypeptides in immunological assays. The kinase and kinase antagonists may also be used to down regulate kinase expression and activity. Diseases related to kinase expression and

XX MO20016689-A2.
 XX 13-SEP-2001.
 XX 05-MAR-2001; 2001MO-US04942.
 XX 07-MAY-2000; 2000US-0519705.
 XX 19-MAY-2000; 2000US-057454.
 XX 17-JUN-2000; 2000US-0596193.
 XX 19-SEP-2000; 2000US-0665463.
 XX 20-OCT-2000; 2000US-0693267.
 XX (HSE)- WISGO INC.
 FI Tang Y, Liu C, Asundi R, Ren F, Ma Y, Zhou P;
 FI Zhao QA, Yang Y, Diamant R, Zhang J, Chen R, Xue AJ, Wang J;
 FI NPT: 2001-589934/56.
 DR P-FSDB; AND28087.
 XX Novel polypeptides and nucleic acids obtained from cDNA libraries
 FI prepared from various human tissues, for diagnosis and treatment of
 FI cancer, neurological, inflammatory, and autoimmune disorders -
 FI Claim 1; SEQ ID NO 68; 107pp; English.
 XX The invention relates to novel isolated human secreted polypeptides (I)
 CC and polynucleotides (II) and (III) are useful for treating
 CC ischemic reperfusion injury, shock, sepsis, immune responses, and is
 CC involved in increasing haematopoiesis, stem cell survival, bone growth
 CC and remodeling. (I) and (II) are modulators of cell adhesion, cell
 CC creating transgenic animals useful for studying the in vivo effects of
 CC the polypeptide as well as for studying modulators of the polypeptides.
 CC (I) induces the proliferation of neural cells and regeneration of nerve
 CC peripheral nervous system diseases and neuropathies, such as Alzheimer's,
 CC Parkinson's disease, Huntington's disease, and amyotrophic lateral
 CC sclerosis. (II) is useful for the treatment of hematologic disorders
 CC or lymphoid cell disorders, platelet disorders such as thrombocytopenia
 CC and for regeneration of bone, cartilage, tendon, ligament and/or nerve
 CC tissue. (III) is useful for the treatment of bone degenerative
 CC disorders, or peritoneal disease. Furthermore, (I) is also useful for
 CC gut protection or regeneration and treatment of lung or liver fibrosis,
 CC and for the treatment of various autoimmune diseases. (I) and (II) are
 CC disorders including severe combined immunodeficiency (SCID), bacterial or
 CC fungal infections, autoimmune disorders e.g. multiple sclerosis,
 CC rheumatoid arthritis, diabetes mellitus, myasthenia gravis, allergic
 CC reactions, and other autoimmune diseases. (I) and (II) are also useful
 CC in addition, (I) affects blood homeostasis and circadian cycles of rhythms.
 CC fertility, metabolism, catabolism, anabolism, storage or elimination of
 CC dietary fat, lipid, protein, carbohydrate, vitamins, minerals, provides
 CC activity and can act as an antigen in a vaccine composition to raise an
 CC immune response. AAS4920-AAS4925 represent novel human secreted protein
 CC coding sequences of the invention.
 XX Sequence 1366 BP: 331 A; 374 G; 377 G; 284 T; 0 other;
 Query Match 22-24; Score 527 2; Db 527 2; Length 1366;
 Matches 734; Percent 54; O: 1; Mismatches 313; Indels 9; Gaps 1;
 OY 261 TTCTCTCCACAGCTCTTCTGACCAATCAACCTTGGCCGCTGCTGCACTCATCC 320
 DB 213 TCCAGAGCTCCAGGCCCATGGGACATGATGCTGGGCTCTTCAGCCAGCCAAATCC 272
 OY 331 TAAACCATCTGACTTCTGCTTCTTAAGATGATGCTGGAAAGGAGCTTTTGGAAAGGCTTC 380

DB 273 CGAGCCCGCGAGCTTGGGTTCTCTTCCCTCAATGCTTGGGCGGAGGACTACGGGAGTCTCT 332
 OY 381 TCTACGACAGCAACAAGCAAGAGAGTGTCTATCTGAGTCAAGATTTTATGACGAAGAC 440
 DB 333 ACTGCCGAGCTGCAAGTCTGAGGCTTCTATCTGAGTCAAGTCTACATACGAAATCT 492
 OY 441 AATCTCGAAGAAAGAGAGAGACATATATATCTGCGAGCGAGATGTTTCTCTACAGCA 500
 DB 393 CATCTTAAAGAGAAAGAGAGACATACATGCGAGGCGAGCTTCTCTTAAAGAA 452
 OY 501 TGTGAG 560
 DB 453 CTGCGCGCGCTCTCTCTGCGGCTGGAGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 612
 OY 561 CTCTGCTCTAGAGCTACATTAATGTGGAGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 620
 DB 513 CTCTGCTCTAGAGCTATGATGAGGCGGAGAGAGCTCTCTCTCTCTCTCTCTCTCTCTCT 572
 OY 621 CTCTCTGGAACAGCGGCT 680
 DB 573 CTCTCTGGAACAGCGGCT 632
 OY 632 GATCTCTGGAACAGCGGCT 740
 DB 633 GATCTCTGGAACAGCGGCT 692
 OY 741 GGAACAGCT 800
 DB 693 GGAACAGCT 752
 OY 801 AAGTCT 860
 DB 753 CACATCT 812
 OY 861 TTATGACAGAGCTGAGCT 920
 DB 813 TTATGACAGAGCTGAGCT 872
 OY 921 CTCTGCGGCTCTTTTATGCGCAACACAGCTGAATGTACGACAGATTTCTGACAGAGCT 980
 DB 873 CTCTGCGGCTCTTTTATGCGCAACAGCTGAATGTACGACAGATTTCTGACAGAGCT 932
 OY 981 TCTGACAGCTGAACCAATATATGCAATATATGCAATATATGCAATATATGCAATATATGCA 1040
 DB 933 CTGACAGCTCTGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 992
 OY 1041 GAAGGAG 1100
 DB 993 CAGGAG 1052
 OY 1101 CT 1160
 DB 1053 ATCT 1112
 OY 1161 CCAAAATCTGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1220
 DB 1113 CCAAAATCTGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1172
 OY 1221 TGTCT 1280
 DB 1173 TGTCT 1223
 OY 1281 ACTGCGGAGGCT 1316
 DB 1224 GGTCT 1259

RESULT 14
 AF447373
 XX AAF44737 standard; cDNA; 1812 bp.
 XX AAF44737;

[illegible]

Db 933 GTTACCC-TTGTGCGAGCCGACCTGACAGCATCTTACAAGAGATTGCATCT 875
 1452 CTGACGCTATGACAGCTATATGACAGCTGCTGCTGCA-ATTTTGTGAAGCGATCTC 1510
 Db 874 CTGAGCACTTATGCAACTTATTCGACAGCTGCTGCGAGCTTTTGAAGACGATTC 815
 1511 TCGTCACTGACGCTATGACAGCTGCTGCTGCA-ATTTTGTGAAGCGATCTC 1570
 Db 814 TCGTCACTGACGCTATGACAGCTGCTGCTGCA-ATTTTGTGAAGCGATCTC 755
 1571 GAAAGCGAGCTTATGACAGCTGCTGCTGCA-ATTTTGTGAAGCGATCTC 1629
 Db 754 GAAAGCGAGCTTATGACAGCTGCTGCTGCA-ATTTTGTGAAGCGATCTC 695
 1630 TCGTCACTGACGCTATGACAGCTGCTGCTGCA-ATTTTGTGAAGCGATCTC 1689
 Db 695 TCGTCACTGACGCTATGACAGCTGCTGCTGCA-ATTTTGTGAAGCGATCTC 635
 1689 TCGTCACTGACGCTATGACAGCTGCTGCTGCA-ATTTTGTGAAGCGATCTC 1749
 Db 634 TCGTCACTGACGCTATGACAGCTGCTGCTGCA-ATTTTGTGAAGCGATCTC 575
 1750 TCGTCACTGACGCTATGACAGCTGCTGCTGCA-ATTTTGTGAAGCGATCTC 1809
 Db 574 TCGTCACTGACGCTATGACAGCTGCTGCTGCA-ATTTTGTGAAGCGATCTC 515
 1810 TCGTCACTGACGCTATGACAGCTGCTGCTGCA-ATTTTGTGAAGCGATCTC 1869
 Db 514 TCGTCACTGACGCTATGACAGCTGCTGCTGCA-ATTTTGTGAAGCGATCTC 455
 1870 TCGTCACTGACGCTATGACAGCTGCTGCTGCA-ATTTTGTGAAGCGATCTC 1929
 Db 454 TCGTCACTGACGCTATGACAGCTGCTGCTGCA-ATTTTGTGAAGCGATCTC 395
 1930 TCGTCACTGACGCTATGACAGCTGCTGCTGCA-ATTTTGTGAAGCGATCTC 1989
 Db 394 TCGTCACTGACGCTATGACAGCTGCTGCTGCA-ATTTTGTGAAGCGATCTC 335
 2049 TCGTCACTGACGCTATGACAGCTGCTGCTGCA-ATTTTGTGAAGCGATCTC 2019
 Db 2050 TCGTCACTGACGCTATGACAGCTGCTGCTGCA-ATTTTGTGAAGCGATCTC 2109
 2174 TCGTCACTGACGCTATGACAGCTGCTGCTGCA-ATTTTGTGAAGCGATCTC 2169
 Db 2110 TCGTCACTGACGCTATGACAGCTGCTGCTGCA-ATTTTGTGAAGCGATCTC 156
 2174 TCGTCACTGACGCTATGACAGCTGCTGCTGCA-ATTTTGTGAAGCGATCTC 2229
 Db 2174 TCGTCACTGACGCTATGACAGCTGCTGCTGCA-ATTTTGTGAAGCGATCTC 2289
 2289 TCGTCACTGACGCTATGACAGCTGCTGCTGCA-ATTTTGTGAAGCGATCTC 2334
 Db 2289 TCGTCACTGACGCTATGACAGCTGCTGCTGCA-ATTTTGTGAAGCGATCTC 2334
 2334 TCGTCACTGACGCTATGACAGCTGCTGCTGCA-ATTTTGTGAAGCGATCTC 2334
 Db 2334 TCGTCACTGACGCTATGACAGCTGCTGCTGCA-ATTTTGTGAAGCGATCTC 2334

RESULT 4

BM455819
 LOCUS BM455819.1 1072 bp mRNA linear EST 05-FEB-2002
 DEFINITION BM455819.1 Homo sapiens cDNA clone IMAGE1549261
 5' UTR sequence.
 ACCESSION BM455819.1 GI:18504859
 VERSION BM455819.1
 KEYWORDS EST, apolipoprotein A2, apolipoprotein A2 (human)
 SOURCE Homo sapiens
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 K14-MC2 http://mc2.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Population Genomics Project
 Contact: Robert Strausberg, Ph.D.
 Email: cgrubbs-f@mail.nih.gov
 Tissue Procurement: Lou Staudt
 DNA Library Prepared by: The J.M.A.P. Consortium (JMLP)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone Distribution: MGC clone distribution information can be
 found through the J.M.A.G.P. Consortium/JMLP at:
 http://www.jmga.org/
 Plasmid: Lambda2129 row: 1 column: 06
 High quality sequence stop: 640.
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /db_xref="taxon:9606"
 /tissue_type="lymphoma, cell line"
 /clone_11b="NH_MGC_85"
 /size="1.867 kb"
 /vector="pGW-SPO6E; Site1; NCI;
 Site2; SalI; Cloned unidirectionally; oligo-dT primed.
 full-length clones and constructed by Life Technologies.
 NCBI accession # U05362.2
 282 a 277 c 250 g 262 t 1 others

BASE COUNT
 282 a 277 c 250 g 262 t 1 others
 Query Match: Score 916.4; Db 12; Length 1072;
 Best Local Similarity 34.9%; Pred. No. 4.7e-101;
 Matches 1011; Conservative 0; Mismatches 47; Indels 7; gaps 6;
 8 GAGCGTAAAGCTCTTCTCTCCCGCGGTGTGACGCGTGAACATGAGCTGCTA 67
 Db 8 GAGCGTAAAGCTCTTCTCTCCCGCGGTGTGACGCGTGAACATGAGCTGCTA 69
 10 GAGCGTAAAGCTCTTCTCTCCCGCGGTGTGACGCGTGAACATGAGCTGCTA 127
 Db 10 GAGCGTAAAGCTCTTCTCTCCCGCGGTGTGACGCGTGAACATGAGCTGCTA 129
 127 GAGCGTAAAGCTCTTCTCTCCCGCGGTGTGACGCGTGAACATGAGCTGCTA 187
 Db 127 GAGCGTAAAGCTCTTCTCTCCCGCGGTGTGACGCGTGAACATGAGCTGCTA 189
 187 GAGCGTAAAGCTCTTCTCTCCCGCGGTGTGACGCGTGAACATGAGCTGCTA 247
 Db 187 GAGCGTAAAGCTCTTCTCTCCCGCGGTGTGACGCGTGAACATGAGCTGCTA 249
 249 GAGCGTAAAGCTCTTCTCTCCCGCGGTGTGACGCGTGAACATGAGCTGCTA 307
 Db 249 GAGCGTAAAGCTCTTCTCTCCCGCGGTGTGACGCGTGAACATGAGCTGCTA 309
 307 GAGCGTAAAGCTCTTCTCTCCCGCGGTGTGACGCGTGAACATGAGCTGCTA 367
 Db 307 GAGCGTAAAGCTCTTCTCTCCCGCGGTGTGACGCGTGAACATGAGCTGCTA 369
 369 GAGCGTAAAGCTCTTCTCTCCCGCGGTGTGACGCGTGAACATGAGCTGCTA 427
 Db 369 GAGCGTAAAGCTCTTCTCTCCCGCGGTGTGACGCGTGAACATGAGCTGCTA 429
 429 GAGCGTAAAGCTCTTCTCTCCCGCGGTGTGACGCGTGAACATGAGCTGCTA 487
 Db 429 GAGCGTAAAGCTCTTCTCTCCCGCGGTGTGACGCGTGAACATGAGCTGCTA 489
 487 GAGCGTAAAGCTCTTCTCTCCCGCGGTGTGACGCGTGAACATGAGCTGCTA 547
 Db 487 GAGCGTAAAGCTCTTCTCTCCCGCGGTGTGACGCGTGAACATGAGCTGCTA 549


```

/clone="CS0K011902"
/cell_type="HELA CELLS COT 25-NORMALIZED"
/notes="HELA CELLS COT 25-NORMALIZED"
/clone_lib="Homo sapiens HELA CELLS COT 25-NORMALIZED"
/notes="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five primes end enriched, double-strand cDNA was generated. The cDNA was ligated into the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT      325 a 193 c 171 g 238 t 15 others
ORIGIN
Query Match      36.5%; Score 864.8; DB 13; Length 942;
Best Local Similarity 96.9%; Pred. No. 7.9e-95;
Matches 907; Conservative 13; Mismatches 12; Indels 4; Gaps 4;
QY 1397 CTTTGTGGAGCCGACGATGACAGAGACATCTTACAGATCTCTGGA 1456
Db 942 SCITTTGTGGAGCCGACGATGACAGAGATTTTACAGAGATTTGAG 883
QY 1457 AGCTAGCAATCTATTGACATCTGCTGGGA-TTTTGTGAAGACATCTCTC 1515
Db 892 AGCTAGCAATCTATTGACATCTGCTGGGA-TTTTGTGAAGACATCTCTC 823
QY 3516 AGTGAAGTCTGCTGAGATCTGCTTATCTCTCTCCAGAGTGGTCTGGAAC 1575
Db 822 AGTGAAGTCTGCTGAGATCTGCTTATCTCTCTCCAGAGTGGTCTGGAAC 763
QY 1576 GAGCTTAGAGTCCGCTCTAGAGAGGAGAGATTTGTGAAGAGCGAG-CTCTTC 1634
Db 762 GAGCTTAGAGTCCGCTCTAGAGAGGAGAGATTTGTGAAGAGAGAGCTCTTC 703
QY 1635 TAAANAAGTCTCTGAGATCTGCTGGCTGTGATGAGCAATATATGAATGTGCT 1694
Db 702 TAAANAAGTCTCTGAGATCTGCTGGCTGTGATGAGCAATATATGAATGTGCT 643
QY 1695 TTCTGAAGAGATTTGTAGTCTGCAAGATTTCTCATGAGGTCTTCAATCTTAT 1754
Db 642 TTCTGAAGAGATTTGTAGTCTGCAAGATTTCTCATGAGGTCTTCAATCTTAT 583
QY 1755 TTCTCTGTGGATGATCTGTGTGAGACGCTGTGTGAGTGTGTATGCTTGACAGAT 1814
Db 582 TTCTCTGTGGATGATCTGTGTGAGACGCTGTGTGAGTGTGTATGCTTGACAGAT 523
QY 1815 GATTTTGTATGATCAATGTGATGATCTGAGAGACCTACAGAGGAGCATTTT 1874
Db 522 GATTTTGTATGATCAATGTGATGATCTGAGAGACCTACAGAGGAGCATTTT 463
QY 1875 GTTCTTCATATTGAGAGATTAATTTATGTGAATTTTGTGAAGATGGGTAA 1934
Db 462 GTTCTTCATATTGAGAGATTAATTTATGTGAATTTTGTGAAGATGGGTAA 403
QY 1935 ACTAATAATTTATGATGCTCTGCAATGATCTGTATGATGCTTAAAGAGAGAT 1994
Db 403 ACTAATAATTTATGATGCTCTGCAATGATCTGTATGATGCTTAAAGAGAGAT 343
QY 1995 TCTGTCAATGATATTCTATTATTGAAGAGGTTTATGAGCAATGCCAGAGTCTC 2054
Db 342 TCTGTCAATGATATTCTATTATTGAAGAGGTTTATGAGCAATGCCAGAGTCTC 283
QY 2055 AGTGAAGCTGTGCTGTTTTCATCTTATGATCTGATCTGTAATATGCGCATTT 2114
Db 283 AGTGAAGCTGTGCTGTTTTCATCTTATGATCTGATCTGTAATATGCGCATTT 2054
QY 2114 AGTGAAGCTGTGCTGTTTTCATCTTATGATCTGATCTGTAATATGCGCATTT 2174
Db 2054 AGTGAAGCTGTGCTGTTTTCATCTTATGATCTGATCTGTAATATGCGCATTT 1904
QY 2175 GGTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2234
Db 1904 GGTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 164
QY 2234 ATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2294
Db 164 ATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 134
QY 2294 ATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 312
Db 134 ATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 104
QY 312 ATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
Db 104 ATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 74
QY 74 ATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 48
Db 48 ATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 24
QY 48 ATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 24
Db 24 ATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 12
QY 12 ATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6
Db 6 ATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3
QY 3 ATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1
Db 1 ATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 0

```


http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=us1000039a1.rst
http://fulllength.invitrogen.com/Invitrogen/1600
Paradya Avenue Genoscope sequence ID : CS0A100CF110P1.

FEATURES

Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /db_xref="taxon:604"
 /db_xref="taxon:604"
 /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo dT, digested with NotI and cloned into the NotI and BspRV sites of the pOWSPORT 6 vector. Library was normalized." 301 a 277 c 379 t 42 others

BASE COUNT 301 a 277 c 379 t 42 others

ORIGIN
 Query Match 35.1%; Score 832; Db 13; Length 1201;
 Best Local Similarity 92.81; Pred. No. 5.7e-91; Indels 4; Gaps 4;
 Matches 903; Conservative 10; Mismatch 56;

QY 9 AGGCTGTAAGCTCTTCTGCTCCGCGGTGGTGGTGAAGCTGAGGCTGCTAA 68
 QY 77 ATCTGTAAGCTCTTCTGCTCCGCGGTGGTGGTGAAGCTGAGGCTGCTAA 136
 QY 69 GGCACCTCTGCTTATCCAGAGTGGGCGGCTGTCGATCTCATGCTTCATGA 128
 QY 137 GGGACCTCTGCTTATCCAGAGTGGGCGGCTGTCGATCTCATGCTTCATGA 196
 QY 129 CGAGAGAGTGGTCTGAGAGCTTATTCAGAGATGCCAATCTCTTATGCT 188
 QY 197 CGAGAGAGTGGTCTGAGAGCTTATTCAGAGATGCCAATCTCTTATGCT 256
 QY 189 CAAGACCTCTGAGTGGTCTGAGAGCTTATTCAGAGATGCCAATCTCTTATGCT 316
 QY 249 GATGCAAGCTCTGCTCCAGAGCTTCTTCAGAAATCAAGCTGCGCGCTGCTC 308
 QY 317 TATCTGCAAGCTCTGCTCCAGAGCTTCTTCAGAAATCAAGCTGCGCGCTGCTC 376
 QY 309 CATCTCTCTCAAGCTCTGAGCTTCACTCTGAAAGTGGGAGGAGGCAATTT 368
 QY 377 CATCTCTCTCAAGCTCTGAGCTTCACTCTGAAAGTGGGAGGAGGCAATTT 436
 QY 369 TGAAGAGTCTCTGAGACACACAGAGAGAGTGTCTATGAGTCAAGATTT 428
 QY 437 TGAAGAGTCTCTGAGACACACAGAGAGAGTGTCTATGAGTCAAGATTT 496
 QY 429 AGAGAGAGAGCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 488
 QY 497 AGAGAGAGAGCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 556
 QY 489 TCTGTGAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 548
 QY 557 TCTGTGAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 616
 QY 549 TGAAGAGTCTCTGAGACACACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 608
 QY 617 TGAAGAGTCTCTGAGACACACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 676
 QY 609 GAGGAGAGAGCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 668
 QY 676 GAGGAGAGAGCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 736
 QY 669 CTGGGCTCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 728
 QY 737 CTGGGCTCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 796
 QY 729 CTGATGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 788

Db 797 GCTAGTGTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 856
 QY 789 ACACAG 916
 Db 857 ACACAG 846
 QY 848 TTCTATAG 906
 Db 917 TTCTATAG 976
 QY 907 GAGATCTCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 966
 Db 967 GAGATCTCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1034
 QY 977 ATTCGAG 979
 Db 1035 ATTCGAG 1047

RESULT 12
 B1333256 969 bp mRNA lineær EST 10-JUL-2003
 602995596F1 NUL_MUC_12 Homo sapiens CDNA IMAGE:5148951 5',
 mRNA sequence.
 ACCESSION B1333256
 VERSION B1333256.1 GI:15017913
 KEYWORDS EST
 ORIGINISM Homo sapiens (human)
 REFERENCE Homo sapiens; Metazoa; Chordata; Craniata; Vertebrata; Kutei; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 TITLE 1 (bases 1 to 969)
 AUTHORS Robert Strausberg, Ph.D.
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: rstraus@nsl.jhu.edu
 Title: Cytochrome P-450
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: Incyte Genomics, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Note: This sequence was obtained from a cDNA library prepared through the T.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
 Place: LLNL1341 row. P. column: 24
 High quality cDNA clones. Size 1.4 kb. Library prepared by Life Technologies.
 Location/Qualifiers
 1. 969
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /db_xref="taxon:9606"
 /clone_lib="IMAGE:5148951"
 /clone_lib="IMAGE:5148951"
 /clone_lib="IMAGE:5148951"
 /clone_lib="IMAGE:5148951"
 /note="Organ: Cervix; Vector: pCMV-Sport6; Site: 1; NotI; Site 2; Salt: Cloned unidirectionally. Primer: oligo dT. Size 1.4 kb. Library prepared by Life Technologies." 236 a 255 c 229 g 249 t

BASE COUNT 236 a 255 c 229 g 249 t

ORIGIN
 Query Match 34.9%; Score 826.4; Db 12; Length 969;
 Best Local Similarity 98.2; Pred. No. 3.1e-90;
 Matches 878; Conservative 0; Mismatch 11; Indels 5; Gaps 4;

QY 632 CAGGGCTCTTCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 691
 Db 1 CAGGGCTCTTCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 60
 QY 692 ACATGCTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 751

BASE COUNT	314	a	178	c	146	g	228	t	18	others
Query Match	34.3%						Score 812.2;	Da 9;	Length 884;	
Best Local Similarity	95.94;						Prod. No. 1.7e-88;			
Matches 848;	Conservative 185;	Mismatches 177;	Indels 3;	Gaps 3;						
Oy	1457	ACGTTCACATCTATTTCACATCTATGCTGCGCGGAAAT	1877	TTTGAAGACGACATCTCTCTCTC	1515					
Db	884	ACGTTCACATCTATTTCACATCTATGCTGCGCGGAAAT	1877	TTTGAAGACGACATCTCTCTCTC	825					
Oy	3516	ATGCACTCAGTGAAGGTTTCATTTTCTCTCTCCACAGCTGCTATCTCTGAAGC	1575							
Db	876	ATGCACTCAGTGAAGGTTTCATTTTCTCTCTCCACAGCTGCTATCTCTGAAGC	765							
Oy	1524	GAGCGCTTGAAGCTGCGCTGTAGACGCGAGAGGCTTGGTTGNAAGCGAGCGCTGTC	1634							
Db	764	GAGCGCTTGAAGCTGCGCTGTAGACGCGAGAGGCTTGGTTGNAAGCGAGCGCTGTC	705							
Oy	1635	TAAAAAGGCTCTCTCGACATCTCTCTGGCTGTATGAGACAAATTAATGAATGCG-C	1693							
Db	704	TAAAAAGGCTCTCTCGACATCTCTCTGGCTGTATGAGACAAATTAATGAATGCG-C	1645							
Oy	1694	TTTTCTCTGAGAGAGCTTTGTTAGCTCCAGACCTTTCTTCACAGCTGTTTACGTCTCTTGA	585							
Db	644	TTTTCTCTGAGAGAGCTTTGTTAGCTCCAGACCTTTCTTCACAGCTGTTTACGTCTCTTGA	585							
Oy	1754	TTTTCTCTCTGTGATATGCTGTGTGAGACGCGTGTGAGCTGTGTAGCTGATCTACACGA	1813							
Db	584	TTTTCTCTCTGTGATATGCTGTGTGAGACGCGTGTGAGCTGTGTAGCTGATCTACACGA	1823							
Oy	1814	TGGATTTTGGTATAAGCATCATGTGACATCTCGACGAGCTACACAGCGGACATGTT	575							
Db	524	TGGATTTTGGTATAAGCATCATGTGACATCTCGACGAGCTACACAGCGGACATGTT	465							
Oy	1874	TGTTCTCTCATATTGAGAGTAATTTATATGTAGCTTTTTCTTCTGAGTACGGTTAA	1933							
Db	464	TGTTCTCTCATATTGAGAGTAATTTATATGTAGCTTTTTCTTCTGAGTACGGTTAA	1905							
Oy	1934	TACCTAAATTTATGAAGTAGCTTCTGACATGCTGTATCATGCTCTCTGAGAGCA	1993							
Db	404	TACCTAAATTTATGAAGTAGCTTCTGACATGCTGTATCATGCTCTCTGAGAGCA	345							
Oy	1994	TGCTCTCTACAAATTTCTATTTTAAAGAGGGTTTTTATGACCAATCCCGACGTCG	2053							
Db	285	TGCTCTCTACAAATTTCTATTTTAAAGAGGGTTTTTATGACCAATCCCGACGTCG	285							
Oy	3045	CAGCTGAGACGCTGGTGTTTCTTCTTAAATCTACCTTCTGATGATGATGATGATGAT	2113							
Db	284	CAGCTGAGACGCTGGTGTTTCTTCTTAAATCTACCTTCTGATGATGATGATGATGAT	225							
Oy	2114	TATGTGTTTTTTTTTGATCTGCTGATATGATGATGATGATGATGATGATGATGATGAT	2173							
Db	224	TATGTGTTTTTTTTTGATCTGCTGATATGATGATGATGATGATGATGATGATGATGAT	165							
Oy	2174	TGGGTTTATACAGCTATGATTTAACTATACAGGCTTATGTGTATTAACACACGCTAT	2233							
Db	164	TGGGTTTATACAGCTATGATTTAACTATACAGGCTTATGTGTATTAACACACGCTAT	105							
Oy	2234	TAAATCTCTGAATTAAGCTGTTTAAATAGCAATCTGCTCTGCTGCTGCTGCTGCTGCTG	2293							


```

Db 445 GAGTTGAGTACCTGAGTCTGGCAGAGGAGTCTGGCAGAGTGTCTGGTGGAG 504
Oy 391 CACAGGCGCAAGAGAGTGTCTATGCAAGCAAGTCTTACAGAGAGAGCAAGCTCGAA 450
Db 505 GAGAGAGCAGAGAGGAGTCTAGTACGAGTCTTACAGAGAGTCTTACAGAGAGTCTGGC 564
Oy 451 AAGAGAGAGAGAGAGTATATCTGGCAGAGAGTCTTGTGTGAGAGATGAGAGAC 510
Db 565 AAGAGAGAGAGAGAGTCTTACAGAGAGTCTTACAGAGAGTCTTACAGAGAGTCTGGC 621
Oy 511 CTTCTCTGCTGGGCTGACCTGCTCTTCTGAGAGTCTTACAGAGAGTCTTACAGAG 570
Db 622 CTTCTCTGCTGGGCTGACCTGCTCTTCTGAGAGTCTTACAGAGAGTCTTACAGAG 681
Oy 571 GACTACATATATATGAGAGTGTGTCTACATCTTCCAGAGAGAGTCTTCTCGAA 630
Db 682 GAGTACAGAGAGAGAGAGTCTTACAGAGAGTCTTACAGAGAGTCTTACAGAGAG 741
Oy 631 CAGAGAGAGAGAGAGTCTTACAGAGAGTCTTACAGAGAGTCTTACAGAGAG 797
Db 742 GACAGAGAGAGAGAGTCTTACAGAGAGTCTTACAGAGAGTCTTACAGAGAG 801
Oy 688 CTGACATATGTTATAGAGAGTCTTACAGAGAGTCTTACAGAGAGTCTTACAGAG 747
Db 802 AAGAGAGAGAGAGAGTCTTACAGAGAGTCTTACAGAGAGTCTTACAGAGAG 861
Oy 748 ATTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 807
Db 862 ATTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 921
Oy 808 TCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 867
Db 922 ACTTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 981
Oy 868 AGAGAGAGAGAGAGTCTTACAGAGAGTCTTACAGAGAGTCTTACAGAGAG 927
Db 982 CTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1041
Oy 928 CTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 987
Db 1042 CTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1101
Oy 988 CTGAGAGAGAGAGAGTCTTACAGAGAGTCTTACAGAGAGTCTTACAGAGAG 1047
Db 1102 TTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1161
Oy 1048 AGAGAGAGAGAGAGTCTTACAGAGAGTCTTACAGAGAGTCTTACAGAGAG 1104
Db 1162 CTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1221
Oy 1104 TTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1161
Db 1222 TTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1281
Oy 1165 AGTGTGAGAGAGAGAGTCTTACAGAGAGTCTTACAGAGAGTCTTACAGAGAG 1224
Db 1282 CAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1341
Oy 1225 CCAAGTCT 1232
Db 1342 ACCATGTC 1349

```

RESULT 7
 US-09-417-197-138
 ; Sequence 138
 ; Reference 138
 ; General Information
 ; APPLICANT: Ole Terastrup, et al.
 ; METHOD FOR: Method for Extracting Quantitative Information Relating To An
 ; TITLE OF INVENTION: Method for Extracting Quantitative Information Relating To An
 ; FILE REFERENCE: 3759-01109
 ; CURRENT APPLICATION NUMBER: US/09/417, 197

```

; CURRENT FILLING DATE: 1999-10-07
; CURRENT FILLING TYPE: 1
; SUPPLEMENT: PatentIn version 3.0
; SEQ ID NO 138
; LENGTH: 2184
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EDPF-PMB fusion
; NAME/KEY: CUS
; LOCATION: (1)..(2181)
; US-09-417-197-138

```

```

Query Match 10.6%; Score 252; DB #; Length 2184;
Best Local Similarity 57.2%; Pred. No. 60;
Matches 519; Conservative 0; Mismatches 380; Indels 9; Gaps 3;
Oy 331 GACTTCTCACTCTGAGAGTCTGAGAGAGAGAGAGTCTGAGAGAGTCTGAGAGAG 390
Db 1186 GAGTGTGAGTACAGTCTGAGAGAGTCTGAGAGAGTCTGAGAGAGTCTGAGAGAG 1245
Oy 391 CACAGAGAGAGAGAGTCTTACAGAGAGTCTTACAGAGAGAGAGAGTCTTACAGAG 450
Db 1246 GAGAGAGAGAGAGAGTCTTACAGAGAGTCTTACAGAGAGAGAGAGTCTTACAGAG 1305
Oy 451 AAGAGAGAGAGAGAGTCTTACAGAGAGTCTTACAGAGAGAGAGAGTCTTACAGAGAG 510
Db 1306 AAGAGAGAGAGAGAGTCTTACAGAGAGTCTTACAGAGAGAGAGAGTCTTACAGAGAG 1362
Oy 511 CTTCTCTGCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 570
Db 1363 CTTCTCTGCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1422
Oy 571 GACTACATATATGAGAGAGTCTTACAGAGAGTCTTACAGAGAGAGAGAGTCTTACAGAG 630
Db 1423 GAGTACAGAGAGAGAGAGTCTTACAGAGAGTCTTACAGAGAGAGAGAGTCTTACAGAG 1482
Oy 631 CCAAGAGAGAGAGAGTCTTACAGAGAGTCTTACAGAGAGAGAGAGTCTTACAGAGAG 687
Db 1483 GAGAGAGAGAGAGAGTCTTACAGAGAGTCTTACAGAGAGAGAGAGTCTTACAGAGAG 1542
Oy 688 GAGAGAGAGAGAGTCTTACAGAGAGTCTTACAGAGAGAGAGAGTCTTACAGAGAGAG 747
Db 1543 AAGAGAGAGAGAGAGTCTTACAGAGAGTCTTACAGAGAGAGAGAGTCTTACAGAGAGAG 1602
Oy 748 ATTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 807
Db 1602 ATTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1662
Oy 808 CTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 867
Db 1663 ACTTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1722
Oy 868 AGAGAGAGAGAGTCTTACAGAGAGTCTTACAGAGAGAGAGAGTCTTACAGAGAGAG 927
Db 1723 CTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1782
Oy 928 CTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 987
Db 1783 CTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1842
Oy 988 CTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1047
Db 1843 CTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1902
Oy 1048 AGAGAGAGAGAGTCTTACAGAGAGTCTTACAGAGAGAGAGAGTCTTACAGAGAGAG 1104
Db 1903 CCAAGAGAGAGAGTCTTACAGAGAGTCTTACAGAGAGAGAGAGTCTTACAGAGAGAG 1962
Oy 1105 TTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1164
Db 1963 TTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2022

```



```

Oy 571 GACTGATATATGCTGGAGAGTGTGTCTACCATCTCCAGAGGAGAGCGCTCTCTCGAA 630
Db 880 GAGTACGCCAAGGCGGAGCTGTCTCTCCACTGTCCCGGAGAGCTGTGTCTCCGAG 939
Oy 631 CCAAGGCGCTTTTCTATGCTGCTGAAATAGGCGACGCTTTGGCTTACTCTGATC---A 687
Db 940 GACCGGCGCTTTATGCTGCTGAAATAGGCGACGCTTTGGCTTACTCTGATC---A 687
Oy 688 CTGAGAGCTGTATTAGAGAGCTTAAACACAGAGAAATTTTCTAGATCTCAGAGGAC 747
Db 1000 AAGAGCTGTATTAGAGAGCTTAAACACAGAGAAATTTTCTAGATCTCAGAGGAC 747
Oy 748 ATTTGCTTACTGATTTTGGAGCTCTCAGAGGAGAGCTTAAACACAGAGGAGACAT 807
Db 1060 ATTAGATCATAGACTTTGGGCTCTCAGAGGAGAGCTTAAACACAGAGGAGACAT 807
Oy 808 ACTCTGTGCTGAGAGCTGAGTATGCGAGCTGAGTGTCTCTATGAGAGCTATGAC 867
Db 1120 ACTCTGTGCTGAGAGCTGAGTATGCGAGCTGAGTGTCTCTATGAGAGCTATGAC 867
Oy 868 AGAGCTGAGTGTGCTGAGTGTCTCTATGAGAGCTGAGTGTCTCTATGAGAGCTATGAC 927
Db 1180 CTGAGTGTGCTGAGTGTCTCTATGAGAGCTGAGTGTCTCTATGAGAGCTATGAC 927
Oy 928 CTTCTTTTACCGAGAGAGCTGAGTGTCTCTATGAGAGCTGAGTGTCTCTATGAGAG 987
Db 1240 CTTCTTTTACCGAGAGAGCTGAGTGTCTCTATGAGAGCTGAGTGTCTCTATGAGAG 987
Oy 988 CTGAGAGAGAGCTGAGTGTCTCTATGAGAGCTGAGTGTCTCTATGAGAGAGAG 1047
Db 1300 CTGAGAGAGAGCTGAGTGTCTCTATGAGAGCTGAGTGTCTCTATGAGAGAGAG 1047
Oy 1048 AGGAGAGAGAGCTGAGTGTCTCTATGAGAGCTGAGTGTCTCTATGAGAGAGAG 1104
Db 1360 AGGAGAGAGAGCTGAGTGTCTCTATGAGAGCTGAGTGTCTCTATGAGAGAGAG 1104
Oy 1105 TTCTCTTTATGAGAGAGCTGAGTGTCTCTATGAGAGCTGAGTGTCTCTATGAGAG 1164
Db 1420 TTCTCTTTATGAGAGAGCTGAGTGTCTCTATGAGAGCTGAGTGTCTCTATGAGAG 1164
Oy 1165 GAGTGTGCTGAGAGAGCTGAGTGTCTCTATGAGAGCTGAGTGTCTCTATGAGAG 1224
Db 1480 GAGTGTGCTGAGAGAGCTGAGTGTCTCTATGAGAGCTGAGTGTCTCTATGAGAG 1224
Oy 1225 CCGAGCT 1232
Db 1540 ACGAGCT 1547

RESULT 10
US-09-256-465-1
; Sequence 1, Application US/09256465
; Patent No. 6013090
; ORGANISM: Homo sapiens
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowert
; TITLE OF INVENTION: ANTISENSE MODULATION OF AKT-2 EXPRESSION
; CURRENT APPLICATION NUMBER: US/09/256,465
; CURRENT FILING DATE: 1999-02-23
; NUMBER OF SEQ ID NOS: 47
; LENGTH: 1599
; TYPE: DNA
; ORGANISM: Homo sapiens
; APPLICANT: Lex M. Cowert
; APPLICANT: Brett P. Monia
; NAME/KEY: CDS
; LOCATION: (88)..(1533)
US-09-256-465-1
Query Match
Best Local Similarity 55.3%; Pred. No. 3, 9e-58;
Matches 516; Conservative 0; Mismatches 408; Indels 6; Gaps 2;

```

```

Oy 330 TGACCTTCACTCTTGAAGTGTATGGAAGCGGAGTTTCTGGAGAGTTCTTTATGAAAG 489
Db 537 TGACCTTCACTCTTGAAGTGTATGGAAGCGGAGTTTCTGGAGAGTTCTTTATGAAAG 536
Oy 390 GAGAGTGTGAGAGAGAGAGTGTCTTATGCTGACCTCAAGAGTTTACAGAGAGAGAGTAA 449
Db 597 GAGAGTGTGAGAGAGAGTGTCTTATGCTGACCTCAAGAGTTTACAGAGAGAGAGTAA 449
Oy 450 AAGAGAGAGAGAGAGAGAGAGTGTCTTATGCTGACCTCAAGAGTTTACAGAGAGAGAG 509
Db 657 CAGGATGAGAGAGAGAGAGAGTGTCTTATGCTGACCTCAAGAGTTTACAGAGAGAGAG 713
Oy 510 CAGGATGAGAGAGAGAGAGTGTCTTATGCTGACCTCAAGAGTTTACAGAGAGAGAG 569
Db 714 CAGGATGAGAGAGAGAGAGTGTCTTATGCTGACCTCAAGAGTTTACAGAGAGAGAG 773
Oy 570 AAGAGTGTGAGAGAGAGAGTGTCTTATGCTGACCTCAAGAGTTTACAGAGAGAGAG 629
Db 774 AAGAGTGTGAGAGAGAGAGTGTCTTATGCTGACCTCAAGAGTTTACAGAGAGAGAG 833
Oy 630 ACGAGAGAGAGAGAGAGTGTCTTATGCTGACCTCAAGAGTTTACAGAGAGAGAG 689
Db 834 ACGAGAGAGAGAGAGTGTCTTATGCTGACCTCAAGAGTTTACAGAGAGAGAG 893
Oy 690 GAGAGTGTGAGAGAGAGAGTGTCTTATGCTGACCTCAAGAGTTTACAGAGAGAGAG 749
Db 894 GAGAGTGTGAGAGAGAGAGTGTCTTATGCTGACCTCAAGAGTTTACAGAGAGAGAG 953
Oy 750 TGCTGTGAGAGAGAGAGAGTGTCTTATGCTGACCTCAAGAGTTTACAGAGAGAGAG 809
Db 954 TGCTGTGAGAGAGAGAGAGTGTCTTATGCTGACCTCAAGAGTTTACAGAGAGAGAG 1013
Oy 810 GAGAGTGTGAGAGAGAGAGTGTCTTATGCTGACCTCAAGAGTTTACAGAGAGAGAG 869
Db 1014 GAGAGTGTGAGAGAGAGAGTGTCTTATGCTGACCTCAAGAGTTTACAGAGAGAGAG 1073
Oy 870 GAGAGTGTGAGAGAGAGAGTGTCTTATGCTGACCTCAAGAGTTTACAGAGAGAGAG 929
Db 1074 GAGAGTGTGAGAGAGAGAGTGTCTTATGCTGACCTCAAGAGTTTACAGAGAGAGAG 1133
Oy 930 TGCTGTGAGAGAGAGAGAGTGTCTTATGCTGACCTCAAGAGTTTACAGAGAGAGAG 989
Db 1134 TGCTGTGAGAGAGAGAGAGTGTCTTATGCTGACCTCAAGAGTTTACAGAGAGAGAG 1193
Oy 990 GAGAGTGTGAGAGAGAGAGTGTCTTATGCTGACCTCAAGAGTTTACAGAGAGAGAG 1049
Db 1194 GAGAGTGTGAGAGAGAGAGTGTCTTATGCTGACCTCAAGAGTTTACAGAGAGAGAG 1253
Oy 1050 GAGAGTGTGAGAGAGAGTGTCTTATGCTGACCTCAAGAGTTTACAGAGAGAGAG 1106
Db 1254 GAGAGTGTGAGAGAGAGAGTGTCTTATGCTGACCTCAAGAGTTTACAGAGAGAGAG 1313
Oy 1107 TGCTGTGAGAGAGAGAGAGTGTCTTATGCTGACCTCAAGAGTTTACAGAGAGAGAG 1166
Db 1314 TGCTGTGAGAGAGAGAGAGTGTCTTATGCTGACCTCAAGAGTTTACAGAGAGAGAG 1373
Oy 1167 TGCTGTGAGAGAGAGAGAGTGTCTTATGCTGACCTCAAGAGTTTACAGAGAGAGAG 1226
Db 1374 TGCTGTGAGAGAGAGAGAGTGTCTTATGCTGACCTCAAGAGTTTACAGAGAGAGAG 1433
Oy 1227 GAGAGTGTGAGAGAGAGTGTCTTATGCTGACCTCAAGAGTTTACAGAGAGAGAG 1286
Db 1434 GAGAGTGTGAGAGAGAGTGTCTTATGCTGACCTCAAGAGTTTACAGAGAGAGAG 1493

```

```

RESULT 11
US-09-167-322-3
; Sequence 3, Application US/09167322
; Patent No. 6365151
; ORGANISM: Homo sapiens
; APPLICANT: Allipheny University of the Health
; Sciences, Halpern, Michael S.
;

```

1 TITLE OF INVENTOR: CANCER VACCINE
2 NUMBER OF SEQUENCES: 14
3 CORRESPONDING AUTHOR: JAMES M. ENGLAND, JAMES M.
4 ADDRESS: Seidel, Gonda, Lavorgna & Monaco, P.C.
5 STREET: Suite 1800, Two Penn Center Plaza
6 CITY: Philadelphia
7 STATE: PA
8 COUNTRY: USA
9 ZIP: 19102
10
11 COMPUTER READABLE FORM:
12 FILE NAME: us-10-000-039a-1.nri
13 COMPUTER: IBM PC compatible
14 OPERATING SYSTEM: PC-DOS/MS-DOS
15 SOFTWARE: Patent Release M1.0, Version #1.30
16 CURRENT RELEASE DATE: 07-OCT-1998
17 APPLICATION NUMBER: US/09/167,322
18 FILING DATE: 07-OCT-1998
19 PUBLICATION NUMBER: UNKNOWN
20 PRIOR APPLICATION DATA:
21 APPLICATION NUMBER: PCT/US97/00582
22 FILING DATE: <unknown>
23 PRIORITY DATE: <unknown>
24 ATTORNEY: DANIEL A. MONACO
25 NAME: MONACO DANIEL A.
26 REGISTRATION NUMBER: 30,480
27 REFERENCE/DOCKET NUMBER: 7933-33 PC
28 TELEPHONE: (215) 568-5549
29 TELEFAX: (215) 568-5549
30 INFORMATION FOR SEQ ID NO: 1:
31 SEQUENCE LENGTH: 1599 base pairs
32 TYPE: nucleic acid
33 STRANDEDNESS: single
34 DESCRIPTION: SEQ ID NO: 3:
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
986
987
988
989
990
991
992
993
994
995
996
997
998
999
1000

1042 TTCAATTCCTCATGTGTGTGGAGAGGGAGTTTGGAAAGAGTGTCTCTCCGACAG 1101
 GY AAGCAGAGAGAGTGTCTCTCATGCTCAAGTGTTCACAGAGAGAGCAATCTCGAAG 453
 1101 AAGCAGAGAGAGTGTCTCTCATGCTCAAGTGTTCACAGAGAGAGCAATCTCGAAG 1161
 GY AAGCAGAGAGAGTGTCTCTCATGCTCAAGTGTTCACAGAGAGAGCAATCTCGAAG 1161
 454 AAGCAGAGAGAGTGTCTCTCATGCTCAAGTGTTCACAGAGAGAGCAATCTCGAAG 513
 GY AAGCAGAGAGAGTGTCTCTCATGCTCAAGTGTTCACAGAGAGAGCAATCTCGAAG 513
 1102 GATGAGAGAGAGTGTCTCTCATGCTCAAGTGTTCACAGAGAGAGCAATCTCGAAG 1221
 GY AAGCAGAGAGAGTGTCTCTCATGCTCAAGTGTTCACAGAGAGAGCAATCTCGAAG 1221
 514 TTCTGCTGGGCTCTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 573
 GY AAGCAGAGAGAGTGTCTCTCATGCTCAAGTGTTCACAGAGAGAGCAATCTCGAAG 573
 1222 TTCTGCTGGGCTCTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1281
 GY AAGCAGAGAGAGTGTCTCTCATGCTCAAGTGTTCACAGAGAGAGCAATCTCGAAG 1281
 1282 TATCTGAGAGAGAGTGTCTCTCATGCTCAAGTGTTCACAGAGAGAGCAATCTCGAAG 1341
 GY AAGCAGAGAGAGTGTCTCTCATGCTCAAGTGTTCACAGAGAGAGCAATCTCGAAG 1341
 634 CUGGCT 693
 GY AAGCAGAGAGAGTGTCTCTCATGCTCAAGTGTTCACAGAGAGAGCAATCTCGAAG 693
 1394 CAGGCT 1401
 GY AAGCAGAGAGAGTGTCTCTCATGCTCAAGTGTTCACAGAGAGAGCAATCTCGAAG 1401
 694 ATGCTGTATGAGAGAGTGTCTCTCATGCTCAAGTGTTCACAGAGAGAGCAATCTCGAAG 753
 GY AAGCAGAGAGAGTGTCTCTCATGCTCAAGTGTTCACAGAGAGAGCAATCTCGAAG 753
 1402 ATGCTGTATGAGAGAGTGTCTCTCATGCTCAAGTGTTCACAGAGAGAGCAATCTCGAAG 1461
 GY AAGCAGAGAGAGTGTCTCTCATGCTCAAGTGTTCACAGAGAGAGCAATCTCGAAG 1461
 754 CTCTGCTGTGAGAGAGTGTCTCTCATGCTCAAGTGTTCACAGAGAGAGCAATCTCGAAG 813
 GY AAGCAGAGAGAGTGTCTCTCATGCTCAAGTGTTCACAGAGAGAGCAATCTCGAAG 813
 1462 ATGCTGTATGAGAGAGTGTCTCTCATGCTCAAGTGTTCACAGAGAGAGCAATCTCGAAG 1521
 GY AAGCAGAGAGAGTGTCTCTCATGCTCAAGTGTTCACAGAGAGAGCAATCTCGAAG 1521
 814 TGTGAGAGAGAGTGTCTCTCATGCTCAAGTGTTCACAGAGAGAGCAATCTCGAAG 873
 GY AAGCAGAGAGAGTGTCTCTCATGCTCAAGTGTTCACAGAGAGAGCAATCTCGAAG 873
 1522 TGTGAGAGAGAGTGTCTCTCATGCTCAAGTGTTCACAGAGAGAGCAATCTCGAAG 1581
 GY AAGCAGAGAGAGTGTCTCTCATGCTCAAGTGTTCACAGAGAGAGCAATCTCGAAG 1581
 1582 TGTGAGAGAGAGTGTCTCTCATGCTCAAGTGTTCACAGAGAGAGCAATCTCGAAG 1641
 GY AAGCAGAGAGAGTGTCTCTCATGCTCAAGTGTTCACAGAGAGAGCAATCTCGAAG 1641
 934 TATGAGAGAGAGTGTCTCTCATGCTCAAGTGTTCACAGAGAGAGCAATCTCGAAG 993
 GY AAGCAGAGAGAGTGTCTCTCATGCTCAAGTGTTCACAGAGAGAGCAATCTCGAAG 993
 1642 TATGAGAGAGAGTGTCTCTCATGCTCAAGTGTTCACAGAGAGAGCAATCTCGAAG 1701
 GY AAGCAGAGAGAGTGTCTCTCATGCTCAAGTGTTCACAGAGAGAGCAATCTCGAAG 1701
 994 CCAATATCTCAAGTGTCTCTCATGCTCAAGTGTTCACAGAGAGAGCAATCTCGAAG 1053
 GY AAGCAGAGAGAGTGTCTCTCATGCTCAAGTGTTCACAGAGAGAGCAATCTCGAAG 1053
 1702 AAGTCT 1761
 GY AAGCAGAGAGAGTGTCTCTCATGCTCAAGTGTTCACAGAGAGAGCAATCTCGAAG 1761
 1054 AAGTCT 1110
 GY AAGCAGAGAGAGTGTCTCTCATGCTCAAGTGTTCACAGAGAGAGCAATCTCGAAG 1110
 1762 AAGCAGAGAGAGTGTCTCTCATGCTCAAGTGTTCACAGAGAGAGCAATCTCGAAG 1821
 GY AAGCAGAGAGAGTGTCTCTCATGCTCAAGTGTTCACAGAGAGAGCAATCTCGAAG 1821
 1111 TTAATTAATGAGAGAGTGTCTCTCATGCTCAAGTGTTCACAGAGAGAGCAATCTCGAAG 1170
 GY AAGCAGAGAGAGTGTCTCTCATGCTCAAGTGTTCACAGAGAGAGCAATCTCGAAG 1170
 1822 AGGTCT 1881
 GY AAGCAGAGAGAGTGTCTCTCATGCTCAAGTGTTCACAGAGAGAGCAATCTCGAAG 1881
 1171 AGGTCT 1881
 GY AAGCAGAGAGAGTGTCTCTCATGCTCAAGTGTTCACAGAGAGAGCAATCTCGAAG 1881
 1882 TGTGAGAGAGAGTGTCTCTCATGCTCAAGTGTTCACAGAGAGAGCAATCTCGAAG 1882
 GY AAGCAGAGAGAGTGTCTCTCATGCTCAAGTGTTCACAGAGAGAGCAATCTCGAAG 1882

RESUB: 13

US-09-772-647-3

Sequence 3, Application US/09772647

Patent No. 6521815

GENERAL INFORMATION

APPLICANT: Reddig, Peter J

APPLICANT: Jansen, Aaron P

TITLE OF INVENTION: Animal Model System for Squamous Cell Carcinoma

CURRENT APPLICATION NUMBER: US/09/772,647

CURRENT FILING DATE: 2001-01-30

NUMBER OF SEQ ID NOS: 6

SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 1
 LENGTH: 2274
 TYPE: DNA
 ORGANISM: Artificial Sequence
 OTHER INFORMATION: Description of Artificial Sequence: 97 has and
 OTHER INFORMATION: mouse protein kinase C epsilon coding sequence
 NAME/KEY: CDS
 US-09-772-647-3 (2271)

Query batch: 9, 98; Score 232.6; DS: 4; Length: 2274;

Mismatches: 488; Conservative: 0; Mismatches: 394; Indels: 9; Caps: 3;

1378 TGATCTTCACCTCTTAAAGTATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 389

GY 370 AGCAGTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 449

DB 1338 ACTGAAG 1197

GY 450 AAG 509

DB 1398 ACTGAAG 1457

GY 510 CCGTCT 569

DB 1458 CCGTCT 1517

GY 570 AGCAGTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1577

DB 1518 GGAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1637

GY 630 AGCAGTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 749

DB 1638 TGGAGTCTTACAG 1697

GY 750 TGTCT 809

DB 1698 CAGCT 1757

GY 810 CT 869

DB 1758 TGTCT 1817

GY 870 GATCT 929

DB 1818 CTCAGTCT 1877

GY 930 TTTTATAG 989

DB 1878 CTTTGAAGCTGACAG 1937

GY 990 GAACCAAT 1049

DB 1938 TCTGCT 1997

GY 1050 GACAG 1100

DB 1998 GACAG 2057

GY 1101 CT 1160

DB 2058 ATCT 2117

GY 1161 CCGAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1211

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: August 11, 2003, 08:36:05 ; Search time 514.182 Seconds
(without alignments)
756.292 Million cell updates/sec

Title: US-10-000-039A-4

Perfect score: 85

Sequence: I EAFLGFSYAPPPTDST

Scoring table: BLOSIM62

Secondary antibody	Concentration
Xgapop	10.0
Ygapop	10.0
Fgapop	6.0
Delop	6.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum Dfs seq length: 2000000000

100

Post-processing: Minimum Match 0%

001 4326 UNLTXPW

[illegible]

Database :

1:	em_estbha:*
2:	em_estbha:*
3:	em_estin:*
4:	em_estin:*
5:	em_estov:*
6:	em_estpl:*
7:	em_estro:*
8:	em_hlc:*
9:	gb_esti:*
10:	gb_est2:*
11:	gb_hlc:*
12:	gb_est3:*
13:	gb_est4:*
14:	gb_est5:*
15:	em_estfun:*
16:	em_estcom:*
17:	em_gss_hum:*
18:	em_gss_inv:*
19:	em_gss_pl:*
20:	em_gss_r:*
21:	em_gss_fur:*
22:	em_gss_m:*
23:	em_gss_mv:*
24:	em_gss_p:*
25:	em_gss_ro:*
26:	em_gss_rh:*
27:	em_gss_rv:*
28:	qb_gss1:*

29: qb_qss2: *

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARY

Result No.	Score	Query Match	Length	DB	ID	Descript Ion
1	85	100.0	344	10	B0001610	BS001010 P42-BM008
2	85	100.0	246	9	A3371718	BS7864732
3	85	100.0	376	12	B1032259	BL022555 CH3-NM024
4	85	100.0	404	14	B0623158	BL062358 CH3-NM024
5	85	100.0	404	14	B0623158	R86234 Y86C010 S1
6	85	100.0	427	10	B0481167	BS048167 P40-RM006
7	85	100.0	448	9	A1188198	AL1188198 P46E105.X
8	85	100.0	450	14	B0623158	BL062358 CH3-NM024
9	85	100.0	460	14	B0623158	R86234 Y86C010 S1
10	85	100.0	465	10	B8002051	BS002051 OVA-HN009
11	85	100.0	465	12	B0740999	BL074099 CH3-NM118
12	85	100.0	487	10	B0595000	BS059000 CH3-NM118
13	85	100.0	500	14	B0623158	BL062358 CH3-NM024
14	85	100.0	530	12	B0756003	BL075601 K-EST0034
15	85	100.0	544	13	B0083706	B0083706 K-EST0146
16	85	100.0	552	14	B0623158	BL062358 CH3-NM024
17	85	100.0	552	14	B0623158	R86234 Y86C010 S1
18	85	100.0	572	12	B0756003	BL075601 K-EST0034
19	85	100.0	582	9	A0702971	AV0702971 AV702971
20	85	100.0	586	12	B1003243	BL100324 CH3-NM015
21	85	100.0	586	12	B1003243	BL100324 CH3-NM015
22	85	100.0	630	10	B0350342	BS350342 CH2-HF006
23	85	100.0	630	10	B0350342	BS350342 CH2-HF006
24	85	100.0	630	14	B0216592	BL021652 K-EST0072
25	85	100.0	641	9	A0370805	AN0370805 NC2-HF002
26	85	100.0	651	10	B0370805	BS037080 K-EST0072
27	85	100.0	659	10	B0178455	BL178455 NC2-HF002
28	85	100.0	661	10	B0178442	BL178443 NC3-HF006
29	85	100.0	671	12	B0370805	BS037080 K-EST0072
30	85	100.0	691	12	B0571090	BL571090 G0274-HF050
31	85	100.0	703	10	B04628534	B04628534 G02503677
32	85	100.0	721	12	B0370805	BS037080 K-EST0072
33	85	100.0	721	12	B0370805	BS037080 K-EST0072
34	85	100.0	765	12	B05763006	BL0573006 G02735501
35	85	100.0	767	14	C0007014	CD000714 AGENNCOURT
36	85	100.0	781	10	B0691931	BL691931 G02247446
37	85	100.0	791	10	B0691931	BL691931 G02247446
38	85	100.0	834	12	BL135545	BL135545 G02927667
39	85	100.0	847	13	B0212589	BL212589 AGENNCOURT
40	85	100.0	851	12	B1764956	BL764956 G03051130
41	85	100.0	873	10	B0675681	BL675681 G02710254
42	85	100.0	876	10	B0122846	B0122846 G02535013
43	85	100.0	885	10	B0675681	BL675681 G02710254
44	85	100.0	885	10	B0675681	BL675681 G02710254
45	85	100.0	889	12	B05769333	BL0576933 G02744440

ALIGNMENTS

RESULT 1	DEFINITION	REFERENCE
BE001610	ACCESSION	AUTHORS
LOCUS	VERSION	
	KEYWORDS	
	SOURCE	
	ORGANISM	

LOCUS	344 bp	linear	EST 05-JUN-2000
BE001610	PM2-BN0080-270400-003-a12	BN0080 Homo sapiens cDNA, mRNA sequence.	
DEFINITION			

VERSION BE001610.1 GI:8261843

KEYWORDS EST.

SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens

ORGANISM *Homo sapiens*
Eukaryota: Metazoa: Chordata

Mammalia: Eutheria: pr:

REFERENCE 1 (bases 1 to 344)

AUTHORS Dias Neto, E., Garcia Co

100

Waggoner, M.A., da Silva, N., Jr., Zapp, M.A., Bordin, S., Costa, F.F., de Castro, A.C., Carvalho, A.F., Matsukawa, A., Reis, C.S., Simpson, D.H., Montenegro, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M., de Oliveira, A., de Oliveira, P.S., Reis, L.F., de Souza, S.J. and Simpson, A.J. (2000) Sclerostin sequencing of the human transcript with ORF expressed sequence tags. *Proc. Natl. Acad. Sci. U.S.A.* 97 (7), 3491-3496 (2000).

CONTACT: SIMPSON A.J.G.
LABORATORY OF CANCER GENETICS
LUDWIG INSTITUTE FOR CANCER RESEARCH
RUA PROF. ANTONIO PRUDENTE 109, 4 ANDAR, 01509-010, SAO PAULO-SP,
BRAZIL
TEL: +55-11-2704922
FAX: +55-11-2707001

```

email: asipone@uowb.org.br
This sequence was derived from the FRAP8/ALCN Human Cancer Genomes
Project (http://www.frapp8.org) and can be found in the following URL
(http://www.uowb.org.br/sciutils/genethal2.pl?l=612-PM2-BN0080-270)
400-003-12423-2000-04-77474-1
seq primer: puc 18 forward
High quality sequence: 30
High quality sequence scop: 344
Location/Qualifiers
    1..344
    /organism="Homo sapiens"
    /mol_type="genomic"
    /db_xref="taxon:9606"
    /dev_stage="Adult"
    /clone_lib="BN0080"
    /notes="Organ: breast; normal; Vector: puc18; Size: 1;
    Size: 1; Seal: 68285; Restr: 68285; Seq: 68285;
    Description: Human breast cancer cell line Hs578T
    No. 136.716 - Ludwig Institute for Cancer Research
    profiles into the puc18 vector. Reverse transcription of
    tissue mRNA and cDNA amplification were performed under
    low stringency conditions."
    75..

```

[illegible]

TITLE Initial assessment of human gene diversity and expression patterns based upon 81 million nucleotides of cDNA sequence

JOURNAL GENOME RESEARCH 7: 6347 (Suppl.), 3-174 (1995)

MEDLINE 96025280

PMID 96025280

URN urn:lsid:imsl.org:pubmed/96025280

FORN 96025280

COMMENT Other-ESTs: TNC173211
TNC173212
TNC173213
TNC173214
TNC173215
TNC173216
TNC173217
TNC173218
TNC173219
TNC173220
TNC173221
TNC173222
TNC173223
TNC173224
TNC173225
TNC173226
TNC173227
TNC173228
TNC173229
TNC173230
TNC173231
TNC173232
TNC173233
TNC173234
TNC173235
TNC173236
TNC173237
TNC173238
TNC173239
TNC173240
TNC173241
TNC173242
TNC173243
TNC173244
TNC173245
TNC173246
TNC173247
TNC173248
TNC173249
TNC173250
TNC173251
TNC173252
TNC173253
TNC173254
TNC173255
TNC173256
TNC173257
TNC173258
TNC173259
TNC173260
TNC173261
TNC173262
TNC173263
TNC173264
TNC173265
TNC173266
TNC173267
TNC173268
TNC173269
TNC173270
TNC173271
TNC173272
TNC173273
TNC173274
TNC173275
TNC173276
TNC173277
TNC173278
TNC173279
TNC173280
TNC173281
TNC173282
TNC173283
TNC173284
TNC173285
TNC173286
TNC173287
TNC173288
TNC173289
TNC173290
TNC173291
TNC173292
TNC173293
TNC173294
TNC173295
TNC173296
TNC173297
TNC173298
TNC173299
TNC173300
TNC173301
TNC173302
TNC173303
TNC173304
TNC173305
TNC173306
TNC173307
TNC173308
TNC173309
TNC173310
TNC173311
TNC173312
TNC173313
TNC173314
TNC173315
TNC173316
TNC173317
TNC173318
TNC173319
TNC173320
TNC173321
TNC173322
TNC173323
TNC173324
TNC173325
TNC173326
TNC173327
TNC173328
TNC173329
TNC173330
TNC173331
TNC173332
TNC173333
TNC173334
TNC173335
TNC173336
TNC173337
TNC173338
TNC173339
TNC173340
TNC173341
TNC173342
TNC173343
TNC173344
TNC173345
TNC173346
TNC173347
TNC173348
TNC173349
TNC173350
TNC173351
TNC173352
TNC173353
TNC173354
TNC173355
TNC173356
TNC173357
TNC173358
TNC173359
TNC173360
TNC173361
TNC173362
TNC173363
TNC173364
TNC173365
TNC173366
TNC173367
TNC173368
TNC173369
TNC173370
TNC173371
TNC173372
TNC173373
TNC173374
TNC173375
TNC173376
TNC173377
TNC173378
TNC173379
TNC173380
TNC173381
TNC173382
TNC173383
TNC173384
TNC173385
TNC173386
TNC173387
TNC173388
TNC173389
TNC173390
TNC173391
TNC173392
TNC173393
TNC173394
TNC173395
TNC173396
TNC173397
TNC173398
TNC173399
TNC173400
TNC173401
TNC173402
TNC173403
TNC173404
TNC173405
TNC173406
TNC173407
TNC173408
TNC173409
TNC173410
TNC173411
TNC173412
TNC173413
TNC173414
TNC173415
TNC173416
TNC173417
TNC173418
TNC173419
TNC173420
TNC173421
TNC173422
TNC173423
TNC173424
TNC173425
TNC173426
TNC173427
TNC173428
TNC173429
TNC173430
TNC173431
TNC173432
TNC173433
TNC173434
TNC173435
TNC173436
TNC173437
TNC173438
TNC173439
TNC173440
TNC173441
TNC173442
TNC173443
TNC173444
TNC173445
TNC173446
TNC173447
TNC173448
TNC173449
TNC173450
TNC173451
TNC173452
TNC173453
TNC173454
TNC173455
TNC173456
TNC173457
TNC173458
TNC173459
TNC173460
TNC173461
TNC173462
TNC173463
TNC173464
TNC173465
TNC173466
TNC173467
TNC173468
TNC173469
TNC173470
TNC173471
TNC173472
TNC173473
TNC173474
TNC173475
TNC173476
TNC173477
TNC173478
TNC173479
TNC173480
TNC173481
TNC173482
TNC173483
TNC173484
TNC173485
TNC173486
TNC173487
TNC173488
TNC173489
TNC173490
TNC173491
TNC173492
TNC173493
TNC173494
TNC173495
TNC173496
TNC173497
TNC173498
TNC173499
TNC173500
TNC173501
TNC173502
TNC173503
TNC173504
TNC173505
TNC173506
TNC173507
TNC173508
TNC173509
TNC173510
TNC173511
TNC173512
TNC173513
TNC173514
TNC173515
TNC173516
TNC173517
TNC173518
TNC173519
TNC173520
TNC173521
TNC173522
TNC173523
TNC173524
TNC173525
TNC173526
TNC173527
TNC173528
TNC173529
TNC173530
TNC173531
TNC173532
TNC173533
TNC173534
TNC173535
TNC173536
TNC173537
TNC173538
TNC173539
TNC173540
TNC173541
TNC173542
TNC173543
TNC173544
TNC173545
TNC173546
TNC173547
TNC173548
TNC173549
TNC173550
TNC173551
TNC173552
TNC173553
TNC173554
TNC173555
TNC173556
TNC173557
TNC173558
TNC173559
TNC173560
TNC173561
TNC173562
TNC173563
TNC173564
TNC173565
TNC173566
TNC173567
TNC173568
TNC173569
TNC173570
TNC173571
TNC173572
TNC173573
TNC173574
TNC173575
TNC173576
TNC173577
TNC173578
TNC173579
TNC173580
TNC173581
TNC173582
TNC173583
TNC173584
TNC173585
TNC173586
TNC173587
TNC173588
TNC173589
TNC173590
TNC173591
TNC173592
TNC173593
TNC173594
TNC173595
TNC173596
TNC173597
TNC173598
TNC173599
TNC173600
TNC173601
TNC173602

```
Seq primer: M1 Reverse,
Occurrence: 1
SOURCE: 1, 316
/organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="NCBI (inhost):181558"
/gen_stage="adult"
/note="Intestine 1"
/note="organ: small intestine"
Site_1: ECOR1; Site_2: XhoI
Vector: pBluescript SK-
others: 2 others
```

FEATURES
SOURCE

BASE COUNT

Note: *Organ: Liver; Vector: pCNS-D2; Site₁: KpnI; Site₂: NotI. The poly (A+) RNA was dephosphorylated with alkaline phosphatase (Boehringer-Mannheim) and ligated with bacterial alkaline phosphatase (BAP) and then decapped with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA linker including BamHI and XbaI sites by treatment of RNA ligase I (Roche Diagnostics GmbH) at 37°C for 6 h. The BamHI-XbaI dimerized cDNA was ligated into BamHI-XbaI digested vector. The dimerized vector was adjusted to have about 60nL. The cDNA vector was

labeled single stranded RNA by *in vitro* transcription. The synthesized RNA probes were hybridized with

antisense single stranded cDNAs prepared from original library and incubated with avidin-gel. After removing

DNA-RNA hybrids by centrifuge, the subcloned cDNA libraries were constructed by transformation of the

remaining DNA into competent cells *E. coli* TOP10F with electroporation method.¹⁸

1229 389 113 L

0 00700 1 00841 450

0.00599	Length:	430
85.00	Matches:	16
700.00	Cost:	0

Model	Conservative	Mismatches	Model	Conservative	Mismatches
1	100.00%	100.00%	5	100.00%	100.00%
2	100.00%	100.00%	6	100.00%	100.00%
3	100.00%	100.00%	7	100.00%	100.00%
4	100.00%	100.00%	8	100.00%	100.00%

100.00e	0
14	0
Index:	0
Gaps:	0

6) x CB11428 (1-458)

pHeLeuGlyPheSerTyrAlaProProThrAspSerPheLeu 16

TTCTAGGCTTTTCCATATCGGCCCTCCACGGACTCTTTCCTC 404

460 bp mRNA Linear EST 02-MAY-1995

SP: A48094 A48094 SERUM AND

CT 700212

GI:792113

ens (human)
ens

Eutheria; Primates; Catarrhini; Hominiidae; Homo.
Eutheria; Primates; Catarrhini; Hominiidae; Homo.
Eutheria; Primates; Catarrhini; Hominiidae; Homo.

... I to 460)
... Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman

Man, N., Kucaba, T., Le, N., Lennon, G., Marra, M., Parsons, J., Rohlfs, T., Soares, M., Tan, F., Trevaskis, E., Waterston

lamson, A.; Wohldmann, P. and Wilson, R.
J-Merck EST Project

pared

1

DNA Sequencing by Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Researchers may obtain clones from Research
 Center (see below).
 Seq primer: M3 reverse.

FEATURES

source

Location/Qualifiers

1..505
 /mol_type="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="UT-E-C11" and "UT-E-C12"
 /dev_stage="adult"
 /lab_host="outlog (Life Technologies) (T1 phage resistant)"

/clone_lib="r18008"
 /vector="p773-Pac (Pharmacia) with a
 modified polylinker; Site.1: EcoR I; Site.2: Not I;
 UI-E-C11 is a normalized cDNA library containing the
 following tissues): REE and Choroid. The library was
 constructed by Dr. M. B. Soares and Dr. M. B. Soares
 Genome Research, 6/791-806, 1996. First strand cDNA
 synthesis was primed with an oligo-dT primer containing a
 Not I site. Double stranded cDNA was ligated to an EcoR I
 site. The cDNA was then digested with Not I and EcoR I
 into p773-Pac vector. The oligonucleotide used to prime
 the synthesis of first-strand cDNA contains a library tag
 sequence that is covalently attached to the Not I site and
 the EcoR I site. This library tag sequence is used for
 This library was created for the program, Gene Discovery
 in the Visual System, supported by National Eye Institute

BASE COUNT 124 a 143 c 117 g 121 t
 ORIGIN

Alignment Scores:
 Pred. No.: 0.0044 Length: 505
 Score: 85.00 Matches: 16
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 12 Gaps: 0

US-10-000-039a-4 (1-15) x BM707970 (1-505)

Qy 1 GUAUAPhELenGlyPheSerTyAlaProProthraspserPheLeu 16

Db 455 GAGCGTTCTTCTAGCGTTTCTGATCGCTCCAGCACTCTTCTC 502

RESULT 14

BM756001

DEFINITION K-HST0031463 S18N5 Homo sapiens cDNA clone S18N5-38-E04 5', mRNA

sequence.

ACCESSION BM756001

VERSION 1

KEYWORDS EST

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 530)

AUTHORS Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, H.Y., Kim, M.R.,

Kim, Y.S., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and

Kim, Y.S.

TITLE 21st Frontier Korean EST Project 2001

JOURNAL Unpublished

COMMENT Genomes Research Center

Korea Research Institute of Bioscience & Biotechnology

52 Eonju-dong Yusong-gu, Daegu 305-333, South Korea

TEL: +82-42-860-4470

FAX: +82-42-860-4409

EMAIL: yongsung@mail.krrib.re.kr

Plate: 38 row: E column: 04

FEATURES

source

High quality sequence stop: 530.
 Location/Qualifiers

1..544
 /mol_type="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="UT-E-C11" and "UT-E-C12"
 /dev_stage="adult"
 /lab_host="outlog (Life Technologies) (T1 phage resistant)"

/clone_lib="r18008"

/vector="p773-Pac (Pharmacia) with a

modified polylinker; Site.1: EcoR I; Site.2: Not I;

UI-E-C11 is a normalized cDNA library containing the

following tissues): REE and Choroid. The library was

constructed by Dr. M. B. Soares and Dr. M. B. Soares

Genome Research, 6/791-806, 1996. First strand cDNA

synthesis was primed with an oligo-dT primer containing a

Not I site. Double stranded cDNA was ligated to an EcoR I

site. The cDNA was then digested with Not I and EcoR I

into p773-Pac vector. The oligonucleotide used to prime

the synthesis of first-strand cDNA contains a library tag

sequence that is covalently attached to the Not I site and

the EcoR I site. This library tag sequence is used for

This library was created for the program, Gene Discovery

in the Visual System, supported by National Eye Institute

Full-length enriched cDNA library."

BASE COUNT 125 a 140 c 120 g 145 t
 ORIGIN

Alignment Scores:

Pred. No.: 0.00452 Length: 530

Score: 85.00 Matches: 16

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 12 Gaps: 0

US-10-000-039a-4 (1-16) x BM756001 (1-530)

Qy 1 GUAUAPhELenGlyPheSerTyAlaProProthraspserPheLeu 16

Db 290 GAGCGTTCTTCTAGCGTTTCTGATCGCTCCAGCACTCTTCTC 337

RESULT 15

BM083706

DEFINITION LOCUS

544 bp mRNA linear EST 04-APR-2002

sequence.

ACCESSION BM083706

VERSION 1

KEYWORDS EST

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Bukaryata; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

AUTHORS Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, H.Y., Kim, M.R.,

Kim, J.S., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and

Kim, Y.S.

TITLE 21st Frontier Korean EST Project 2001

JOURNAL Unpublished

COMMENT Genomes Research Center

Korea Research Institute of Bioscience & Biotechnology

52 Eonju-dong Yusong-gu, Daegu 305-333, South Korea

TEL: +82-42-860-4470

FAX: +82-42-860-4409

EMAIL: yongsung@mail.krrib.re.kr

Plate: 63 row: H column: 01

High quality sequence stop: 544.

Location/Qualifiers

1. 544

/organism="Homo sapiens"

/mol_type="cDNA" /taxid="9606"

/clone="S14K402-63-401"

/cell_line="K402"

/lab_host="Top10P"

/clone_from="Site 2"

/vector="pTZ1918; Vector: pTZ1918; Site: 1. EcoRI; Site: 2. NotI; The poly (A) RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tobacco acid phosphatase (TAP). The decapped intact mRNA was ligated with the NotI linker, including EcoRI ends, and transformed into E. coli Top10P cells. The cDNA was synthesized from oligo dT-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was digested with NotI and EcoRI. The cDNA fragment digested with EcoRI which site is also included vector RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10P by electroporation method. The cDNA library was screened by hybridization with full-length enriched cDNA library. This method are

BASE COUNT		ORIGIN		ALIGNMENT SCORES		LENGTH	
116 a	140 c	129 g	159 t	0.00475	544	Matches:	16
				85.00		Conservative:	0
				Percent Similarity:	100.00%	Mismatches:	0
				Best Local Similarity:	100.00%	Indels:	0
				Query Match:	100.00%	Gaps:	0
				DB:	13		

US-10-000-039A-4 (1-16) x EQ083706 (1-544)

Search completed: August 11, 2003, 11:27:48
Job time : 515.182 secs